

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - multiple search, using frame-p2n model

Run on: January 31, 2003, 07:12:56 ; Search time 6558 Seconds
(without alignments)
4544.262 Million cell updates/sec

Title: US-09-697-089-2

Perfect score: 5459

Sequence: 1 MNFKDNRALIQRMGMVTI.....MQPDDDLSTVIGAFKLYTA 1024

Scoring table:

PAM120	4.0	Xgapext 12.0
Xgapop	4.0	Xgapext 12.0
Ygapop	6.0	Ygapext 7.0
Delop	6.0	Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL-frame-p2n.model -DEV-xlh
-O/-cgn2.1/USPPO-spool/US09697089/runat_29012003_092504_19158/app-query.fasta.1.1223
-DB-GenEmbl -QFMT-fastap -SUFFIX-p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=1 -MATRIX-pam120 -TRANS-human40.cdi -LIST=45
-OCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE-LOCAL
-OUTFMT=ptc -NORM-ext -HEAPSIZE=500 -MITEM=0 -MAXLEN=200000000
-USER=US09697089/ecgn_1.1.4449/runat_29012003_092504_19158 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAP -LARGEOQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV-TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=4 -XGAPEXT=12 -FGAPOP=6 -FGAPEXT=7
-XGAPOP=4 -XGAPEXT=12 -DELOP=6 -DELEXT=7

Database :

1:	GenEmbl:*
2:	gb_ba:*
3:	gb_hcg:*
4:	gb_in:*
5:	gb_om:*
6:	gb_ov:*
7:	gb_ph:*
8:	gb_pl:*
9:	gb_pr:*
10:	gb_ro:*
11:	gb_sts:*
12:	gb_sy:*
13:	gb_un:*
14:	gb_vl:*
15:	em_ba:*
16:	em_fun:*
17:	em_hum:*
18:	em_in:*
19:	em_mu:*
20:	em_om:*
21:	em_or:*
22:	em_ov:*
23:	em_pat:*
24:	em_ph:*
25:	em_pl:*
26:	em_ro:*
27:	em_sts:*
28:	em_un:*

29: em_vl:*

30: em_hcg_hum:*

31: em_hcg_inv:*

32: em_hcg_other:*

33: em_hcg_mus:*

34: em_hcg_pln:*

35: em_hcg_rod:*

36: em_hcg_mam:*

37: em_hcg_vrt:*

38: em_sy:*

39: em_hlgo_hum:*

40: em_hlgo_mus:*

41: em_hlgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5459	100.0	3133	9	AY032589 Homo sapi
2	5453	99.9	3219	9	AY035391 Homo sapi
3	5453	99.9	3360	9	BC031555 Homo sapi
4	5448	99.8	3581	9	AE376061 Homo sapi
5	5447	99.8	3355	9	AK095467 Homo sapi
6	5438	99.6	3396	6	AX318091 Homo sapi
7	5438	99.6	3396	6	AY027787 Homo sapi
8	3543	64.9	160583	2	AC010968 Homo sapi
9	3539	64.8	138909	2	CNS01DS3
10	2740	50.2	183469	2	AC101793
11	2300	42.1	1355	9	IR2005417
12	1598	29.3	891	6	AX318174
13	1424	26.1	1395	9	AX318093
14	1424	26.1	1395	9	AY027788
15	1084	19.9	618	6	AX318176
16	853	15.6	768	6	AX318097
17	853	15.6	768	6	AX318097
18	516	9.5	162982	2	CNS01DS8
19	516	9.5	162982	2	AC011232
20	493	9.0	578	6	AX318095
21	493	9.0	578	6	AY027790
22	485	8.9	261	6	AX318172
23	363	6.6	107885	2	AC107111
24	358	6.6	83866	2	AC131423
25	307	5.6	553	11	G55568
26	300	5.5	117791	10	AF242431S1
27	297	5.4	41613	10	AF242433S1
28	296	5.4	206808	2	AC093971
29	292	5.3	6829	10	AF135494
30	289	5.3	5269	10	AF135492
31	289	5.3	179252	10	AF131205
32	287	5.3	165	6	AX318178
33	281	5.1	5362	10	AF135491
34	281	5.1	5497	10	AF007769
35	281	5.1	196486	2	AC116741
36	279	5.1	4013	9	AB048534
37	279	5.1	5366	6	E23944
38	279	5.1	5366	6	E24990
39	279	5.1	5502	6	A64509
40	279	5.1	5984	6	E23943
41	279	5.1	5984	6	E24989
42	279	5.1	5984	6	E38321
43	279	5.1	6124	6	A64529
44	279	5.1	6124	6	AX335820
45	279	5.1	6124	9	HS019251

RESULT 1

ALIGNMENTS

AY032589 Homo sapi
AY035391 Homo sapi
BC031555 Homo sapi
AE376061 Homo sapi
AK095467 Homo sapi
AX318091 Homo sapi
AY027787 Homo sapi
AC010968 Homo sapi
AL121653 BAC seque
AC101793 Mus muscu
AL189934 Homo sapi
AX318174 Sequence
AX318093 Sequence
AY027788 Homo sapi
AX318176 Sequence
AX318097 Sequence
AY027789 Homo sapi
AL121658 BAC seque
AC011232 Homo sapi
AX318095 Sequence
AY027790 Homo sapi
AX318172 Sequence
AC107111 Rattus no
AC131423 Rattus no
G55568 SHGC-100923
AF242431 Mus muscu
AF242433 Mus muscu
AC093971 Rattus no
AF135494 Mus muscu
AF135492 Mus muscu
AF131205 Mus muscu
AX318178 Sequence
AF135491 Mus muscu
AF007769 Mus muscu
AC116741 Mus muscu
AB048534 Homo sapi
E23944 Apoptosis-1
E24990 Apoptosis-1
A64509 Sequence 1
E23943 Excessive 1
E24989 Apoptosis-1
E38321 Monoclonal
A64529 Sequence 21
AX335820 Sequence
U19251 Homo sapien

LOCUS	AY032589	3133 bp	mRNA	linear	PRI 25-MAY-2001
DEFINITION	Homo sapiens caspase recruitment domain protein 12 mRNA, complete cds.				
ACCESSION	AY032589				
VERSION	AY032589.1 GI:13899172				
KEYWORDS					
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens.				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 3133) Geddes,B.J., Wang,L., Huang,W.-J., Lavellee,M., Manji,G.A., Brown,M., Jutman,M., Morganstern,J., Merriam,S., Glucksmann,A., Distefano,P.S. and Bertin,J.				
TITLE	Human CARD12 is a novel CED4/Apaf-1 family member that induces apoptosis				
JOURNAL	Biochem. Biophys. Res. Commun. 284 (1), 77-82 (2001)				
MEDLINE	21268963				
PUBMED	11374873				
AUTHORS	2 (bases 1 to 3133) Bertin,J.				
TITLE	Direct Submission				
JOURNAL	Submitted (15-APR-2001) Neurobiology, Millenium Pharmaceuticals Inc., 640 Memorial Drive, Cambridge, MA 02139, USA				
FEATURES	Location/Qualifiers				
SOURCE	1..3133				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	36..3110				
	/note="CARD12: CED4/Apaf-1 family member"				
	/codon_start=1				
	/product="caspase recruitment domain protein 12"				
	/protein_id="AAK38730.1"				
	/db_xref="GI:13899173"				
	/translation="MNTIKDNRSLIORMGTYIKQTTDLFTVNVNIREEVNICEE KVEDDAAGIITHMLTKRGESCNLFKLSLEWNPPLFDOLGSLFQTSFGDLDLDA QDLDIYHPSPLEPIGDEDIDITIFNFKSTFPPVLRKROHNRVEOLNGLDLD LOSCLIEGESGKSTPLGRIDIALMGSGKALKTRKPYEFLRSNAOGLPFTLDD OLDLPGTRIRKQTFPMAMLRKRVLPFLDLOGNEPQNCDEPALLIKENRFNMVYI VTPTTECLRIHROGALFAEVDMPEDSAQALREVALIKELABELAIQIQSRNLN MKTLEPVITCAIOMGESERHSHQTTLFTFYDLLIQNNKHKGVAADFISLDH CGDIALEGVESHKRDFELQDVSVNEDVLTITGLCKYTQOREPKPKFFKSPQET AGRLSLTISHPEEVTKNGVYLOKWSISDITGLSTYSLRFGSSVEATRAVMKH LAAVYOHGCLGLSIRAKPLRQESLOSVKNTTDELIKAVINISFVPCGHIHQEST SKSLSQEPEAFQFGKSLYINSGNIDPFLDPFPHLPNCAADIPFLIDPYGMASSW EKAADPDGIGIMERAPETIYIPSRVSLFPNNKQEPFLVETLRPSKLKODITYLCK IFSSATSLRLQIKRACAGVAGSLSVLSTCKNTYSLMVEASPLTEDRHNTSVNLT LSIHDLQRLRPGILDSLGMLNKLTKINDINWNEBDAIKLAEGLNKKMCLFYT THSLDIGEGMDYIVKSLSEPCDEIEIQLVSCSANAIVKILANLNLYLSTLDS ENYLEKDEGNALHELIDBMNVLEQTLALMPGCGVQSGSLKLHELVEYDQVKGGL KNWELTDTEIRITLIGAFGKNPLKNFQOLNLAGNVSSDGLAEPGVEENIKQIVFPDP STKEFLDPALVRLKLSQVLSKTLTQLQEARLVGWFPDDDLSVITGAKRLVYA"				
	36..299				
	/note="CARD: Region: caspase recruitment domain"				
	522..1406				
	/note="NBS: Region: nucleotide-binding site"				
	2001..3107				
	/note="LRR: Region: leucine-rich repeats"				
BASE COUNT	903 a	691 c	729 g	810 t	
ORIGIN					
Alignment Scores:					
Pred. No.:	0	Length:	3133		
Score:	5459.00	Matches:	1024		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	100.00%	Indels:	0		
DB:	9	Gaps:	0		
US-09-697-089-2 (1-1024) x AY032589 (1-3133)					
0y	1 Metasphelelyaspasnserrarglaaleuileglnargmetglmethrvalile 20				

Db	36	ATGAATTTCATTAAGGACCAATAGCCGACCCCTTATTCAAAGAAATGGGAATGACTCTTATA	95
QY	21	LysGlnIleThrAspAspLeuPheValaTrpAsnValLeuAsnArgIuGluValaAsnIle	40
Db	96	AAGCAATACACAGATGACCTATTGTATGTGAATGTTCTGAATCCGCAAGCAATAAACATC	155
QY	41	IleCysCysGluLysValaGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys	60
Db	156	ATTTCCTCCGAGAGGTCGAGACAGAGATGCTGTAGAGGAGATTCACATGATGATTTTGAA	215
QY	61	LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTrpProIeu	80
Db	216	AAGGGTTACAGATCCTGTATACCTCTTTTAAATCCCTTAAGAGAGCAATATCTCTTA	275
QY	81	PheGlnAspLeuAsnGlnLysIleSerLeuPheHisGlnThrSerGluLysAspLeuAsp	100
Db	276	TTTCAGGACTTGAAATGGACCAAGCTCTTTTCATCAACACATCAGAAAGACCTTGACAT	335
QY	101	LeuAlaGlnAspLeuLysAspLeuTrpHisThrProSerPheLeuAsnPhetTrpProIeu	120
Db	336	TTGGCTCAGATATTAAAGGACTTGATACCATACCCCATCTTTCTGAATCTTATCCCTT	395
QY	121	GlyGluAspIleAspIleIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTrp	140
Db	396	GGTGAAGATATTGACATTATTTTAACTTGAAAGACCTTCACAGAACCTCTCCTGTGG	455
QY	141	ArgLysAspGlnHisHisAspValaGlnGlnLeuThrLeuAsnGlnLeuLeuGlnAla	160
Db	456	AGGAAGGACCAACACCATCACCGGTGAGACACTACCTGTAAATGCTCTTGACAGCT	515
QY	161	LeuGlnSerProCysIleIleGluGluLysSerGlyLysGlyLysSerThrLeuLeuGln	180
Db	516	CTTGAGACCCCTGCATCATTTGAAGGGGATCTGGCAAGCAAGTCCACTGCTGTGAG	575
QY	181	ArgIleAlaMetIleuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal	200
Db	576	CGCATTTGCCATGCTCTGGGGCTCCGGAAAGTCMAAGGCTGTGCACCAAGTTCAAAATTCCTC	635
QY	201	PhePheLeuArgLeuSerArgAlaGlnGlnGlyLeuPheGlnThrLeuCysAspIleu	220
Db	636	TTCTTCCTCCGTCTCACACAGGGCCCAAGGGTGGACCTTTTGAAACCTCTGTATCACTC	695
QY	221	LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg	240
Db	696	CTGGATATACCTGGCACAAATCAGAAACGACACTTATATGGCCATGCTGTGAAGCTGGGG	755
QY	241	GlnArgValLeuPheLeuLeuAspGlyTrpAsnGluPheLysProGlnAsnCysProGlu	260
Db	756	CAGAGGGTCTTTTCTCTTTGATGGCTCAATGAATTCMAACCCCAAGAACCTGCCAAGAA	815
QY	261	IleGluValLeuIleLysGluAsnHisAspPheLysAsnMetValIleValThrThrThr	280
Db	816	ATCGAAGCCGTGAATTAAGAAACCAACCGCTTAAACAACATGGCTACTCTCAACCACTACC	875
QY	281	ThrGluCysLeuArgHisIleArgGlnPheGlyValaLeuThrAlaGluValaGlyAspMet	300
Db	876	ACTGATGCTCCGAGAGCACATACGGCAGTTTGGTCCCTGACACGTGAGAGTGGGGGATATG	935
QY	301	ThrGluAspSerAlaGlnAlaLeuIleArgGluValaLeuIleLysGluLeuAlaGluGly	320
Db	936	ACAGAAAGACAGCCGCCAGGCTCTCATCCGAGAAAGTCTGATCAAGAGCTTCTCAAGGC	995
QY	321	LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProIeuPhe	340
Db	996	TTGTGTGCTCCAAATTCAGAAATCCAGAGTCTTGAGGAATCTCATGAAGCCCTCTCTT	1055
QY	341	ValValIleThrCysAlaIleGlnMetGlyLysSerGluPheHisSerHisThrGlnThr	360
Db	1056	GTGGCATCACTTGTGCATATCCAGATGGGGAAGAGACTTCCACTCTCACACAAACA	1115
QY	361	ThrLeuPheHisThrPheTrpAspLeuLeuIleGlnLysAsnLysHisLysHisLysGly	380

Db 1116 ACGCTGTCACACCTTCTATGATCTGTTGATACAGAAAAACAAACACAACTAAAGT 1175
 QY 381 ValAlaIaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly 400
 Db 1176 GTGGGCTGACAGAGCTTCACTTCGAGCCCTGGACCACTGTGGACCTGCTCTGGAGGGT 1235
 QY 401 ValIlePheSerHisLysPheAspPheGluLeuGluGlnAspValSerSerValAsnGluAspVal 420
 Db 1236 GTGTCTCTCCCAACAGTTTGATTCGAACTGCAGAGATGTCTCAGCGCTAAATGAGAGATGTC 1295
 QY 421 LeuLeuThrThrGlyLeuLeuGluCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440
 Db 1296 CTGGCAACACTGGGCTCTCTGTAAATATACAGCTCAAAAGTTCAACCAAGATATAA 1355
 QY 441 PhePheHisLysSerPheGlnGluIuThrThrAlaGlyArgGlnLeuSerSerLeuThr 460
 Db 1356 TTCTTTCACAAAGTCACTTCAGAGAGTACACAGAGAGCAACAGATCAGAGATTTTGAAGC 1415
 QY 461 SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480
 Db 1416 TCTCATGAGCCAGAGAGAGTACCAAGGGAATGGTTACTTCAGAAATAGTTCCATT 1475
 QY 481 SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500
 Db 1476 TCGGACATTACATCCACTTATAGACAGCTGCTCGGTAACACCTGTGGTCACTGTGGAA 1535
 QY 501 AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly 520
 Db 1536 GCCACACAGGCTGTATATGAACACCTGCAGACAGTATACACAGGCTGCTCTCTCGGA 1595
 QY 521 LeuSerIleAlaLysArgProLeuThrPargGlnGlnLeuSerLeuGlnSerValLysAsnThr 540
 Db 1596 CTTTCACATCCGCAAGAGAGCCCTCTCGAGACAGCAATCTTTCGAAAGTGGAACAAACACC 1655
 QY 541 ThrGlnGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGlyCysGlyIleHis 560
 Db 1656 ACTAGACAGAAATTCGAAAGCCATTAACATCACTTCTTGTAGAGTGTGGCATCCAT 1715
 QY 561 LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGlnPheGlnAlaPhePheGln 580
 Db 1716 TTATATATCAAGAGATACATCAATCAAGCCCTGAGCCCAAGAAATTTGAAGTTCTTTCAA 1775
 QY 581 GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrIlePheAspPhePheGlu 600
 Db 1776 GGTAAAGCTTATATATCACTCAGGAGAACATCCCGATTAATCTTATTTGACTCTTTGAA 1835
 QY 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyValAla 620
 Db 1836 CATTTGCCAATGTGCAAGTCTCTGAGACTTCAATTAACGTGAACTTTATGGGGAGCT 1895
 QY 621 MetAlaSerTpcLysAlaAlaGluAspThrGlyGlyIleHisMetGlnGluAlaPro 640
 Db 1896 ATGGCTTCATAGGAGAAAGCTCGAGAAACACAGGTGGAATCCACATGGAAGAGGCCCA 1955
 QY 641 GluThrTyrIleProSerArgAlaValSerLeuPhePheAsnTyrLysGlnGluPheArg 660
 Db 1956 GAAACCTACACTCCACAGAGGCTGTATCTTTGTTCTTAACTGGAGAGCAAGAAATTCAGG 2015
 QY 661 ThrLeuGlnValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu 680
 Db 2016 ACTCTGAGAGTACACTCGGGGATTTCCAGCAAGTTGAATTAACAGATATACATATCTG 2075
 QY 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700
 Db 2076 GGGAAAAATATTCAGCTCTCCACAAAGCCCTCAGGCTGCAATTAAGAGATGTCTGTGG 2135
 QY 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu 720
 Db 2136 GCTGGAAGCTCAGTTTGTCTTCACACCTTATAGAACATTTATTTCTCATGTGTGAA 2195
 QY 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740
 Db 2196 GCCAGTCCCTCAGCATAGAGATGAGAGGCCAATCAGATCTGTATACAAACCTGAAACCC 2255

QY 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyLysLeuThrAspSerLeuGly 760
 Db 2256 TTGAGTATTCATGACTACAGAAATCAACAGGCTGGCGGGTGTCTGACTGACACTTGGGT 2315
 QY 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetLsnGlnGluAspAla 780
 Db 2316 AACTTGAAGAACCTTACAAAGCTCATATGATTAACATTAAGATGAAGAAAGATGCT 2375
 QY 781 IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800
 Db 2376 ATAAACTACTGAGAGCCCTGAAAACCTCAAGAGATGTGTATTTTCAATTTGACCCAC 2435
 QY 801 LeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCys 820
 Db 2436 TTGTCTGACATTTGGAGAGGGAATGATATCATATGTCAGATCTGTGCAGTGAACCTGT 2495
 QY 821 AspLeuGlnGluIleGlnLeuValSerCysLysLeuSerAlaAsnAlaValLysIleLeu 840
 Db 2496 GACCTTGAAGAAATTCAAATTAGTCTCTCTGCTGTGTGCAAAATGCAAGTGAATCCTA 2555
 QY 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860
 Db 2556 GCTCAGAACTTTCACAAATTTGGTCAAACTGAGAGATCTTGATTTATCAGAAATTAACCTG 2615
 QY 861 GluLysAspCysAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGln 880
 Db 2616 GAAAAAGATGGAATTAACCTCTTCATGAACTGATGACAGATGATGATGATGATGATGATG 2675
 QY 881 LeuThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900
 Db 2676 CTACAGGCACTGATGTGCTGCTGGGGCTGTGACGTGCAAGGCAAGGCTGAGCGCTGTGG 2735
 QY 901 LysHisLeuGlnGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrPargLeuThr 920
 Db 2736 AAACATTTGGAGAGAGTCCCAACACTCGCAAGCTTGGGTGAAATCGAGAGATCCACA 2795
 QY 921 AspThrGluIleArgIleLeuGlnLysAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940
 Db 2796 GATACAGAGATTAAGATTTAGTGCATTTTGGAAAAACCCCTGTAACATTTCCG 2855
 QY 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPheAlaPheMetGlyVal 960
 Db 2856 CAGTTGAATTTGGCGGGAATCGTGTGAGCATGTATGATGATGATGATGATGATGATGATG 2915
 QY 961 PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980
 Db 2916 TTTGAGAAATCTTAACCAATTAATGATTTTGTGACTTAAAGATTTCTACCTGAT 2975
 QY 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla 1000
 Db 2976 CCAGATTAATGACAGAAACCTTAAGCCAAAGTGTATCCAAATCTTTCTGCAAGAAAGCT 3035
 QY 1001 ArgLeuValGlyTyrGlnPheAspAspAspAspLeuSerValIleThrGlyAlaPheLys 1020
 Db 3036 AGGCTTGTGGGTGGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3095
 QY 1021 LeuValThrAla 1024
 Db 3096 CTAGTAACCTGCT 3107
 RESULT 2
 LOCUS AY035391 3219 bp mRNA linear PRI 24-JUL-2001
 DEFINITION Homo sapiens ICE-protease activating factor mRNA, complete cds.
 ACCESSION AY035391
 VERSION AY035391.1 GI:14334214
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 3219)

AUTHORS Poeyt,J.L., Srinivasula,S.M., Tnani,M., Razmara,M.,
 TITLE Fernandes-Alnemri,T. and Alnemri,E.S. Identification of Ipa1, a human caspase-1-activating protein related to Apaf-1
 JOURNAL J. Biol. Chem. 276 (30), 28309-28313 (2001)
 MEDLINE 21359454
 PUBMED 11390368
 REFERENCE 2 (bases 1 to 3219)
 AUTHORS Poeyt,J.-L., Srinivasula,S.M., Fernandes-Alnemri,T. and Alnemri,E.S.
 TITLE Direct Submission
 JOURNAL Submitted (16-MAY-2001) Microbiology and Immunology, Thomas Jefferson University, 233 S. 10th Street, Philadelphia, PA 19107, USA

FEATURES
 source location/Qualifiers
 1..3219
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="2"
 /map="p21-22"
 145..3219
 /note="IPAF: CED4/Apaf-1 family member; caspase-associated recruitment domain containing protein"
 /product="ICE-Protease activating factor"
 /protein_id="AAK59843.1"
 /db_xref="GI:14334215"
 /translation="WNFKDNRALIQKMTVTKQTDDLFVWVNLREVNITTCCE
 RVEQDARGIIMILKSGESCNLFKSLKEWNYLFQDLNGQSLEFHTSGLDDLA
 ODLDKLYPSFLNPLYGLEDIDIFENKSTPEYLVKRDQHNHRVQLTNGLLQA
 LOSPCIIEESGKSKSTLLQRIAMLMGSGKALKAFKFEVFLRLSRAGGGLFETLQ
 OLDDIPGTRKQRTFMALIKLQROVLFILFDGYNKRPQCPRIEALIKENHFKNMVI
 VYTTTECPHTRPGATRTAEVGMTEDSAQALIRVILIKELAGLILQISRCRLNL
 MKTPILEVYTTCAIQMGSEFPHSHQTOTTFHTHYDILQKMKHKGVASDPTBSLD
 CGDLAEVFSKEDPELDVSSVNEVDLITGLCKTKTAQFKRYKFRKSEPEYT
 AGRRLSLTISHEPEVTKNGNYLQKMSISDITYSLSLNTYTGSSVEATRAVMKH
 LAAVVOHGLGLSLAKRPLROESLOSAYKNTBOEILKAINISFVEGHLVQEST
 SKSALSGEFAEFQGSILYINGNIPDYLFDFEHLPCNSALDFIKLDFYEGAMASW
 EKAAEDTGFIHMEAPETYIPRAVSLFENKQEPTELVTLRDSKLNKODIRILGK
 IFSASTSLPIQIKCAQVAGSISLVISTCKNYSIMAVEASPLTIDEBRITSTVNLKT
 LSHLDLONRPLRGCLDLSIGNIKNLTKLIMDKIKNNEBPAITLASEGILKMKCLPHL
 THLSIDGEMDYTVKSLSEPCDLBIQVSCCLSNAYKIIAONLHNLYKSIIDLS
 ENYLDEGNEALHELIDRMNVLEQLTALMLPWGCDVQSSLSLHLHLEVPQLVGLG
 KNWRLDTEIRILIGAFGRKNPLKFNQOLMLAGNRVSSDQMLAFMGVFNMLQDLVDFD
 STRKEFLPDALVAKLSQVLSKLTFLQEARLVGMQEDDDLVTITGAFKLVTAA"

BASE COUNT 934 a 696 c 748 g 841 t

ORIGIN

Alignment Scores:
 Pred. No.: 0 Length: 3219
 Score: 5453.00 Matches: 1023
 Percent Similarity: 99.90% Conservative: 0
 Best Local Similarity: 99.90% Mismatches: 1
 Query Match: 99.89% Indels: 0
 DB: 9 Gaps: 0

US-09-697-089-2 (1-1024) x AY035391 (1-3219)

QY 1 MetasnpheilelsaspasnerArgAlaleuileglnarwmetglymethrvalille 20
 Db 145 ATGAATTTCATTAAGGACAAATGCCGACCTTATTCAAGAAATGGGAATGACGTGTA 204
 QY 21 LysGlnIlethrAspAspLeuPheValITrpAsnValLeuAsnArgIugluValAsnIle 40
 Db 205 AAGCAAAATCACAGATGACCTATTGTATGAAATGTCTCGAATCCGAAAGATTAACATC 264
 QY 41 IlecyScyGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
 Db 265 ATTGCTCGCGAAGGTGGAGACAGATGCTCTAGAGGAGCATTCACATGATTTTGAAA 324
 QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluITrpAsnITyrProleu 80
 Db 325 AAGGTTTCAGAGTCTCTGTAACCTCTTTCTTAATCCCTTAAGAGAGTGAACATATCCTTA 384

QY 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnIthrSerGluGlnAspLeuAspAsp 100
 Db 385 TTTCAGAGACTTGATGACCAAAAGCTTTTTCATCAGACATCAGAGAGACTGGACAGAT 444
 QY 101 LeuAlaGlnAspLeuLysAspLeuITyrHisIThrProSerPheLeuAsnPheITyrProleu 120
 Db 445 TTGGCTCGAGATTTAAAGAGACTTGATACCATACCCCATCTTTTGAACTTTTATCCCTT 504
 QY 121 GlyGlnAspLeuAspIleIlePheAsnLeuLysSerIThrPheITrpGluProValIleITrp 140
 Db 505 GGTGAAGATATTGACATTAATTTTAATCTGAAAAGCACCTTCACAGAACCTGTCCTGG 564
 QY 141 ArgLysAspGlnHisHisHisArgValGluGlnLeuIThrLeuAsnGlyLeuGlnAla 160
 Db 565 AGAAGACCAACACACATCACCCTGGAGACAGCTGACCCGATGGCCTCTGCAAGCT 624
 QY 161 LeuGlnSerProCysIleIleGluGlyLysSerGlyLysGlyLysSerIThrLeuGln 180
 Db 625 CTTCAGAGCCCTGATCATGTAAGGGGAATCTGGCAAAAGGCAAGTCCACTCTCTGACAG 684
 QY 181 ArgIleAlaMetLeuITrpGlySerGlyLysCysLysAlaLeuIThrLysPheLysPheVal 200
 Db 685 CGAATTGGCATGCTCTGGGCTCCGAAAGTGCAAGGCTGACCACTTAATTTGCTC 744
 QY 201 PhePheLeuArgLeuSerArgAlaGlnGlyLysLeuPheGluIThrLeuCysAspGlnLeu 220
 Db 745 TTCTTCCTCCGCTCAGACAGGCCAGGCTGACTTTTGAACCTCTGATCACTC 804
 QY 221 LeuAspIleITrpGlyIThrIleArgLysGlnIThrPheMetAlaMetLeuLysLeuAla 240
 Db 805 CTGGATTAATCCCGGACATCAGGAAGACACATTCACATGCGCATGCTGCTAAGCTGGG 864
 QY 241 GlnArgValLeuPheLeuLeuAspGlyITyrAsnGluPheLysProGlnAsnCysProGlu 260
 Db 865 CAGAGGCTTCTTCTCTTCTTATGCTACATGATTAATCAAGCCCAATGCGCCACAA 924
 QY 261 IleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValIThrIThr 280
 Db 925 ATCGAAGCCCTGATGAAGAAACACACGCTTCAGAAACATGCTATGCTACCACTCC 984
 QY 281 ThrGluCysLeuAsnArgHisIleArgGlnPheGlyAlaLeuIThrAlaGluValGlyAspMet 300
 Db 985 ACTGATGCTCTAAGGACATACGAGAGTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1044
 QY 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGlu 320
 Db 1045 ACAGAAAGACAGGCCAGCTCTCATCCGAAAGTGTGATCAAGAGCTTGTGAAAGGC 1104
 QY 321 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysIThrProleuPhe 340
 Db 1105 TTGTTCTCTCAAAATTCAGAAATCCAGAGTCTTGAGAAATCTATAGAACCCCTCTCTTT 1164
 QY 341 ValValIleIThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisIThrGlnIThr 360
 Db 1165 GTGGTATCACTGTGCATTCAGATGGGTGAAGTGAATTCACCTCACACACAAACA 1224
 QY 361 ThrLeuPheHisIThrPheITyrAspLeuLeuIleGlnLysAsnLysHisLysITrsGly 380
 Db 1225 ACCGTGTCATACCTTATGATCTGTGATACGAAACCAACCAACCAATCAAGAGT 1284
 QY 381 ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly 400
 Db 1285 GTGGCTGCAAGTACTTCATTCGAGACCTGGACACCTGGAGACCTTACTCTGAGAGGT 1344
 QY 401 ValIPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420
 Db 1345 GTGTCTCCACAAAGTTTGAATTCGAACAGCAGAGATGTGTCAGCTGAATGAGATGTC 1404
 QY 421 LeuLeuIThrIThrGlyLeuLeuCysLysITyrIThrAlaGlnArgPheLysITrpLysITrs 440
 Db 1405 CTGCTGACACTGGGCTCTCTGTAATAATVACAGTCAAAAGGTTCAAGCCAAAGTATTA 1464

QY 441 PhePheHisLysSerPheGlnGluTrpThrAlaGlyArgGluSerLeuLeuThr 460
 |||||
 Db 1465 TTCTTCAACAAGTCATTCACAGAGGTACACAGCAGCAAGACATCAGCATTTATTGAGG 1524
 QY 461 SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGluLysMetValSerIle 480
 |||||
 Db 1525 TCTCAATGACCCAGAGAGGTGACCAAGGGGAATGGTTACTGACGAATAATGGTTCCATT 1584
 QY 481 SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerValGlu 500
 |||||
 Db 1585 TCGGACATTCATCATCCTTATACAGCCGTGCTCGGTACACCTGTGGTCATCTGGGAA 1644
 QY 501 AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly 520
 |||||
 Db 1645 GCGACACGAGGCTGTATGAAAGACCTCGCAGAGTGTATCAACAGCGCTTCCTCGGA 1704
 QY 521 LeuSerIleAlaLysArgProLeuThrPargGlnGluSerLeuGlnSerValLysAsnThr 540
 |||||
 Db 1705 CTTTCCATGCGCAAGAGGCTCTGTGGAGACAGAAATCTTTCGAAAGTGTGAAACACCC 1764
 QY 541 ThrGlnGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGlnGlyGlyIleHis 560
 |||||
 Db 1765 ACTGACCAAGAAATTTCTGAAGCCATTAACATCATCTTGTGTAGAGTGGCATCCAT 1824
 QY 561 LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln 580
 |||||
 Db 1825 TTATATCAAGAGAGTACATCAAAATCAGCCCTGAGCCAGAAATTTGAACTTCTTTCA 1884
 QY 581 GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhePheGlu 600
 |||||
 Db 1885 GGTAAAGCTTATATATCTCACTCAGGGAACATCCCGATCTTATTTGACTTCTTTGAA 1944
 QY 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyAla 620
 |||||
 Db 1945 CATTTGCCCAATTTGTGCAGAGTCCCTGGACTTCATTAACCTGGACTTTATGGGAGCT 2004
 QY 621 MetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaPro 640
 |||||
 Db 2005 ATGGCTCATGTGGAAAGGCTGCAGAGACACAGGTGGATCCACATGGAAGAGGCCCA 2064
 QY 641 GluThrTyrIleProSerArgAlaValSerLeuPhePheAsnTyrPlyGlnGluPheArg 660
 |||||
 Db 2065 GAAACCTCATCTCCAGCAGGCGCTATCTTGTCTTCACTGAGAGAGGAATTCAGG 2124
 QY 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu 680
 |||||
 Db 2125 ACTCTGGAGGTCACACTCGGAGTTTCAGCAAGTGAATTAACAGATATCGATATCTG 2184
 QY 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyAla 700
 |||||
 Db 2185 GGGAAATATATTCAGCTCGCCCAAGCCTCAGCGTCCAAATTAAGATGTCTGTGTG 2244
 QY 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu 720
 |||||
 Db 2245 GCTGGAAAGCTTCAGTTGTCTCTCAGCACCTGTAGAACATTTATTCCTCATGTGTGAA 2304
 QY 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740
 |||||
 Db 2305 GCCATCTCCCTTCACCATGAAAGATAGAGGCCATCATCTGTATCAAAACCTGAAACCC 2364
 QY 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 760
 |||||
 Db 2365 TTGACTATTCATGACCTACAGATCAAGCGCTCGCGGTGGTCTACCTGACAGCTTGCGT 2424
 QY 761 AsnLeuLysAsnLeuThrLysLeuIleMetLysAsnIleLysMetAsnGluGluAspAla 780
 |||||
 Db 2425 AACCTGAAGAACCTTACAAAGCTCATTAATGATTAACATTAAGATGAATGAAGAAGATGCT 2484
 QY 781 IleLysLeuAlaGluGlyLeuLysAsnLeuLysMetCysLeuPheHisLeuThrHis 800
 |||||
 Db 2485 ATAAACTAGCTGAGAGGCTCTGAAAGCTGAAGAGATGTCTTATTCATTTGACCCAC 2544
 QY 801 LeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCys 820

Db 2545 TTGTCTGACATTTGGAGAGGAGTATGATTCATATGTCATCTCTGTCAAGTAAACCTGT 2604
 QY 821 AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840
 |||||
 Db 2605 GACCTTGAAGAAATCAATTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2664
 QY 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860
 |||||
 Db 2665 GCTCAGAAATCTTCACAAATTTGGTCAAACTGACACTTCTGATTTATCAGAAAAATTAACCTG 2724
 QY 861 GlyLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGln 880
 |||||
 Db 2725 GAAAAAGAGTGAAGAAATGAAGCTTTTCATGACGATCGACAGATATACCTGTTAAACAG 2784
 QY 881 LeuThrAlaLeuMetLeuProTyrPglyCysAspValGlnGlySerLeuSerSerLeuLeu 900
 |||||
 Db 2785 CTCACCGCAGCTGATCTGCTCGCTGGGGCTGTGACGTGCAAGGACAGCCTGAGCAGCTGTTG 2844
 QY 901 LysHisLeuGlnGluValProGlnLeuValLysLeuGlyLysAsnTyrPargLeuThr 920
 |||||
 Db 2845 AAACATTTGGAGAGGCTCCACAACTCGTCAAGCTTGGGTTGAAAACTGGAGACTCACA 2904
 QY 921 AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940
 |||||
 Db 2905 GATACAGAGATTAAGATTTTATGATGTCATTTTGGAAAGAACCTCTGAAAAACTTCCAG 2964
 QY 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPleuAlaPheMetGlyVal 960
 |||||
 Db 2965 CAGTTGAATTTGGCGGGAATCGTGTGAGCAGTGTGATGATGCTGCTCATGGGTGA 3024
 QY 961 PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980
 |||||
 Db 3025 TTGGAATCTTAACCAATATGATGTTTGTGACTTATGACTTAAAGAAATTTCTACCTGAT 3084
 QY 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla 1000
 |||||
 Db 3085 CCAGCATTAAGCAGAAATTAAGCAAGTGTATTCAGATTAACCTTCTGCAAGAGACT 3144
 QY 1001 ArgLeuValGlyTyrPglPheAspAspAspAspLeuSerValIleThrGlyAlaPheLys 1020
 |||||
 Db 3145 AGGCTTGTGGGTGGCAATTTGATGATGATGATCATCTGTATATACAGGTGCTTTTAA 3204
 QY 1021 LeuValThrAla 1024
 |||||
 Db 3205 CTAGTAAGTCT 3216
 |||||
 RESULT 3
 BC031555 3360 bp mRNA linear PRI 26-JUN-2002
 LOCUS BC031555
 DEFINITION Homo sapiens, caspase recruitment domain protein 12, clone
 MGC:35330 IMAGE:5179909, mRNA, complete cds.
 ACCESSION BC031555
 VERSION BC031555.1 GI:21594975
 KEYWORDS MGC.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 3360)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (06-JUN-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: http://mgc.ncl.nih.gov
 CONTACT MGC help desk
 REMARK
 COMMENT Email: gcabs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome

Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Huiyk, S.W., Hale, S.M.,
 Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
 Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/ILN at: <http://image.llnl.gov>
 Series: IRAC Plate: 50 Row: a Column: 10
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Hexamer frequency OR
 analysis.

FEATURES

location/Qualifiers
 1..3360
 /organism="Homo sapiens"
 /db_xref="LocusID:38484"
 /db_xref="taxon:9606"
 /clone="MGC:35330 IMAGE:5179909"
 /tissue_type="Brain, Lung, Testis, adult, pooled whole"
 /clone_id="NH_MGC_115"
 /lab_host="DH10B"
 /note="Vector: pCMV-Sport6"
 232..3306
 /codon_start=1
 /product="caspase recruitment domain protein 12"
 /protein_id="AAH3155.1"
 /db_xref="GI:21594976"
 /translation="MNFIKNSRALIORMGMYIKQITDDLYWVNLNREVNITCE
 KVEQDARGLIIMHILKRGSECNFLSKLEWNPYLPQDINGSLHQTSGLDIDA
 QDLKDLHPSPFNFPYPLGEDIDIFNLKSTFEPVLMKQDHHNREQLGLDA
 LQSPCIIEGSGSGKSTLQRIAMLMWSGSKALTKRFFYRLSRVAGQLEETLD
 QLDIDGTTIKQTFMALIKLRQVLELFDGKQFQKQNPQELALIKENHRKNVY
 VTTTCTLRHRIORFALAEVDMTEDSNALIREVILKLAGLILLOKSCILNL
 MKTPPLPVYTICAIOMGESEFHSHTQTTLEFTFTDILQKKHKNKYAEDFRSDH
 GDLALEGVESHKFEDELQVSVNEDELFTLDTLCKYTAQKRPKFFKHSFOET
 AGRRLSLTSHPEEYTKNGYLOKRVYSIDTSTYSLRLRTCGSVATRAVMK
 LAAYVHGCLGLSIAKRPLOBESLOSVCNTEOEILKAININSFEGCIHYOEST
 SKALSGEFAFGKSLYINSINIPYLFDFEHLNFCASALDFIKLDYGGAMSM
 EKAAEDGGTHMEAPERTYIPSAVSIFFMKQEPFRLTYLDELSEKLNQDRIYLGK
 IPSASTSLRQITRCAGVAGSLSLVSTCKNITSIMAEASPLITEDRHITSYTNLT
 LSHIDUNORLPGLDSDGNLKNLTKLINDTKMNEEDAIKLBGLKKNKCLFHL
 TSLSDIGEMDYIVKSLSSPCDLEIQLVSCCLSAVAVKILQNLHNLVKLISLDS
 ENYLEKXGNELHLEIDRMNVLEQLTALMPGCDVGSLSLKLHLEVPOLVKGL
 KNMRLEDTETIRLIGAFGRKNPLNFQOLNLAGKRVSDGMALFAGVEENKQVFEDE
 STKEFLDPPLVLRKLSQVLSKLPLOEARLVGMQFDDDDSVITGARKLVTVA"

CDS
 1011 a 718 c 768 g 863 t
 BASE COUNT
 ORIGIN

Alignment Scores:
 Pred. No.: 0 Length: 3360
 Score: 5453.00 Matches: 1023
 Percent Similarity: 99.90% Conservative: 0
 Best Local Similarity: 99.90% Mismatches: 1
 Query Match: 99.89% Indels: 0
 DB: 9 Gaps: 0

US-09-697-089-2 (1-1024) x BC031555 (1-3360)

QY 1 Metasnphellieysaspasnserrargalaleuileglnatgmetcylmetthrvalille 20
 Db 232 ATGAATTTCAATVAAAGCAATAAGCCGACCTTATTCAAAGAAATGGGAATGACTGTATTA 291
 QY 21 LysglnlietnhraspaspleuPheValtrypasnvallleuasnarglugluValasnlle 40
 Db 292 AAGCAAAATCACAGATGACCTATTGTATGGAATGTTGAAATCGGAAAGAAAGTAACATC 351
 QY 41 IleCysCysglulysValaGluglnaspAlaalaarglylleIleHisMetIleuLys 60
 Db 352 ATTTCCTCGAGAGAGGTGAGCAGATGCTCTTAAGGATCATTCACATGATTTTGA 411
 QY 61 LysglSerGlusSerCysasnleuPheleuLysSerleuLysglutrpAsnIyrProleu 80

Db 412 AAGGTTACAGACGTCGTAACTCTTTCTTAATCCCTTAAGAGATGAACTATCCCTTA 471
 QY 81 PheGlnaspLeuasnnglInserleuPheHisglInThrSerClnuLysaspLeuasp 100
 Db 472 TTTTCAGACTTGAATGAGCAAAAGCTTTTTCATCAACATCAACAAAGAGATGGAGAT 531
 QY 101 LeuAlaGlnaspLeuLysaspLeuTyrHisThrProSerPheLeuasnPheYrProleu 120
 Db 532 TTGGCTCAGATTTAAAGACTTGTACACATACCCCATCTTTCTGAACTTTATCCCTT 591
 QY 121 GlyLnuaspIleaspIleIlePheasnLeuLysSerThrPheThrClnuProValleuTyr 140
 Db 592 GGTGAAGATATGTACATTTATTTTAACTTGMAAAGCAACCTTCACAAACCTGCTGTG 651
 QY 141 ArgLysaspGlnHisThrAsrValaGluglnLeuThrleuasnnglLeuGlnAla 160
 Db 652 AGGAGAGACCAACACCTTCCCGGTGAGACACTGACCTGAAATGGCTCTGCGAGGCT 711
 QY 161 LeuGlnSerProCysIleIleGluGlnSerGlyLysGlyLysSerThrleuLeuGln 180
 Db 712 CTTCAGAGCCCTGCATCATTTGAAGGGGAACTGGCAAAAGCAAGTCCACTGTGTCAG 771
 QY 181 ArgIleAlaMetleuTyrpglySerGlyLysCysAlaLeuThrLysPheLysPheVal 200
 Db 772 CGAATTCGATGCTGTGGGCTCGGAAAGTGAAGGCTTGACCAAGTTCAATTCGTC 831
 QY 201 PhePheLeuArgLeuSerArgAlaGlnGlyLysLeuPheGlnThrleuCysAspGlnLeu 220
 Db 832 TTCTCTCTCCGCTGCAGACAGGCCCGGAGGTGACTTTTGAACCCCTGTGATCAACTC 891
 QY 221 LeuAspIleProGlyThrIleArgLysglInThrPheMetAlaMetleuLysLeuArg 240
 Db 892 CTGATATTAACCTGGCACAAATCAGGAACAGACATTCATGCGCAATGCTGGAAGCTGCGG 951
 QY 241 GlnArgValleuPheleuLeuAspGlyTyrAsnGlnuPheLysProGlnAsnCysProGln 260
 Db 952 CAGGGGCTTTCTTCTCTGTTGATGAGGCTACAAATCAAGCCCGCAACTGCGCCAGAA 1011
 QY 261 IleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValIThrThr 280
 Db 1012 ATCGAACCCTCGAATAAGAAACACCGCTTCAGAAACATGTCATCGTACACACTAC 1071
 QY 281 ThrClnuLysLeuArgHisIleArgGlnPheGlnAlaLeuThrAlaGlnValGlyAspMet 300
 Db 1072 ACTGAGGCGCTGAGGCGCAACAGCGCACTGTGCTGCTGCTGAGTGGGGGGAATG 1131
 QY 301 ThrGlnuSpSerAlaGlnAlaLeuIleArgGlnValleuIleLysGlnuAlaGlnGly 320
 Db 1132 ACAGAGACACGCGCCAGGCTCTATCCGAGAACTGTCATCAAGAGCTTGGCTGAAGGC 1191
 QY 321 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysTrpProleuPhe 340
 Db 1192 TTGTTGCTCCCAATTCAGAAATCCAGGCGCTTGAGAAATCCAGAAACCCCTCTT 1251
 QY 341 ValValIleThrCysAlaIleGlnMetGlyClnuSerClnuPheHisSerHisThrGlnThr 360
 Db 1252 GTGTCATCACTGTGCAATCCAGATGAGTGAAGTGAATGCCACTCTCCACACCAACA 1311
 QY 361 ThrleuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysGly 380
 Db 1312 ACGGTGTCATTCATCTTATGATCTGTGATACAGAAACCAACCAACATTAAGGT 1371
 QY 381 ValAlaAlaSerAspPheIleArgSerleuAspHisCysGlyAspLeuAlaLeuGlnGly 400
 Db 1372 GTGGCTGCAATGACTTATTCGAGAGCTGAGACACACTGTGAGACACTGTGAGAGGT 1431
 QY 401 ValPheSerHisLysPheAspPheClnuLeuGlnaspValSerSerValasnGlnaspVal 420
 Db 1432 GTGTTCTCCCAAGATTGATTTGAACTGCAAGATGATGTCACAGTGAATGAGAGATGTC 1491
 QY 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440

Db 1492 CTGTCGACACTGGGCTCCCTCTGTAATATACACCTCAAAAGCTTCAAGCCAAAGTATATAA 1551
Qy 441 PhePheHisLysSerPheGlnGluTyrThrAlaGluValArgLeuSerSerLeuThr 460
Db 1552 TTCTTTCAACAAGTATTCACAGAGTACACAGCAGAGCAAGAGCTTATATGAGC 1611
Qy 461 SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480
Db 1612 TCTCATGAGCAGAGAGGAGTGACCAAGGGAATGGTTACTTGCAGAAATGGTTCCATT 1671
Qy 481 SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500
Db 1672 TCGGACATTCATCCACTTATAGAGCGCTCTCCGGTACACCTGTGGGTTCATCTGGAA 1731
Qy 501 AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly 520
Db 1732 GCCACCAAGGCTTTATGAAGACCTCGAGCAGTGTATACACAGCGCTGCCCTTCGGA 1791
Qy 521 LeuSerIleAlaLysArgProLeuTyrArgGlnGluSerLeuGlnSerValLysAsnThr 540
Db 1792 CTTTCATTCGCCCAAGAGCGCTCTCGAGACAGAAATCTTTGCAAGTGTGAAGAAACACC 1851
Qy 541 ThrGlnGlnLutIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560
Db 1852 ACAGAGCAAGAAATTCGAAAGCCATTAACATCAATTCCTTTAGAGTGTGCATCCAT 1911
Qy 561 LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGlnAlaPhePheGln 580
Db 1912 TTATATCAAGAGTATCATCAATCAAGCCCTGAGCCAGAAATTTAAGCTTCTTCAA 1971
Qy 581 GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPheGlu 600
Db 1972 GGTAAAGCTTATATATCAACCTCAGGAACATCCCGATTACTTATTGACTCTTGA 2031
Qy 601 HisLeuProAsnLysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyIleAla 620
Db 2032 CATTTCCCAATGTGCAGTGCCTCGAGCTTCATTAACCTGCACTTTATGGGAGACT 2091
Qy 621 MetAlaSerTrpGluLysAlaAlaGluAspThrGlyIleHisMetGluGluAlaPro 640
Db 2092 ATGGCTTCATGGAAAGGCTGCAGAGACACAGGTGATCCACATGGAAGAGGCCCA 2151
Qy 641 GluThrTyrIleProSerArgAlaValSerLeuPheAsnTrpLysGlnGluPheArg 660
Db 2152 GAACCTACATTCGCCAGAGGGGCTGATCTTTGTTCTTCACTGGAAGAGAGATTCAG 2211
Qy 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu 680
Db 2212 ACTCTGGAGGTACACTCGGGAATTCACCAAGTTGAATACCAAGATATCAGATATCTG 2271
Qy 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700
Db 2272 GGGAAATATTCAGCTCTGCCACAAAGCCCTCAGGCTGCAAATTAAGAGATGCTGGTGTG 2331
Qy 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu 720
Db 2332 GCTGGAAAGCTCAGTTGGTCTCTCAGACCTGTAAGAACATTTATCTCTCATGGGAA 2391
Qy 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuTyrThr 740
Db 2392 GCCAGTCCCTCACCATTAAGATAGAGGACATCACTCTGTAAACAACTGAAACCC 2451
Qy 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 760
Db 2452 TTGAGATATCATGACCTACAGAAATCAAGCGTCCGGGTGTCTACAGCAGCTTGGCT 2511
Qy 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAla 780
Db 2512 AACCTGAAGAACCTTACAAAGCTCATATGATTAACATTAAGATGAAGAGAAATGCT 2571
Qy 781 IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800
Db 2572 ATTAAGAACTGCTGAAGGCTGAAACCTGAGAGAGATGTATTATTCATTTGACCCAC 2631

Qy 801 LeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCys 820
Db 2632 TTGTCTGACTTGTGAAGGGAATGATGATACATGATCAAGTCTCTGTCAAGTGAACCTGT 2691
Qy 821 AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840
Db 2692 GACCTGAAGAAATTCATATTAGTCTCTGCTGCTGTCTGTGCAAAATCAGTGAATCTTA 2751
Qy 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860
Db 2752 GCTCAGAAATCTTCACATTTGGTCAAACTGAGACTTCCTTGATTATACAGAAATTAACCTG 2811
Qy 861 GluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGln 880
Db 2812 GAAAGAGATGGAATGAACCTCTTCATGAACTGATGACAGAGTGAACGTGTAGAACAG 2871
Qy 881 LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900
Db 2872 CTCACCGCACTGATGCTGCCCTGGGCTGTGACGTGCAGAGCGAGCTGAGCCTGTG 2931
Qy 901 LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThr 920
Db 2932 AAACATTTGGAGAGGTCCACAACTGCAAGCTTGGGTTGAAAACTGGAGACTCACA 2991
Qy 921 AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940
Db 2992 GATACAGAGATTAAGAAATTTAGGTGATTTTGGAAAGAACCTCTGAAAACTTCCAG 3051
Qy 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyVal 960
Db 3052 CAGTTGAATTTGGCGGAAATCTGTGACCATGTGATGATGCTTGCCTTCATGGGTGA 3111
Qy 961 PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980
Db 3112 TTTGAGAAATCTTAACCAATTAGTGTTTTGTGACTTATAGTAAAGAAATTTCTACTGAT 3171
Qy 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla 1000
Db 3172 CCAGATTAATGAGAAACTTATGCAAGTGTATTCAGATTAACCTTCTGCCAAGAACT 3231
Qy 1001 ArgLeuValGlyTrpGlnPheAspAspAspAspLeuSerValIleThrGlyAlaPheLys 1020
Db 3232 AGCCTGTTGGGTGGCANTTTCATGATGATGATCTCAAGTGTATTACAGGTCTTTTAA 3291
Qy 1021 LeuValAlaAla 1024
Db 3292 CTAGTAAGTGTCT 3303
RESULT 4
LOCUS AF376061 3581 bp mRNA linear PRI 15-MAY-2001
DEFINITION Homo sapiens caspase recruitment domain protein 12 mRNA, complete cds.
ACCESSION AF376061
VERSION AF376061.1 GI:14040074
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3581)
AUTHORS Gingras, M.-C., Qiu, J. and Margolin, J.F.
TITLE Differential expression of the caspase recruitment domain protein 12 (CARD12) during monocytic differentiation
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3581)
AUTHORS Gingras, M.-C., Qiu, J. and Margolin, J.F.
TITLE Direct Submission
JOURNAL Submitted (03-MAY-2001) Pediatric/Texas Children's Cancer Center, Baylor College of Medicine, 6621 Fannin St. MC3-3320, Houston, TX 77030, USA
FEATURES
Location/Qualifiers

```
source
1. .3581
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/map="2p21-22"
/cell_line="0937"
/cell_type="peripheral blood-derived CD14 mature monocyte"
490. .3564
/note="CARD12"
/codon_start=1
/product="caspase recruitment domain protein 12"
/protein_id="AAK3443.1"
/db_xref="GI:14040075"
/translation="MNFKIDNSRALIQMGMTVIKQITDLEFVNVNLRREVNITCC
KVEDDARGIITMILIKGSECNFLKFKEMNYLFODLNGOSLFQTSFGDLDLA
ODKLDYTPSPFLPGLDEDIIPNKSTFTEVLMRKQHHRYRLQNLNGILOA
LOSPCITGEGSEKSKSTLQRIAMMGSKKALIKFPEVFLISRAQGLFETICD
QLDIPGIRKQITPMALIKRQYLFLLDQYNEKRPONCEPIALIKENHREKMTVI
VTTECLRH1RQFGALTAEVGDMTEDAQALIREVLIKELAEGLLIQISRLRL
MKTPLFVITCAIQMGSESEFHSHTQTLTFHFYDILLQKNHKKHGVASDFIRSLDH
CGDLAEGVFSHKFDELDQVSVNEDALFTGLCKTYAORFKPKYKFFPKSFOEY
AGRLSILTSHPPEVTKNGYLQKMWISDITSTSLRYTCGSSVEATRAVMKH
LAAYOHGCLIGLSIAKRPIMROESIOSVKTTQTOELIKATINISFVPCGHLIOEST
SKSALDSFEAFQGSKITYSNGNPDLTFPFEHLPCASALDPRIKIDFYGAMASR
EKAEDTGTGIHMEARPEYIPSRVSLFENKQERLLEVLTRDFSKLNKODIRLAK
IFSSATSLRQIKCAGVAGSLSVLSTCKNIYSIMVEASPLTEDEKHITSVNLKT
LSIHDLQRLPGSLTDSIGLNLKNTKLIMDKINMEDAIKLEGLNKKMCLFHL
THLSDIGEMDYIVKSLSEPCDLEEIQVSCCSANAKVILIAONLHLVRLSTLDS
ENYLEKQENALHYEIDRMNYLEOLTLMLPMGCDVQGISLKLKHEVQVQVIGL
KNMRLTDEIRITILGAFECNPLKNFQOLNAGNRYSSGMLAFMGEVFNKLQDLFFDF
STKEFLPDPALVRKLSQVLSKTLFQEARLVGWQFDDDLSTVITGAFLVA"
502. .741
/misc_feature
/note="Region: caspase recruitment domain"

BASE COUNT 1033 a 781 c 843 g 924 t
ORIGIN

Alignment Scores:
Pred. No.: 0 Length: 3581
Score: 5448.00 Matches: 1022
Percent Similarity: 99.80% Conservative: 0
Best Local Similarity: 99.80% Mismatches: 2
Query Match: 99.80% Indels: 0
DB: 9 Gaps: 0

US-09-697-089-2 (1-1024) x AF376061 (1-3581)
QY 1 MetAspPheIleIysAspSnsSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
Db 490 ATGAATTTCAATAAGACAAATAGCCGACCTTATTCAAGAATGGGAATGACTGTATA 549
QY 21 LysGlnIleThrAspAspLeuPheValITrPasnValIleuAsnArgGluGluValAsnIle 40
Db 550 AAGCAATATCAGATGACCTATTGTATGGAATGCTTGAAATGCCAAGAAGAAACATC 609
QY 41 IleCysCysGluIysValGluGlnAspAlaIaArgGlyIleIleHisMetIleLeuIys 60
Db 610 ATTTCGTCGAGAGAGCTGAGCAGCATGCTGTAGAGGATCATTCACATGATTTGAAA 669
QY 61 LysGlySerGluSerCysAsnLeuPheLeuIysSerIleuIysGluIrrPasnIrrProLeu 80
Db 670 AAGGGTTCAGAGTCCGTGTAACCTCTTTCTTAAATCCCTTAAGAGAGTGAATATCCCTTA 729
QY 81 PheGlnAspLeuAsnGlyGlnSerIleuPheHisGlnThrSerGluGluIysAspAsp 100
Db 730 TTTCAGGACTTGATATGCAAAAGCTTTTTCATCAGACATCAGAAAGGAACCTTGACGAT 789
QY 101 LeuAlaGlnAspLeuIysAspLeuIrrHisIthrProSerPheLeuAsnPheIrrProLeu 120
Db 790 TTGGCCTCAGAGATTAAAGACTTGATACCAATACCCCATCTTTCTGAACTTTATCCCTT 849
QY 121 GlyGluAspIleAspIleIlePheAsnLeuIysSerThrPheThrGluProValIleutrr 140
Db 850 GGTGAAGATATGACATTTATTTTAACTTGAAAGACACCTTCACAGAACCACTGCTGTGG 909

141 ArgIysAspGlnHisHisIleArgValGluGlnIleuThrLeuAsnGlyLeuLeuGlnAla 160
Db 910 AGGAAGGACCAACACCATCACCAGCGGTGAGCAGCTGACCTGAAATGGCTCTTCAGAGCT 969
QY 161 LeuGlnSerProCysIleIleGluGluIysIleSerGlyIysGlyIysSerThrLeuLeuGln 180
Db 970 CTTCAGAGCCCTGCATCATGTAAGAGGGAATCTGGCAAGGCAAGTCCACTCTCTGCAG 1029
QY 181 ArgIleAlaMetIleuThrGlySerGlyIysCysIysAlaLeuThrIysPheIysPheVal 200
Db 1030 CGCATTCGCATGCTCTGGGGCTCCGGAAGTGCAAGGCTTGACCAAGTTCAAAATGCTC 1089
QY 201 PhePheLeuArgLeuSerArgAlaGlnGlyIysLeuPheGluIrrThrLeuCysAspGlnIleu 220
Db 1090 TTCTTCCTCCCGCTCAGAGAGGGCCAGGGTGAGACTTTTGAACCCCTGTGATCAACTC 1149
QY 221 LeuAspIleProGlyIthrIleArgGlyGlnThrPheMetAlaMetLeuLeuIysLeuArg 240
Db 1150 CTGGATATACCTGGCACAATCAGGAACGACATTCATGAGCCATGCTCAAGCTGCGG 1209
QY 241 GlnArgValIleuPheLeuAspGlyIrrAsnGluPheIysProGlnAsnCysProGlu 260
Db 1210 CAGAGGTTCTTCTCTTGATGCTACATGATTAATTCAGCCAGAACTGCCAGAA 1269
QY 261 IleGlnAlaLeuIleIysGluAsnHisArgPheIysAsnMetValIleValIthrThr 280
Db 1270 ATCGAAGCCCTGATTAAGAAACACCGCTCAAGAACATGTCATGTCACACCTAC 1329
QY 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300
Db 1330 ACTGAGTCCCTGAGGACACATACGCGCATTTGGTGCCTGACTGCTGAGAGTGGGGATATG 1389
QY 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValIleuIleIysGlnLeuAlaGluGly 320
Db 1390 ACAGAAAGACAGCGCCAGGCTCTCATCCGAGAGTGTGATCTAGAGAGACTTGCTGAAGC 1449
QY 321 LeuLeuLeuGlnIleGlnIysSerArgCysLeuArgAsnLeuMetIysThrProLeuPhe 340
Db 1450 TTGTTGCTCCCAAAATTCAGAAATCCAGGTGCTTGAGGAATTCATGAAGACCCCTCTCT 1509
QY 341 ValValIleThrCysAlaIleGlnMetGlyIleSerGluPheHisSerHisIthrGlnThr 360
Db 1510 GTGGTCATCATCTTGTCATTCAGATGGGTGAAGTGAAGTTCACCTCCACACAAACA 1569
QY 361 ThrLeuPheHisIthrPheThrAspLeuLeuIleGlnIysAsnIysHisIysGly 380
Db 1570 ACGCTGTTCCATACCTTCTATGATCTGTGATACGAAACAAACAAACATTAAGGT 1629
QY 381 ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly 400
Db 1630 GTGGCTGCAAGTACTTATTCGAGGCTGAGACCACTGTGGAGACTGCTGAGAGGT 1689
QY 401 ValPheSerHisIysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420
Db 1690 GTGTTCTCCCAACAAGTTGATTTGCAACGTGCGAGATGTGTCAGCGGTGAATAGAGATCC 1749
QY 421 LeuLeuThrThrGlyLeuLeuCysIysIrrThrAlaGlnArgPheIysProIstIrrIys 440
Db 1750 CTGCTGACACACTGGGCTCTCTGTAATATACAGCTCAAGGTTTAAGCCAAAGTATAAA 1809
QY 441 PhePheHisIysSerPheGlnGlnIrrThrAlaGlyArgArgLeuSerSerLeuLeuThr 460
Db 1810 TTCTTTCACAATCATCTCCAGAGATACACAGCAGGACGAAAGCTGACAGTTATTGACG 1869
QY 461 SerHisGluProGluGluValIthrIysGlyAsnGlyIrrLeuGlnIysMetValSerIle 480
Db 1870 TCTCATGACCCAGAGAGGTGACCAAGGGGAATGTGTTACTTCAAAAAATGGTTTCCATT 1929
QY 481 SerAspIleThrSerThrIrrSerSerLeuLeuAlaGlyIrrThrCysGlyIysSerValGlu 500
Db 1930 TCGGACATTACATTCACATTATGACAGCCGCTCGGTACACCTGTGGGTCACTGTGGAA 1989
```

QY 501 AAlarhArgAlaValMetLysHisLeuAlaValTyrGlnHisGlyCysLeuLeuGly 520
 |||||
 Db 1990 GCCACAGGCGCTTATGAGACCTCCGACAGTGTATCAACACGCGCTTCCGA 2049
 QY 521 LeuSer11eAlaLysArgProLeuTrpArgGlnGlnSerLeuGlnSerValLysAsnThr 540
 |||||
 Db 2050 CTTTCCATCGCCAGAGGCGCTCTCGAGACAGGAATCTTTCGAAAGGTGAAAAACACC 2109
 QY 541 ThrGlnGlnGluLeuLysAlaLeuAsnLeuSerPheValGluCysGlyLeuHis 560
 |||||
 Db 2110 ACTGACAGAAATTTCTAAAGCCATAAATCAATTCCTTTGTAGAGTGTGGCATTCAT 2169
 QY 561 LeuTyrGlnGlnSerThrSerLysSerAlaLeuSerGlnGlnPheGlnAlaPhePheGln 580
 |||||
 Db 2170 TTATATCAAGAGAGTACATCCAAATACACCTCGAGCCAGAAATTTGAAGCTTTCTTCAA 2229
 QY 581 GlyLysSerLeuTyrLeuAsnSerGlyAsnLeuProAspTyrLeuPheAspPheGln 600
 |||||
 Db 2230 GGTAAACCTTATATATCACTCAGGGAACATCCCGATTTACTTATTTGACTCTTTGAA 2289
 QY 601 HisLeuProAsnGlyAlaSerAlaLeuAspPheLeuLysLeuAspPheTyrGlyAla 620
 |||||
 Db 2290 CATTTGCCCAATGTGCAAGGCGCTGGACTTCATTAACCTGACTTTATGGGGAGCT 2349
 QY 621 MetaLaserTrpGluLysAlaAlaGluAspThrGlyGlyLeuHisMetGluGluAlaPro 640
 |||||
 Db 2350 ATGGCTTCATGGAAAGCGTGCAGAGACACAGAGTGAATCCACATGGAAGAGCCCA 2409
 QY 641 GluThrTyrLeuProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArg 660
 |||||
 Db 2410 GAAACCTACATTTCCAGAGGCGTGTATCTTTGTTCTTCACTGGAAGCAGAAATTCAGG 2469
 QY 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnGlnAspThrTyrLeu 680
 |||||
 Db 2470 ACTGTGAGGCGACACCTCCGGATTTCAACAGTTGAATGAGCAAGATACATCAATCTCG 2529
 QY 681 GlyLys11ePheSerSerAlaThrSerLeuArgLeuGlnLeuLysArgCysAlaGlyVal 700
 |||||
 Db 2530 GGGAAATATTCACGCTCGCCACAAGCCTGACGCTGCAAAATTAAGAGATGTGGGTG 2589
 QY 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnLeuTyrSerLeuMetValGlu 720
 |||||
 Db 2590 GCTGGAAGCCTCACTTTGGTCTCCAGACCTGTAAGAACATTTTCTCATGCTGTGAA 2649
 QY 721 AlaSerProLeuThr11eGluAspGluArgHis11eThrSerValThrAsnLeuLysThr 740
 |||||
 Db 2650 GCCAGTCCCTCACATAGAAAGATGAGACGACATCTGTAACAAACCTGAAACACC 2709
 QY 741 LeuSer11eHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 760
 |||||
 Db 2710 TTGAGTATTCATGACCTACAGAAATCAACGCGCTCCGGGTGTGACTGACAGCTTGGGT 2769
 QY 761 AsnLeuLysAsnLeuThrLysLeu11eMetAspAsn11eLysMetAsnGlnGluAspAla 780
 |||||
 Db 2770 AACTGGAAGAACTTACAAAGGCTCATATGATGAATCAATTAAGATGAAGAGATGCT 2829
 QY 781 11eLysLeuAlaGluGlyLysLeuAsnLeuLysMetCysLeuPheHisLeuThrHis 800
 |||||
 Db 2830 ATAAACTAGCTGAAAGCCGTAAGAAACCTGAAAGATGTGTTATTTCACTTTGACCCAC 2889
 QY 801 LeuSerAsp11eGlyGlyGlyMetAspTyr11eValLysSerLeuSerSerGluProCys 820
 |||||
 Db 2890 TTGCTGTACATTTGGAGGGAATGGATGATGATCAATGCTCTGTCACTGAAACCTGT 2949
 QY 821 AspLeuGlnGlu11eGlnLeuValSerCysLysSerAlaAsnAlaValLys11eLeu 840
 |||||
 Db 2950 GACCTTAAAGAAATTCATTAATGCTCTGCTGCTTGTCTCAATGAGGAAATCTCTA 3009
 QY 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSer11eLeuAspLeuSerGluAsnTyrLeu 860
 |||||
 Db 3010 GCTCAGAAATCTCAATTTGGTCAAACTGAGCATCTTGATTTATTCAGAAATTTACCTG 3069
 QY 861 GluLysAspGluAsnGlnAlaLeuHisGluLeu11eAspArgMetAsnValLeuGluGln 880

Db 3070 GAAAAAGTGGAAATGAAAGCTTTCATGAACTGATCCGACAGATGAACGTGTAAGACAG 3129
 QY 881 LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900
 |||||
 Db 3130 CTCACCGCAGCTGATGCTGCCCTGGGGCTGTGACCTGCAAGGACAGCCTGAGACGCTGTG 3189
 QY 901 LysHisLeuGlnGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThr 920
 |||||
 Db 3190 AAACATTTGGAGGAGGTCGCCCAACTCGTCAAGCTTGGGTTGAAAAAACTGAGACTCACA 3249
 QY 921 AspThrGlu11eArgGlyLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940
 |||||
 Db 3250 GATACAGAGATTAATAATTTTATAGTGCATTTTGTGAAAGAACCTCTGAAAACTTCACG 3309
 QY 941 GlnLeuAsnLeuAlaGluAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyVal 960
 |||||
 Db 3310 CAGTTGAATTTGGCGGGAATCGTGTGACGAGTGTGATGATGGCTTGCCTCATGGGTGTA 3369
 QY 961 PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980
 |||||
 Db 3370 TTGTGAGATCTTAAGCAATTAAGTGTGTTTGTGACTTGTACTAAAGAAATTTCAACCTGAT 3429
 QY 981 ProAlaLeuValArgGlyLysSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla 1000
 |||||
 Db 3430 CCAGCATTAATGACGAAAACTTAGCCAGATGTATTCAGAACTTTCTTGTGCAGAGAGCT 3489
 QY 1001 ArgLeuValGlyTrpGlnPheAspAspAspLeuSerVal11eThrGlnAlaPheLys 1020
 |||||
 Db 3490 AGCCTGTTGGGTGGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3549
 QY 1021 LeuValThrAla 1024
 |||||
 Db 3550 CTAGTAATCTCT 3561

RESULT 5
 AK095467 3355 bp mRNA linear PRI 15-JUL-2002
 LOCUS Homo sapiens cDNA FLJ38148 f1s, clone D90ST2003791, highly similar
 DEFINITION to Homo sapiens ICE-protease activating factor mRNA.
 ACCESSION AK095467
 VERSION AK095467.1 GI:21754727
 KEYWORDS oligo capping; f1s (full insert sequence).
 SOURCE Homo sapiens CD34+ Cells cDNA to mRNA, clone_1lb:D90ST2
 clone:D90ST2003791.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1
 Nishimura, K., Wagatsuma, M., Kanda, K., Kondo, H., Yokoi, T.,
 Kodaira, H., Furuya, T., Takahashi, M., Kikkawa, E., Omura, Y., Abe, K.,
 Kamihara, K., Katseta, N., Sato, K., Tanikawa, M., Yamazaki, M.,
 Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S.,
 Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T.,
 Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M.,
 Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi-Fujii, A.,
 Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,
 Nagahara, K., Masuno, Y., Nagai, K., and Isogai, T.
 NEDO human cDNA sequencing project
 Unpublished
 2 (bases 1 to 3355)
 REFERENCE Isogai, T. and Yamamoto, J.
 AUTHORS Direct Submission
 TITLE Submitted (04-Jul-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
 JOURNAL

COMMENT

kazusa-kamatari, kisarazu, Chiba 292-0812, Japan
 (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
 NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:
 Research Association for Biotechnology (RAB); cDNA library
 construction: Helix Research Institute (HRI) (supported by Japan
 Key Technology Center etc.); 5'- and 3'-end one pass sequencing: RAB,
 HRI, and Biotechnology Center, National Institute of Technology and
 Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.
Location/Qualifiers
FEATURES
Source
1. .3355
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="D9OST2003791"
/cell_type="CD34+ Cells"
/clone_id="D9OST2"
/note="cloning vector: pME18SFL3-mRNA from CD34+ cells
after 9-days ODF induction.-primary culture, CD34+ cells"
BASE COUNT 986 a 726 c 774 g 869 t
ORIGIN
Alignment Scores:
Pred. No.: 0 Length: 3355
Score: 5447.00 Matches: 1022
Percent Similarity: 99.80% Conservative: 0
Best Local Similarity: 99.80% Mismatches: 2
Query Match: 99.78% Indels: 0
DB: Gaps: 0
US-09-697-089-2 (1-1024) x AK095467 (1-3355)
QY 1 MetAspHeIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
DB 262 ATGATTTCTAAAGGACAAATAGCCGACCTTATTCAAGAAATGGAAATGACTGTATA 321
QY 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluValAsnIle 40
DB 322 AAGCAATTCACAGATGACATATTGTATGGAATTTCTGATTCGCGAAGAACTAAACATC 381
QY 41 IleCysCysGluLysValGluGlnAspAlaAlaArgIleIleIleHisMetIleLeuLys 60
DB 382 ATTTGCTGCGAAGAGTGAGAGGATGCTGTAGAGGATCATTCATGATGATTTTGAAA 441
QY 61 LysGlySerGlySerCysAsnLeuPheLeuLysSerIleuLysGluTrpAsnTrpProLeu 80
DB 442 AAGGTTTCAAGATCTCTAACTCTTTCTTAATCCCTTAAGAGTGGAATACCTACTA 501
QY 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAsp 100
DB 502 TTTCAGACTTGAATGACAAAGCTTTTCAATCAGACATCAGAGAGACTTGAGCAT 561
QY 101 LeuAlaGlnAspLeuLysAspLeuTrpHisThrProSerPheLeuAsnPheTrpProLeu 120
DB 562 TTGGCTCAGATTTAAAGGACTTGTACCATACCCCATCTTTCGAACTTTATCCCTT 621
QY 121 GlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTrp 140
DB 622 GGTGAAGATATGTACATTATTTAACTTGAAGACCTTCACAGAACTGTCTGTGG 681
QY 141 ArgLysAspGlnHisHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla 160
DB 682 AGGAGAGACCAACACATCACCAGCTGAGCAGCTGACCTGATAGGCTCTCTGAGGCT 741
QY 161 LeuGlnSerProCysIleIleGlyGlyGluSerGlyLysGlyLysSerThrLeuLeuGln 180
DB 742 CTTCAGAGCCCTGCATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACTGCTCAG 801
QY 181 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 200
DB 802 CGAATTGCCATGCTCTGGGGCTCCGGAAATGCAAGGCTGTGACCAAGTTCAAAATTCGTC 861
QY 201 PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGlnThrLeuCysAspGlnLeu 220
DB 862 TTCTCTCCGCTCAGCAGAGGCGCCAGGGTGAGCTTTTGAACCCCTCTGTATCAATC 921
QY 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 240
DB 922 CTGGAAATACCTTGCAAAATCAGGAAGCAAGACATTCATGCTGCTGGAAGCTGGCG 981
QY 241 GlnArgValLeuPheLeuLeuAspGlyTrpAsnGluPheLysProGlnAsnCysProGlu 260

DB 982 CAGAGGCTTTTCCCTTCTGTGATGGCTTACAAATGAATTCAGGCCCAAGAACTGCCAGAA 1041
QY 261 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr 280
DB 1042 ATCAACACCTGTATTAAGGAAACACCCGTTCAAGAACATGGTATGTCACACACTACC 1101
QY 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300
DB 1102 ACTGAGCTCGTAGGACATACGCAAGTTGGTGCCCTGACTGCTGAGTGGGGGAATATG 1161
QY 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 320
DB 1162 ACAGAAACAGCCGCCAGGCTTCATCCGAAAGTGTGATCAAGAGAGCTTGTGAAGGC 1221
QY 321 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340
DB 1222 TTGTGTGCTCAAAATTCGAAATCCAGGTGCTTGAAGATCTCATGAAGACCTCTCTTT 1281
QY 341 ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr 360
DB 1282 GTGGTATCAGCTTGTGCAATCCAGATGGGTGAAGAGTGTCCACTGCACACAAACA 1341
QY 361 ThrLeuPheHisThrPheTrpAspLeuLeuIleGlnLysAsnLysHisLysGly 380
DB 1342 ACCTGTTCATACCTTCATGATCTGTGATACAGAAAAACAACAACATAAAGGT 1401
QY 381 ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly 400
DB 1402 GTGGCTGCAAGTACTTCATTCGAGCTTGACACCTGTGACACCTGAGACCTGTGGAGGGT 1461
QY 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420
DB 1462 GTGTTCCTCCACAAGTTTGATTCGAATCAGAGATGTGTCCAGCGATGATGAGATGTC 1521
QY 421 LeuLeuThrThrGlyLeuLeuCysLysTrpThrAlaGlnArgPheLysProLysTrpLys 440
DB 1522 CTGCTGACAACCTGGCTCCCTGTAAATATACGCTCAAGAGGTTCAAGCCAAAGTATAA 1581
QY 441 PhePheHisLysSerPheGlnGluTrpThrAlaGlyArgArgLeuSerLeuLeuThr 460
DB 1582 TTCTTTCACAGTCATTCACGGAGTACACAGCGACGAAAGACTCAGCACTTTATGAGT 1641
QY 461 SerHisGluProGluGluValThrLysGlyAsnGlyTrpLeuGlnLysMetValSerIle 480
DB 1642 TCTCATGAGCAGAGAGGAGTGACCAAGGGAATGGTACTTCAGAAATGGTTCCATT 1701
QY 481 SerAspIleThrSerThrTrpSerSerLeuLeuArgTrpThrCysGlySerSerValGlu 500
DB 1702 TCGGACATTTACATCCACTTATACACCTGTCCGGTACACCTGTGGGTATCTGTGAA 1761
QY 501 AlaThrArgAlaValMetLysHisLeuAlaAlaValTrpGlnHisGlyCysLeuLeuGly 520
DB 1762 GCCACCAAGGCTTTATGAAGCACTTCGCAAGCTTATCAACACGCGCTCTTCGGA 1821
QY 521 LeuSerIleAlaLysArgProLeuTrpArgGlnGluSerLeuGlnSerValLysAsnThr 540
DB 1822 CTTCATCGCCCAAGAGCCCTCTCTGAGACAGAAATCTTTGCAAGGTGGAAGAAACACC 1881
QY 541 ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560
DB 1882 ACTGACCAAGAAATTTCTGAAGGCCATTAACATCAATCTTGTGTAAAGTGTGCAATCCAT 1941
QY 561 LeuTrpGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGlnAlaPhePheGln 580
DB 1942 TTATATCAAGAGATCATCCAAATAGCCCTGAGCAAGATTTTAAGCTTTCTTTCAA 2001
QY 581 GlyLysSerLeuTrpIleAsnSerGlyAsnIleProAspTrpLeuPheAspPhePheGlu 600
DB 2002 GGTAAAGAGCTTATATATCAACTCAGGGAACATCCCGGATTAATTAATGACTCTTTGAA 2061
QY 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTrpGlyGlyAla 620
DB 2062 CATTTGCCCAATTTGTCAAGTGGCTGTGACTTCATTAACTGCACTTTATATGGGGAGCT 2121

QY 621 MetAlaSerTrpGluLysAlaIleAspThrGlyIleHisMetGluGluAlaPro 640
DB 2122 ATGGCTTCATGGGAAAGAGCTGCAGACAGACAGAGGATCCACTGGAGAGGCCCA 2181
QY 641 GluThrTyrIleProSerArgAlaValSerLeuPheAsnTyrPlyGlnIupheArg 660
DB 2182 GAACCTACATTCACAGCAGGAGCTGATCTTGTCTTCACTGGAAGCAGGAATTCAG 2241
QY 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu 680
DB 2242 ACTCGAGAGCTACACCTCGGAGATTTCACAGATTGAATACAGATATTCAGAAATCTG 2301
QY 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700
DB 2302 GGGAAATATTTACGCTCTGCCACAGCCTCAGGCTGCCAATTAAGAGATGCTGTGTG 2361
QY 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu 720
DB 2362 GCTGGAAGCTCAGTTGTGCTCTCAGACCTGTAAGAACATTTATCTCTCATGGTGCA 2421
QY 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740
DB 2422 GCCAGTCCCCCTACCATTAAGATGAGAGGACATCATCTGTATACAAACCTGAAAAAC 2481
QY 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 760
DB 2482 TTGAGATATCATGACCTACAGATACAGCGCTGCCGGTGTCTGATCAGCTGGTGGT 2541
QY 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluLysAla 780
DB 2542 AACTGGAAGAACCTTACAAAGCTCATATGATTAACATTAAGATTAAGAAAGATGCT 2601
QY 781 IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800
DB 2602 ATAAACTACGCTGAAGGCCCTGAAAAACCTGGAAGAGTGTGTTATTTTCATTGTGACCCAC 2661
QY 801 LeuSerAspIleGlyLysGlyMetAspTyrIleValLysSerLeuSerSerGluProCys 820
DB 2662 TTGCTGCACATTCGAGAGGAGGATGATTACATGATCAAGTCTCTCAAGTGAACCTGT 2721
QY 821 AspLeuGluGluIleGlnLeuValSerCysLysLeuSerAlaAsnAlaValLysIleLeu 840
DB 2722 GACCTTGGAAGAAATTCATTAATCTCCCTGCTGCTGCTGCAAAAGCAGTGAATAATCTCT 2781
QY 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860
DB 2782 GCTCAGAAATCTTCACAATTTGGTCAAACTGACATTTCTTGATTTATTCAGAAATTAACCTG 2841
QY 861 GluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGln 880
DB 2842 GAAAAAGATGGAATGAGAGCTCTTCATGACATGATGACAGATGACAGTGTCTAGAACAG 2901
QY 881 LeuThrAlaLeuMetLeuProTrpGlyLysAspValGlnGlySerLeuSerSerLeuLeu 900
DB 2902 CTCACCGACATGATCTCCCTCGGGGCTGTGACGTCAGAGGAGCCTCAGCAGCCTGTGTG 2961
QY 901 LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThr 920
DB 2962 AAACATTTGGAGAGAGTCCCACTCACTCAAGCTTGGGTTGAAAAAATCGGAGACTCAC 3021
QY 921 AspThrGluIleArgIleLeuGluValAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940
DB 3022 GATACAGAGATTAAGAAATTTAGGTGCATTTTGGAAAAAGAACCCCTGAAAAAATCTCCAG 3081
QY 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPleuAlaPheMetGlyVal 960
DB 3082 CAGTTGAATTTGGCGGAAATCGTGTGAGCAGTGTGATGCTGCTTCATGGGTGTA 3141
QY 961 PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980
DB 3142 TTTCGAAATCTTAAGCAATTAAGTGTGTTTTCAGCTTTAGTACTAAAGAAATTTCTACTGAT 3201

QY 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla 1000
DB 3202 CCAGCATTTAGTAGAAACTTATGACAGTGTATCCAACTTACTTCTGTGCAAGAGCT 3261
QY 1001 ArgLeuValGlyTrpGlnPheAspAspAspLeuSerValIleThrGlyAlaPheLys 1020
DB 3262 AGCGTTGTTGGGTGGCAATTTGATGATGATGATTCACAGTGTATTAACAGCTCTTTAA 3321
QY 1021 LeuValThrAla 1024
DB 3322 CTAGTAACGTCT 3333
RESULT 6
AX318091
LOCUS AX318091 3396 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 96 from Patent WO0190156.
ACCESSION AX318091
VERSION AX318091.1 GI:17900820
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Reed,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,
Oliveira,V.A., Hayashi,H. and Pawlowski,K.
TITLE Card domain containing polypeptides, encoding nucleic acids, and
methods of use
JOURNAL Patent: WO 0190156-A 96 29-NOV-2001;
The Burnham Institute (US)
FEATURES
source
location/Qualifiers
1..3396
/organism="Homo sapiens"
/db_xref="taxon:9606"
277..3351
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD19340.1"
/db_xref="GI:17900821"
/translation="MNFITKDSRALIORMKPTVYKQITDDLFVWNVLNREEVNITCE
KVEDDARGITIHMLTKRGSESCNLEFLSKEMWNPYLEPQDNGSLFHOJSEGLDDLA
QNDLVAHTPSFLNFPYLEDIDITFNMKSTFEPIEDKRDONHHRVQDLNLGLDA
LOSPCIIIEGSESGKSTLQRIAMLMGSGKALTKRFKFEFLRSAGGLFEFTLCD
QLDIPETIRKOTPMAMLIKROVLEFLDQYNEKFPONCEITALLKRRKRNVT
VTTFTECLRHROGALTAEDMTESAOALREVLIKELASLILQIQKRSRRL
MKPLFVYICAIOMGSESPSHQITLFFRYDILLQKKKKHKVYASDIFRSIDH
RGDIALRGVSHKFDPELDQVSYNEVDLITFGLLTKTKOREPKTKFHSFOET
AGRLSSLLTSHPEEYTKNGYLOKNVLSIDTITSTYSLRLRYTGSSVASTRAVMH
LAAVYOHGCLLGSLIAKRPMLROESQVNTTEOEILKAININSFVEGCIHLVQEST
SKSALSOEFAFPOGKSLYINSQNPYLFDFEFLHFNCSALDFIKLDPYGGAMSM
EKAEDRGTHIMEEAPETYPISRAVSLFFNMKOEFLLEYLIRDFSKLKNODIRYLGK
IFSASTSLRIQKRCAGVAGSLSTYSCNKIYSLMPEASPLTIEDRHRTSYNLT
LSTHDONQRLPGSLDPSGLKMLTILMDNITKMEDEIKLAEGLKMLKKLFL
THSIDGEMDYIVKSLSSSEPCDLEELIVSCCLSAANVILKQNLNLVLSLIDS
ENYLEKNGEALHELIDRMNVLDQTLTLMIPWGDVQSGLSLKLHEEYPOVLKGL
KNMRLTDETRILIRIIGAEPKMLKFNQNLNAGNVSDDGMIAFWGVENKQIVFDFE
STKEFLDPLLVRLSOVLSKIFLEQARLVQMFDDDDLSVTIGARKLVTA"

BASE COUNT 992 a 737 c 793 g 874 t
ORIGIN

Alignment Scores:
Pred. No.: 0 Length: 3396
Score: 5438.00 Matches: 1021
Percent Similarity: 99.80% Conservative: 1
Best Local Similarity: 99.71% Mismatches: 2
Query Match: 99.62% Indels: 0
DB: 6 Gaps: 0

US-09-697-089-2 (1-1024) x AX318091 (1-3396)

QY 1 MetAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
DB 277 ATGAATTCATTAAGAGACATTAAGCCCTTATTCAGAAAGAGGAGATGACTGTATA 336

QY 21 LysGlnIleThrAspAspIleuPheValITrpAsnValIleuAsnArgGluGluValAsnIle 40
|||||
Db 337 AAGCAATTCACAGATGACACTTTTGTATGGAAATTTCTGAATCCCGAAGAAAGTAAACATC 396
QY 41 IleCysCysGluIuValGluGlnAspAlaIlaArgGlyIleIleHisMetIleLeuLys 60
397 ATTGTGTCGAGAGGTGGACAGAGATGCTCTAGAGGAGATCATTCATCATTTTGGAA 456
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluITrPAsnTyrProLeu 80
457 AAGGGTTTCAGAGTCTCTAACCTTTCTTAAATCCCTTAAAGGATGGAACTATCCCTTA 516
QY 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp 100
517 TTTAGAGACTTGAAATGACAAAGTCTTTTCATCATGACATAGAAAGAGACTTGGACAT 576
QY 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu 120
577 TTGGCTCAGAGATTAAAGAGCTTGACCATCCCATCTTTTGAACCTTTATCCCTT 636
QY 121 GlyIuAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuITrp 140
637 GGTAAATATATGACATTAATTTTAACCTGAAAGCAACCTTCACAGAACTTACTCTG 696
QY 141 ArgLysAspGlnHisHisArgValGluGlnLeuThrIleuAsnGlyLeuLeuGlnAla 160
697 AGGAAGACCAACACACATCACCGGCTGGAGACGCTGACCCGGAATGGCCTCTCGAGCT 756
QY 161 LeuGlnSerProCysIleIleGluGlyLysSerGlyLysSerThrLeuLeuGln 180
757 CTTCAGAGCCCTCATCATGATGAAGGGGAATCTGGCAAGCAAGTCCACTCTCTGAG 816
QY 181 ArgIleIleMetLeuITrpGlySerGlyLysCysLysAlaLeuIThrLysPheLysPheVal 200
817 CGCATTCGCACTCTGCGGGCTCGGAAAGTGAAGGCTCTGACCAAGTTAAATTCGTC 876
QY 201 PhePheLeuITrArgLeuSerITrArgAlaGlnGlyLeuPheGluIThrLeuCysAspGlnLeu 220
877 TTCTTCCTCCGCTCAGACAGGCCAGGGTGGACTTTTGAAGCCCTCTGTGATCAACTC 936
QY 221 LeuAspIleITrProGlyIThrIleITrGlyGlnIThrPheMetAlaMetLeuLeuLysLeuITrG 240
937 CTGATITACCTGGCACAAATCAGGAACGACATTCATGGCCATGCGCTGAACCTGGG 996
QY 241 GlnITrValIleuPheLeuLeuAspGlyTyrITrAsnGluPheLysProGlnAsnCysProGlu 260
997 CAGAGGCTCTTTTCTTTCTTTGATGGCTACAAATGAAITTCAAAGCCCCCAGAACTGCCAGAA 1056
QY 261 IleGluAlaLeuIleLysGluAsnHisITrPheLysAsnMetValIleValIThrIThr 280
1057 ATCGAAGCCCTGATTAAGGAACACACCGCTTCAAGAACATGTCATGTCACACACTACC 1116
QY 281 ThrGluCysLeuITrArgHisIleITrGlnPheGlyAlaLeuIThrAlaGluValGlyAspMet 300
1117 ACTAGTGTCCGAGGACAAITACGGCAGATTTGTGTGCTCCCTGACTGCTGAGAGTGGGAAATG 1176
QY 301 ThrGluAspSerITrAlaGlnAlaLeuIleITrGlyValLeuIleLysGluLeuAlaGluGly 320
1177 ACAGAAGACAGCCGCCAGGCTCTATCCGAGAATGCTGATCAAGAGACTTGGTGAAGGC 1236
QY 321 LeuLeuLeuGlnIleGlnLysSerITrGlySerITrArgAsnLeuMetLysIThrProLeuPhe 340
1237 TTGTGTCCCAAAATTCAGAAATTCAGAGTGTGAGGAATTCATGAGAACCCCTCTCTTT 1296
QY 341 ValValIleIThrCysAlaIleGlnMetGlyLysITrGluPheHisSerHisIThrGlnIThr 360
1297 GTGTGTCAATCACTTGTGCAATTCAGATGGTGAAGTGAATTCACCTCCACACCAACAA 1356
QY 361 ThrIleuPheHisIThrPheTyrAspLeuLeuIleGlnLysAsnLysHisITrLysGly 380
1357 ACCTGTTCATACCTTCTATGATCTGTGTATACGAAACAAACAAACATTAAGGT 1416
Db

QY 381 ValAlaIleAspPheIleITrArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly 400
1417 GTGGCTCAGAGTACTTCATTCGAGAGCTGGACCAACCGTGGAGACCTTAGAGGT 1476
QY 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420
1477 GTGTTCCTCCACAGATTGTAATTTGCAACTGACAGATGTGTCCACCGTAATGAGAGATGC 1536
QY 421 LeuLeuIThrITrGlyLeuLeuCysLysITrThrITrAlaGlnITrPheLysITrLys 440
1537 CTGCTGAACACTGGGCTCTCTGTAAATATACACTCAAAAGTTCAAGCCAAAGTATATA 1596
QY 441 PhePheHisLysSerPheGlnGluTyrIThrAlaGlyITrArgLeuSerSerLeuLeuIThr 460
1597 TTCTTTCACAAGTATATCCAGAGATACACAGCAGAGAGAAAGTACAGATTATTCAGC 1656
QY 461 SerHisGluProGluGluValIThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480
1657 TCTCATGAGCCAGAGAGGTGACCAAGGGGAATGTTACTTGACAGAAATGGTTCCATT 1716
QY 481 SerAspIleIThrSerITrLysSerSerLeuLeuITrIThrCysGlySerSerValGlu 500
1717 TCGGACATTCATCCACTTATAGCAGCTCTCGGTACACCTGTGGTCAATCTGTGGA 1776
QY 501 AlaITrArgAlaValMetLysHisLeuAlaAlaValITrGlnHisGlyCysLeuLeuGly 520
1777 GCCACCAAGGGCTGTATTAAGACACCTCGCAGCACTGATATACACAGGCTGCTCTGGA 1836
QY 521 LeuSerIleAlaLysITrProLeuITrPArgGlnGluSerLeuGlnSerValLysITrThr 540
1837 CTTCCTCATCGCAAGAGCCCTCTCTGAGACAGGAATCTTGGAAATGTGAAACAC 1896
QY 541 ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGlyCysGlyIleHis 560
1897 ACTGACGACAAATTCGAAAGCCATTAACATCAATTCCTTTAGAGTGTGGATCAT 1956
QY 561 LeuITrGlnGluSerIThrSerLysSerITrAlaLeuSerGlnGluPheGluAlaPheGln 580
1957 TTATATCAAGAGATACATCCAAATTCAGCCCTGAGCCAAAGAAATTTGAAGCTTCTTCAA 2016
QY 581 GlyLysSerLeuITrIleAsnSerGlyAsnIleITrAspITrLeuPheAspPheGlu 600
2017 GGTAAAGCTTATATATCACTACGAGGAACATCCCCATTAATTTGACTTTTGAA 2076
QY 601 HisLeuITrAsnCysAlaSerITrAlaLeuAspPheIleLysLeuAspPheITrGlyAla 620
2077 CATTTGCCAATTTGCAAGTGGCTCGAGCTTCAATTAACITGACCTTTATGGGGAGCT 2136
QY 621 MetAlaSerITrGluLysAlaIleGluAspIThrGlyIleHisMetGluGluAlaPro 640
2137 ATGGCTTCATGGGAAAGGCTGCGAGAAACACACAGTGGAAATCCACATGGAAGAGGCCCA 2196
QY 641 GluIThrITrIleProSerITrArgAlaValSerITrLeuPheAsnITrPlysGlnITrPheArg 660
2197 GAAACCTTACATTCACAGAGGGCTGTATCTTTGTTTCAACTGGAAGACGGAATTTAGG 2256
QY 661 ThrLeuGlnValIThrLeuITrAspPheSerLysLeuAsnLysGlnAspIleIThrITrLeu 680
2257 ACTGTGAGGTGACACACCTCGGAGATTTCAGCAAGTGTGAATAAGATATCAGATATCTG 2316
QY 681 GlyLysIlePheSerSerITrAlaIThrSerLeuITrGluGlnIleLysITrArgCysAlaGlyVal 700
2317 GGGAAATATATCACCTGTGCCACAAAGCTCAGCTGCAAAATTAAGAATATGGCTGGTGTG 2376
QY 701 AlaGlySerLeuSerITrValLeuSerIThrCysLysAsnIleITrSerLeuMetValGlu 720
2377 GCTGGAAGCCTCAGATTGGTCTCAGCACCTGTAAAGAACATTTATCTCTCATGTGGA 2436
QY 721 AlaSerProLeuIThrIleGluAspGluITrArgHisIleIThrSerValIThrAsnLeuLysIThr 740
2437 GCCAGTCCCTCAGCATTAGAAAGATGAGAGGCACATCATCTGTATACAAACCTTAAGAC 2496
QY 741 LeuSerIleHisITrAspLeuGlnAsnGlnITrArgLeuProGlyLeuIThrAspSerLeuGly 760

```
|||||
Db 2497 TTGAGATTTCATGACCTACGAAATCAACGGCTCCGGGTGCTGACGTACGACCTGGGT 2556
Qy 761 AsplLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetLsnGluLysAla 780
Db 2557 AACTTGAAGAACTTACAAAGCTCATTAATGATGAATGAATGAATGAATGAATGAATGCT 2616
Qy 781 IleLysLeuAlaGluLysLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800
Db 2617 ATAAACTAGCTGCAAGGCTGAAAAACCTGAACAAATGCTGTTATTTCATTGACCCAC 2676
Qy 801 LeuSerAspIleGlyLysGluLysMetAspTyrIleValLysSerLeuSerGluProCys 820
Db 2677 TTGCTGACATTGAGAGGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 2736
Qy 821 AsplLeuGluLysLeuLysLeuValSerCysLeuSerLysAlaValLysIleLeu 840
Db 2737 GACCTTGAAGAAATTCATTAATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2796
Qy 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860
Db 2797 GCTCACAATCTTCACAAATTTGGTCAAACTGAGCATTCCTGATTATTCAGAAAATTCCTG 2856
Qy 861 GluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGln 880
Db 2857 GAAAAAGATGGAATGAACCTCTTCATGAACTGATGACAGATGAACTGATGAACTGATG 2916
Qy 881 LeuThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerLeuLeu 900
Db 2917 CTCACCGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2976
Qy 901 LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrPargLeuThr 920
Db 2977 AAACATTTGGAGAGAGTCCCACTCCGCAAGCTTGGGTTGAAAACTGGAGACTCACA 3036
Qy 921 AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940
Db 3037 GATACAGATTAAGATTTAGGTGATGATTTTGGAAAGAACCCCTCTGAAAACTTCAG 3096
Qy 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPheLysAlaPheMetGlyVal 960
Db 3097 CAGTTGAATTTGGCGGGAATGCTGTGACAGATGATGATGATGATGATGATGATGATGATG 3156
Qy 961 PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980
Db 3157 TTGGAGAATCTTAAGCAATTAAGTGTGTTTGGACTTACCTTAAGCAATTTCTACTGAT 3216
Qy 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla 1000
Db 3217 CCAGCATTTAGTCAGAAAACCTTAGCCAAAGCTTATCCAAATGTTTCTGCAAGAGCT 3276
Qy 1001 ArgLeuValGlyTyrGlnPheAspAspAspAspLeuSerValIleThrGlyAlaPheLys 1020
Db 3277 AGGCTGTGGTGGCGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3336
Qy 1021 LeuValThrAla 1024
Db 3337 CTAGTAACCTCT 3348

RESULT 7
AY027787 3396 bp mRNA linear PRI 20-JUL-2001
LOCUS Homo sapiens CLAN1 (CLAN1) mRNA, complete cds.
DEFINITION AY027787
ACCESSION AY027787.1 GI:14324112
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3396)
AUTHORS Damiano,J.S., Stehlik,C., Pio,F., Godzik,A. and Reed,J.C.
TITLE Clan, a novel human ced-4-like gene
```

```
JOURNAL Genomics 75 (1-3), 77-83 (2001)
MEDLINE 21365712
PUBMED 11472070
REFERENCE 2 (bases 1 to 3396)
AUTHORS Stehlik,C., Damiano,J.S., Pio,F., Godzik,A. and Reed,J.C.
TITLE Direct Submission
JOURNAL Submitted (21-FEB-2001) Program on Apoptosis and Cell Death
Research, The Burnham Institute, 10901 North Torrey Pines Road, La
Jolla, CA 92037, USA

FEATURES
source
1..3396
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/map="2p22-p21"
/feature_type="lung"
1..3396
/gene="CLAN1"
277..3351
/gene="CLAN1"
/feature="alternatively spliced; similar to Ced-4"
/codon_start=1
/product="CLAN1"
/protein_id="AAK14776.1"
/db_xref="GI:14324113"
/translation="MNFIDKNSRLIORMGVTYIKOITDOLFVNNVLRREVNITICE
KVEDDAAGITIMILKSGESCNLFPLSKRWNPILRODLNGSLPHOTSGDLDLDA
ODKDLHTPSFLNTPLEGIDIDIFNLKSTFTEPLMKRODHHRYOQLINLDA
LQSPCITIEGSESGKSTLQRIAMLWSGCKALTKRFEFLRSRAOGLFETLAD
QULIDPTIRKQTFWAMMLKLRORYLFELGDKNEFKPQNCPEIALIKENRFRNMYI
VTTTECLRHIFQALAEVDMQTEDSOALIREVLIKELEGLLQIORSCLNL
MKTPLFVITTCALOMGESESHQNTITLFFHFYLLLOKNNKHKGVAAPLTSISDH
RGDLALBEVFSHKRDELODYSVNEVDLITGLCKTADRFKRYFKPSQERT
AGRLSSULTSHEBEVTKNGVYLQKMSISDITSTYSLTRYCGSSVEYTRVMKH
LAAVYOHGCLLGLSTAKRPLMRQESLOSVKNTTQELIKAININSFEGCITHLOEST
SKSALDSQFEAFFOGSKLYINSNPDLFDFEPLPCASALDFIKLDFYGMAASV
EKAAEDTGIEHMEAPETYIPSRVSLFENKOEPRLETLRDESKLNKODIRYLG
IFSSATSLRLQIKRCAGVAGSLVLSICKKITYSLMVEASPLTLEDRHITSYNIKT
LSIDHONORLPGLGIDSGNLKLNLRKININIKENEDAKILABGLKNLKKLFIH
THSDIGEMDTYKSLSSSEPCDEIOLVSCCLSANVKILAOHLNHLVLTUDLS
ENVLEKDSNEALHELIDRMNVLEQITFALMLPWGCDVQSGSLSLKHLKEVQALVGL
KNMRLTDEIRLILFAFGKNPLKRFQOINLAGNVSSDGMWLAFMGVENLQVLFDFE
STKEFLPDPALVRKLSQVLSKLTFLQEARLVGMQFDDDDLSVITGARLVYA"
```

```
Db 517 TTTCAGAGCTTGAATGGACAAAGTCTTTTCATCAGACATCAGAAGGACTTGGACAT 576
Qy 101 LeuAlaGlnAspLeuLysAspLeuThrHisThrProSerPheLeuAsnPheTyrProLeu 120
Db 577 TTGGCTCGAGGATTTAAAGACTTTGACCATACCCCATCTTTCTGAACTTTATACCCCTT 636
Qy 121 GlyLysAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuThrP 140
Db 637 GGTGAAGATATTGACATTATTTTAACTTTGAAAAGCACCTTCCACAGAACCTATCTGTGG 696
Qy 141 ArgLysAspGlnHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla 160
Db 697 AGGAAGGACCAACACATCACCGGTGGAGCAGCTGACCTGAAATGGCTCTGGACAGCT 756
Qy 161 LeuGlnSerProCysIleIleGluGlyLeuSerGlyLysSerThrLeuLeuGln 180
Db 757 CTTGAGAGCCCTCGATCATTTGAAGGGGAATCTGGCAAAAGGCAAAGTCCACTCTGCTGCAG 816
Qy 181 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 200
Db 817 CGCATTTGCCATGCTCTGTGGGCTCCCGAAAGTGCAAAGCTCTGACCAAGTTCAAATTCGTC 876
Qy 201 PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu 220
Db 877 TTCTTCCCTCCGCTCAGCAGGGGCCAGGCTGGAACCTTTTGAAACCCCTCTGATCAACTGC 936
Qy 221 LeuAspIleProGlyThrIleArgGlyGlnThrPheMetAlaMetLeuLeuLysLeuArg 240
Db 937 CTGGATATATCTGGCACAAATCAGAAAGCAGACATTTCATGCCCATGCTCTGAAAGCTGGCG 996
Qy 241 GlnArgValLeuPheLeuLeuAspGlyTyrArgGlnPheGlyAlaLeuThrAlaGlyAspMet 260
Db 997 CAGAGGGTTCTTTCTTCTCTTGATGGCTACAAATGAAATTCAGAGCCCAAGACTGGCCACAGA 1056
Qy 261 IleGluAlaLeuIleLysGlyAsnHisArgPheLysAsnMetValIleValIleThrThr 280
Db 1057 ATCGAAGCCCTGATAAAGAAACCAACCGCTTCAGAAACATGTCATGTCACCCCTACCC 1116
Qy 281 ThrGlyCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGlyValAlaGlyAspMet 300
Db 1117 ACTGAGTCCCTGAGGACACATACGCGAGTGTGGTGGCTGCATGCTGCGAGGTGGGGATATG 1176
Qy 301 ThrGlnAspSerAlaGlnAlaLeuIleArgGlnValLeuIleLysGlyLeuAlaGly 320
Db 1177 ACAGAAAGACAGGCCCGACGCTCATCCGAAAGTGTGATCAAGAGACTTGGCTGAAGGC 1236
Qy 321 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340
Db 1237 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAACCCCTCTCTTT 1296
Qy 341 ValValIleThrCysAlaIleGlnMetGlyLysSerGlnPheHisSerHisThrGlnThr 360
Db 1297 GTGGTCATCAGTGTGCATATCCAGATGGGTGAAAGTGAATTCACATCTCACACACAAACA 1356
Qy 361 ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysGly 380
Db 1357 ACGCTGTTCCATACCTCTATGATCTGTGATACAGAAACCAACAAACATATAAGT 1416
Qy 381 ValAlaAlaSerAspPheLeuArgSerLeuAspHisCysGlyAspLeuAlaLeuGly 400
Db 1417 GTGGCTGCAAGTGTTCATTCGTGGAGCTGGACACCGCTGGAGACTGAGCTTGAGAGGT 1476
Qy 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420
Db 1477 GTGTTCTCCCAAGTGTGATTTCGAACCTGCAGAGATGTGTCTCAGCGTGAATGAGAGATGC 1536
Qy 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440
Db 1537 CTGGTGACAACCTGGGCTCTCTGTAAATATACAGCTCAAGGTTCAAGCCAAAGATATAA 1596
Qy 441 PhePheHisLysSerPheGlnGlyTyrThrAlaGlyArgGluSerSerLeuLeuThr 460
|||||
Db 1597 TTCTTCAAGATCATTCACAGACTACACAGACGAAAGACTCAGACTTATATGACG 1656
Qy 461 SerHisGluProGlyGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480
Db 1657 TCTCATGAGCCAGAGAGGTGACCAAGGGGAATGTTACTTTCGAGAAATGTTCCATT 1716
Qy 481 SerAspIleThrSerThrLysSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500
Db 1717 TCGGACATTCATCAGCTTATAGCAGCGCTGCTCGGATACACCTGTGGGTATCTGTGGAA 1776
Qy 501 AlaThrArgAlaValMetLysHisLeuAlaValIleGlyGlnHisGlyCysLeuLeuGly 520
Db 1777 GCCACAGAGGCTGTATGAAACACCTCGCAGCAGATGATACAAACAGCGCTGCTCGGA 1836
Qy 521 LeuSerIleAlaLysArgProLeuThrArgGlnGluSerLeuGlnSerValLysAsnThr 540
Db 1837 CTTTCCATGCGCAAGAGGCTCTCTGGAGAGGAATCTTTGAAAGCTGTGAAACACCC 1896
Qy 541 ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGlyCysGlyIleHis 560
Db 1897 ACTGAGCAGAAATTCGAAAGCCATTAACATCAATTCCTTGTAGAGTGGCATCCAT 1956
Qy 561 LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln 580
Db 1957 TTATATCAAGAGATACATCCAAATCAGCCCTGAGCCAGAAATTTGAAGCTTCTTCCAA 2016
Qy 581 GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPheGlu 600
Db 2017 GGTAAAGACTTATATATCAACTCAGGAGACATCCCCGATTTACTTATTTGACTTCTTGA 2076
Qy 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyVal 620
Db 2077 CATTTGCCCAATTTGCAAGTGCCTCGACTTCAATTAACAGGACTTTTATGGGGAGCT 2136
Qy 621 MetAlaSerTrpGlyLysAlaAlaGluAspPheArgGlyIleHisMetGluAlaPro 640
Db 2137 ATGGCTTCATGGAAAGCTGTCAGAAACACAGGTGAATCCACATGGAAGAGGCCCA 2196
Qy 641 GluThrTyrIleProSerArgAlaValSerLeuPheAsnTrpLysGlnGluPheArg 660
Db 2197 GAACCTTCATTTCCAGCAGAGGCTGTATCTTGTCTTCACTGGAAGCAGGATTCAG 2256
Qy 661 ThrLeuGlnValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu 680
Db 2257 ACTCTGAGGTCACACTCCGGGATTTTCAGCAAGTGTGAATACGAATATCATGATCTG 2316
Qy 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700
Db 2317 GGGAAATATTCAGCTGTGCCACAAAGCTCAGGCTGCAAATTAAGAGATGTGTGTGTG 2376
Qy 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu 720
Db 2377 GCTGGAACCTTCAGTGTGTCTCAGCAGCCTGTAAAGACATTTATCTCATGTGTGAA 2436
Qy 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740
Db 2437 GCCAGTCCCTCCACCATGGAAGATGAGAGGCACATCATCTGTGAACAAACCTGAAACCC 2496
Qy 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 760
Db 2497 TTGAGTATTCATGACCTTACAAATTCACAGGCTGCCGGGTGTGTGACTGACAGCTTGGGT 2556
Qy 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAla 780
Db 2557 AACTTGAAGAACCTTACAAAGCTCATATATGATATAACATAAAGATGAAGAGAGATGCT 2616
Qy 781 IleLysLeuAlaGlyGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800
Db 2617 ATAAACTAGCTGAAGGCTGAAAAACCTGAAGAGATGTTTATTTTCATTTGACCCAC 2676
Qy 801 LeuSerAspIleGlyGlyLysMetAspTyrIleValLysSerLeuSerSerGluProCys 820
Db 2677 TTGTCTGACATTGGAGAGGGAATGATTACATAGTCAAGTCTCTGTCAAGTGAACCCCTGT 2736
```

```

QY 821 AsplEugluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840
    |||||||
Db 2737 GACCTGGAAGAAATTCATTAAGTCTCTCTCTCTCTGCAAAATGCACTGAAATCTTA 2796
QY 841 AlagInAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGlnAsnTrpLeu 860
    |||||||
Db 2797 GCTCAGAAATCTTCACAAATTTGGTCAAACTGACCATTTCTGATTATTCAGAAATTAACCTG 2856
QY 861 GlnTrpAspGlyAsnGlnAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGln 880
    |||||||
Db 2857 GAAAAAGAGAAATGAACCTCTTCATGAAATGATCGACAGATGAACCTGCTAGAACAG 2916
QY 881 LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900
    |||||||
Db 2917 CTCACCGCACATGATGCTGCTGGGCTGTGACGTGCAGACGACCTGACGACCTGTGG 2976
QY 901 LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThr 920
    |||||||
Db 2977 AAACATTTGGAGAGAGTCCACACACTCGTCAGCTTGGTTGAAAACTGGAGACTCACA 3036
QY 921 AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940
    |||||||
Db 3037 GATACAGACATTAAGATTTAGTGCATTTTGGAAAGAACCTCTGAAAAACTTCCAG 3096
QY 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyVal 960
    |||||||
Db 3097 CAGTTGAATTTGGCGGGAATCGTGTGACAGCTGATGATGAGTGCCTTGCATGGTGTGA 3156
QY 961 PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGlnPheLeuProAsp 980
    |||||||
Db 3157 TTTGAGAACTTAAGCAATTAAGTCTTTTGTGACTTACTTAAGAAATTTTACTGAT 3216
QY 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGlnAla 1000
    |||||||
Db 3217 CCAGCATTAAGTCAAGAACTTACCAAGTCAATCAAGTCAATCTTCTGCAAGAGCT 3276
QY 1001 ArgLeuValGlyTrpGlnPheAspAspAspAspLeuSerValIleThrGlyAlaPheLys 1020
    |||||||
Db 3277 AGCGTTGTGGTGCAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3336
QY 1021 LeuValThrAla 1024
    |||||||
Db 3337 CTAGTAAGTCTGT 3348

RESULT 8
AC010968 160583 bp DNA linear HTG 18-AUG-2000
LOCUS Homo sapiens chromosome 2 clone RP11-9302, WORKING DRAFT SEQUENCE,
DEFINITION 11 unordered pieces.
ACCESSION AC010968.5 GI:9845170
VERSION AC010968.5
KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 160583)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 160583)
REFERENCE Direct Submission
AUTHORS Waterston,R.H.
TITLE Submitted (28-SEP-1999) Genome Sequencing Center, Washington
JOURNAL University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Aug 18, 2000 this sequence version replaced gi:8439959.
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml

```

```

----- Project Information -----
Center project name: H_NH0093002
----- Summary Statistics -----
Sequencing vector: plasmid; 418
Chemistry: Dye-primer ET; 47% of reads
Chemistry: Dye-terminator Big Dye; 53% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: bases at least Q40
Consensus quality: bases at least Q30
Consensus quality: bases at least Q20
Insert size: 147000; agarose-ff
Insert size: 159583; sum-of-contigs
Quality coverage: 6.64 in Q20 bases; agarose-ff
Quality coverage: 6.38 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 1080: contig of 1080 bp in length
* 1081 1180: gap of unknown length
* 1181 2476: contig of 1296 bp in length
* 2477 2576: gap of unknown length
* 2577 5035: contig of 2459 bp in length
* 5036 5135: gap of unknown length
* 5136 9606: contig of 4471 bp in length
* 9607 9706: gap of unknown length
* 9707 17078: contig of 7372 bp in length
* 17079 17178: gap of unknown length
* 17179 27158: contig of 9980 bp in length
* 27159 27258: gap of unknown length
* 27259 45137: contig of 17879 bp in length
* 45138 45237: gap of unknown length
* 45238 65522: contig of 20285 bp in length
* 65523 65623: gap of unknown length
* 65623 91498: contig of 25876 bp in length
* 91499 91598: gap of unknown length
* 91599 116835: contig of 25237 bp in length
* 116836 116936: gap of unknown length
* 116936 160583: contig of 43648 bp in length.
Location/Qualifiers
1. 160583
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/clone="RP11-9302"
1. 1080
/note="assembly_name:Contig9"
1181. 2476
/note="assembly_name:Contig12"
2577. 5035
/note="assembly_name:Contig13"
5136. 9606
/note="assembly_name:Contig14"
9707. 17078
/note="assembly_name:Contig15"
17179. 27158
/note="assembly_name:Contig16"
27259. 45137
/note="assembly_name:Contig17"
45238. 65522
/note="assembly_name:Contig18
/clone_end=:77
vector_side:right"
65623. 91498
/note="assembly_name:Contig19"
91599. 116835
/note="assembly_name:Contig20

```

clone_end:SP6
vector_side:right"
misc_feature 116936..160583
/note="assembly_name:Contig21"
BASE COUNT 44349 a 33843 c 33703 g 47641 t 1047 others
ORIGIN

Alignment Scores:

Pred. No.: 0 Length: 160583
Score: 3543.00 Matches: 664
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 64.90% Indels: 0
DB: 2 Gaps: 0

US-09-697-089-2 (1-1024) x AC010968 (1-160583)

QY 88 SerleuPheHisGlnThrSerGluGlyAspLeuAspAspLeuAlaGlnAspLeuLysAsp 107
Db 49187 GGTCTTTTCATCAGACATCAGAAAGAGACTTGGACGATTTGGCTCAGAGATTTAAAGGAC 49246
QY 108 LeuTyRHsIsthProSerPheLeuAsnPhetTyProLeuGlyGluAspIleAspIleIle 127
Db 49247 TTGTACCATACCCCATCTTTCTGAACTTTATCCCTTGGTGAAGATATTGACATTAT 49306
QY 128 PheAsnLeuLysSerThrPheThrGluProValLeuTrpArgLysAspGlnHisHis 147
Db 49307 TTTAACTTGAAGAACCTTCACAGAACCTGCTGTGGAGGAAGCAACACCATCAC 49366
QY 148 ArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaGlnSerProCysIleIle 167
Db 49367 GCGGTGGAGCGCTGACCTTAATGCTCCTGAGGCTTTCAGGCCCCGCTGCATCAT 49426
QY 168 GluGlyGlnSerGlyGlyGlySerThrLeuLeuGlnArgIleAlaMetLeuTrpGly 187
Db 49427 GAAGGGGATCTGGCAAGGCAAGCCACTCTGCTGCAGCCCATTTGCCATGCTCGGGC 49486
QY 188 SerGlyCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSerArg 207
Db 49487 TCCGAAAGTGCAGGCGCTGACCAAGTCAAAATTCGCTTCCTCCGCTCAGCAGG 49546
QY 208 AlaGlnGlyGlyLeuPheGlnThrLeuCysAspGlnLeuLeuAspIleProGlyThrIle 227
Db 49547 GCCCAGGGGTGACTTTTGGAAACCTCTGTATCAACCTCGGATATTCCTCGGCCAATTC 49606
QY 228 ArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArgValLeuPheLeu 247
Db 49607 AGGAAGCAGACATTCATGCGCATGCTGTAAGCTGCGGCGAGAGGTTCTTTCTTCTT 49666
QY 248 AspGlyTyraGlnLupPheLysProGlnAsnCysProGluIleGluAlaLeuIleLysGlu 267
Db 49667 GATGGCTCAATGAATCAAGCCCCAGAACTGCCAGAAATCGAAGCCCTGATAAGGAA 49726
QY 268 AsnHisArgPheLysAsnMetValIleValThrThrThrThrGluCysLeuArgHisIle 287
Db 49727 AACCAACCCCTTCAGAAACATGATGATCTCACCACTACCTGATGATGCTTGAAGCATA 49786
QY 288 ArgGlnPheGlyAlaLeuThrAlaGluValAlaGlyAspMetTrpGluAspSerAlaGlnIle 307
Db 49787 CGGCAGTTGGTGGCTTACCTGCTGAGGTGGGGGATATGACAGAAAGAGGCCCAAGGCT 49846
QY 308 LeuIleArgGluValLeuIleLysGluLeuAlaGluGlyLeuLeuLeuGlnIleGlnLys 327
Db 49847 CTCATTCGAGAAAGTGTATATCAGAGAGCTTGTCTGAAGCTTGTGCTCCAAATTCAGAAA 49906
QY 328 SerArgCysLeuArgAsnLeuMetLysThrProLeuPheValIleThrCysAlaIle 347
Db 49907 TCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTTGTGGTCATGACATGTCATTC 49966
QY 348 GlnMetGlyGlnSerGluPheHisSerHisThrGlnThrThrLeuPheHisIsthPheLys 367
Db 49967 CAGATGGGTGAAGTGAAGTTCACCTTCACACACAAACAGCGTGTTCATACCTTCAT 50026

QY 368 AspLeuLeuIleGlnLysAsnLysHisLysHisLysGlyValAlaAlaSerAspPheIle 387
Db 50027 GATCTGTGATACAGAAAAACAAACATTAAGGTGTGGCTCGCAAGTGCATTCAT 50086
QY 388 ArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGlyValPheSerHisLysPheAsp 407
Db 50087 CGGAGCCGAGCACCTGTGGAGACTGACTCTGGAGGTGTGTCTCCCAAGTATTGAT 50146
QY 408 PheGluLeuGlnAspValSerSerValAsnGluAspValLeuThrThrGlyLeuLeu 427
Db 50147 TTCCAGCTGCAGATGTGTCTCCAGGCTGATAGATGTCCCTCGACACAGCTGCTCTC 50206
QY 428 CysLysTyThrAlaGlnArgPheLysProLysTyThrLysPhePheHisLysSerPheGln 447
Db 50207 TGTAATATACAGCTCAAGAGTTCAAGCCAAAGTATTAATCTTTCACAAAGTCAATCCAG 50266
QY 448 GluTyThrAlaGluArgArgLeuSerSerLeuLeuThrSerHisGluProGluGluVal 467
Db 50267 GAGTTCACAGCAGAGCAGAACTCAGAGTATTGACGTCTCATGAGCCAGAGAGGTG 50326
QY 468 ThrLysGlyAsnGlyTyThrLeuGlnLysMetValSerIleSerAspIleThrSerThrTy 487
Db 50327 ACCAAGGGGATGGTTACTTTCAGAAATGTTTCCATTTGCGACATTAATCCACTTAT 50386
QY 488 SerSerLeuLeuArgTyThrThrCysGlySerSerValGluAlaThrArgAlaValMetLys 507
Db 50387 AGCAGCCGTCTCCGTTACACCTGTGGTCATCTGTGGAAGCCACAGGCGCTTATGAG 50446
QY 508 HisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGlyLeuSerIleAlaLysArgPro 527
Db 50447 CACCTCGAGCAGTGTATCAACACGGCTGCTTCTCGACTTTCATGTCGCAAGAGGCT 50506
QY 528 LeuTrpArgGlnLysSerLeuGlnSerValLysAsnThrThrGlnGlnGluIleLeuLys 547
Db 50507 CTCGGAGACAGGATCTTTTCCAAAGTGTGAAAAACACACTGAGCAAGAAATTCGAAA 50566
QY 548 AlaIleAsnIleAsnSerPheValGluCysGlyIleHisLeuTyrglnLysSerThrSer 567
Db 50567 GCCATAAACATCAATTCCTTTGTAGAGTGTGCAATCCATTTATATCAAGAGATACATCC 50626
QY 568 LysSerAlaLeuSerGlnLupPheGlnAlaPhePheGlnGlyLysSerLeuTyriAsn 587
Db 50627 AAATCAGCCCTGAGCCCAAGATTTGAACTTTTCAAGGTAAAGCTTATATATCAAC 50686
QY 588 SerGlyAsnIleProAspTyThrLeuPheAspPhePheGlnHisIleProAsnCysAlaSer 607
Db 50687 TCAGGGAACATCCCGGATTAATTGACTTCTTTGAACATTTGCCAATGTGCAAGT 50746
QY 608 AlaLeuAspPheIleLysLeuAspPheTyrglyAlaMetAlaSerTrpGluLysAla 627
Db 50747 GCTCTGACCTTCATTAACCTGACTTTTATGGGAGGCTATGCTTCATGGGAAAGGCT 50806
QY 628 AlaGluAspThrGlyGlyIleHisMetGluGluAlaProGluThrTyriIleProSerArg 647
Db 50807 GCAGAAACAGAGGTGATGATCAGATGAGAAAGGCCCAAGAACTCATTTCCAGAGG 50866
QY 648 AlaValSerLeuPhePheAsnTrpLysGlnLupPheArgTrpLeuGluValThrLeuArg 667
Db 50867 GCTGTATCTTTGTTCTTCAACTGCAAGCAGAAATTCAGAGACTGTGGAGGTACACTCCG 50926
QY 668 AspPheSerLysLeuAsnLysGlnAspIleThrTyThrLeuGlyLysIlePheSerSerAla 687
Db 50927 GATTTACAGCAAGTTGAATAAACCAAGATATCAGATATGCGGAAATATTCAGCTCGCC 50986
QY 688 ThrSerLeuArgLeuGlnIleLysArgCysAlaGlyValAlaGlySerLeuSerLeuVal 707
Db 50987 ACAAGCCCTCAGCTGCAGAAATGAAGATGTGCTGTGTGGCTGGAAGCCTCAGATTGGTC 51046
QY 708 LeuSerThrCysLysAsnIleTyrrSerLeuMetValGluAlaSerProLeuThrIleGlu 727
Db 51047 CTCAGCACTGTAAAGAACATTTATTTCTCATGTGGGAAGCCAACTCCCTCACCATTGAA 51106
QY 728 AspGluArgHisIleThrSerValThrAsnLeuLysThrLeuSerIleHisAspLeuGln 747

|||||
Db 51107 GATGAGAGCACAATCTGTACAAACGTAACCTTGATTCATTCACCTACAG 51166
Oy 748 AsglnArgLeuProGly 753
|||||
Db 51167 AATCAACGGCTGCCGGT 51184
RESULT 9
CNS01DS3/c 138909 bp DNA linear PRI 18-APR-2002
LOCUS BAC sequence from the SPG4 candidate region at 2p21-2p22 BAC 164M19
DEFINITION of 11bpary C17B_978_SKB from chromosome 2 of Homo sapiens (Human).
ACCESSION AL121653
VERSION AL121653.2 GI:7159616
KEYWORDS SPG4 genomic DNA interval.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 138909)
AUTHORS Hazan,J., Fonknechten,N., Mavel,D., Paternotte,C., Samson,D.,
Artiguenave,F., Davoine,C.S., Cruaud,C., Durr,A., Mincker,P.,
Brothier,P., Catolico,L., Barbe,Y., Burgunder,J.M.,
Prud'Homme,J.F., Brice,A., Fontaine,B., Heilig,R. and
Weissenbach,J.
TITLE Spastin, a novel AAA protein, is altered in the most frequent form
of autosomal dominant spastic paraplegia
JOURN. Nat. Genet. (1999) In press
REFERENCE 2 (bases 1 to 138909)
AUTHORS Genoscope.
TITLE Direct Submission
JOURN. Submitted (18-APR-2002) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT On Mar 6, 2000 this sequence version replaced gi:6002386.
FEATURES
source location/Qualifiers
1..138909
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/clone_id="C17B_978_SKB"
BASE COUNT 39243 a 28424 c 29121 g 42121 t
ORIGIN
Alignment Scores:
Pred. No.: 0 Length: 138909
Score: 3539.00 Matches: 664
Percent Similarity: 99.85% Conservative: 1
Best local Similarity: 99.70% Mismatches: 1
Query Match: 64.83% Indels: 0
Gaps: 0
US-09-697-089-2 (1-1024) x CNS01DS3 (1-138909)
Oy 88 SerLeuPheHisGlnThrSerGluGlyAspLeuAspAspLeuAlaGlnAspLeuLysAsp 107
:::|||||
Db 75310 GGTCTTTTTCATCAGACATCAGAAAGAGACTTGACGATTTGGCTCAGAGATTTAAAGAC 75251
Oy 108 LeuTyrHisThrProSerPheLeuAsnPheTyrProLeuGlyGluAspIleAspIleIle 127
|||||
Db 75250 TTGTACCATCCCATCTTTCTGAACTTTATCCCTTGGTGAAGATATGACATATAT 75191
Oy 128 PheAsnLeuLysSerThrPheThrGluProValLeuThrPAuGlyAspGlnHisHisHis 147
|||||
Db 75190 TTTTAACTTGAAGACCTTACAGAAACCTGCTCGTGAGAGAGAACCAACACCATAC 75131
Oy 148 ArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuGlnSerProCysIleIle 167
|||||
Db 75130 CGCGTGAAGACAGCTACACCTGAATGGCTCTCGACGGCTCTTCAGAGCCCTGCATCTAT 75071
Oy 168 GluGlyGluSerGlyLysGlyLysSerThrLeuLeuGlnArgIleAlaMetLeuTrpGly 187
|||||

Db 75070 GAAGGGAAATCTGGCAAGGCAAGTCACCTGCTGACGCAAAATGCCATGCTGGGGC 75011
Oy 188 SerGlyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLysSerArg 207
|||||
Db 75010 TCCGAAAGTGCAGAGCTCTGACCAGTTCAAAATTCCTTTCTCTCTCCCTCAGCAGG 74951
Oy 208 AlaGlnGlyGlyLeuPheGlnThrLeuCysAspGlnLeuLeuAspIleProGlyThrIle 227
|||||
Db 74950 GCCCAGGTGGACTTTTGAACCTCTGTGATCAATCTGGGATATACCTGGCAATTC 74891
Oy 228 ArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArgValLeuPheLeu 247
|||||
Db 74890 AGGAAGCAGACATTCATGCGCATGCTGTAAGCTGGCGCAGAGGCTCTTTCTCTCTT 74831
Oy 248 AspGlyTyrAsnGluPheLysProGlnAsnCysProGluIleGluAlaLeuIleLysGlu 267
|||||
Db 74830 GATGGCTCAATGAAATTCACCCCGAAGCTCCAGAAATCGAAGCCCTGATAAAGGA 74771
Oy 268 AsnHisArgPheLysAsnMetValIleValThrThrThrThrGluCysLeuArgHisIle 287
|||||
Db 74770 AACCAACCTTCAGAACATGATGTCATGTCACCACTACCTGAGTGCATGACACATA 74711
Oy 288 ArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMetThrGluAspSerAlaGlnAla 307
|||||
Db 74710 CGGCAGTTTGGTGGCTTACGCTGAGTGGGGGATATACAGAAAGACAGCCCGCAGCT 74651
Oy 308 LeuIleArgGluValLeuIleLysGluLeuAlaGluGlyLeuLeuLeuGlnIleGlnLys 327
|||||
Db 74650 CTCATCCGAGAAAGCTCTATCAGAGAGCTGCTGAAAGCTTGCTCAATTCAGANA 74591
Oy 328 SerArgCysLeuArgAsnLeuMetLysThrProLeuPheValIleThrCysAlaIle 347
|||||
Db 74590 TTCAGGCTTGAAGAACTGATGATGAGACCCCTCTTGTGGTATCATCTGGCAATTC 74531
Oy 348 GlnMetGlyGluSerGluPheHisSerHisThrGlnThrThrLeuPheHisThrPheTyr 367
|||||
Db 74530 CAGATGGGTGAAGAGTGAAGTCCACTGCACACAAACAGCGTTCATACCTTTAT 74471
Oy 368 AspLeuLeuIleGlnLysAsnLysHisLysHisLysGlyValAlaAlaSerAspPheIle 387
|||||
Db 74470 GATCTGTGATACAGAAACAAACAAACATAAAGGTGGGCTGCAGAGCTTCATT 74411
Oy 388 ArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGlyValAlaPheSerHisLysPheAsp 407
|||||
Db 74410 CGAGACCTGGAGACCACTGTGAGACCTACCTGAGAGGCTGTCTCCCAAGATTGAT 74351
Oy 408 PheGluLeuGlnAspValSerSerValAsnGluAspValLeuLeuThrThrGlyLeuLeu 427
|||||
Db 74350 TTCCGAATGCGAGATGTGTCCAGCGGTGAATGAGATGTCTGTGACAACTGGGCTCCTC 74291
Oy 428 CysLysTyrThrAlaGlnArgPheLysProLysTyrLysPhePheHisLysSerPheGln 447
|||||
Db 74290 TGTAAATATACAGCTCAAAAGGTCAAGGCCAAAGTAAATCTTTCAAAATCATCTCAG 74231
Oy 448 GluTyrThrAlaGlyArgArgLeuSerSerLeuLeuThrSerHisGluProGluGluVal 467
|||||
Db 74230 GAGTACACAGACAGACGAAAGACTCAGCAGTTTATGACGTCTCATGAGCCAGAGAGGTG 74171
Oy 468 ThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIleSerAspIleThrSerThrTyr 487
|||||
Db 74170 ACCAAGGGGAATGCTTACTTCAGAAATGGTTTCCATTTGCGACATTCACCATTTAT 74111
Oy 488 SerSerLeuLeuArgTyrThrCysGlySerSerValGluAlaThrArgAlaValMetLys 507
|||||
Db 74110 AGCAGCTGTCTCCGTTACACTGTGGGTCACTGTGGAAAGCACAGGGGCTTTATGAAG 74051
Oy 508 HisLeuAlaIaValTyrGlnHisGlyCysLeuLeuGlyLysSerIleAlaLysArgPro 527
|||||
Db 74050 CACCTCGAGACAGTGTATCAACACAGGCTGCTTCTCGACTTTCATTCGCCAAAGAGCT 73991
Oy 528 LeuThrArgGlnGluSerLeuGlnSerValLysAsnThrThrGlnGlnGluIleLysLys 547
|||||
Db 73990 CTCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACCACTGAGCAAGAAATCTGAAA 73931

QY 548 A1a11easnilleasSerpheValGluCysGlyIleHisLeuTyrGlnGluSerThrSer 567
 |||||
 Db 73930 GCCATAAACATCATTCCTTGTGAGAGTGGCATCATTAATATCAAGAGATACATCC 73871
 QY 568 LysSerSerAlaLeuSerGlnGluPheGluAlaPhePheGlnGlyLysSerLeuTyrIleAsn 587
 Db 73870 AAATCACCCTCGAGCCAGAAATTTGAAGCTTCTTCAAGGTAAACCTTAATATATCAAC 73811
 QY 588 SerGlyAsnIleProAspTyrLeuPheAspPhePheGlnHisLeuProAsnCysAlaSer 607
 Db 73810 TCAGGGAACATCCCGATTAATTTGACTCTTTGACACTTTGGCCAAATGTGGCAAGT 73751
 QY 608 A1a1eunaspheIleLysLeuaspPheTyrGlyAlaMetAlaSerTyrPgluLysAla 627
 Db 73750 GCCCTGACCTCATTAACCTGACTTTATGAGGAGCTATGCGTCAATGGAAGAGGCT 73691
 QY 628 A1a1eunaspheIleLysLeuaspPheTyrGlyAlaMetAlaSerTyrPgluLysAla 647
 Db 73690 GCAGAGACACAGGTGGAATCCACATGCAAGAGGCCCCAGAAACCTACATTCACAGCAGG 73631
 QY 648 A1a1a1SerLeuPhePheAsnTyrPlyGlnGluPheArgThrLeuGluValThrLeuArg 667
 Db 73630 GCTGTATCTTGTCTTCACTGCAAGCAGAGATTCAGAGACTCTGAGAGTACACTCCGG 73571
 QY 668 AspPheSerLysLeuAsnLysGlnAspIleThrTyrLeuGlyLysIlePheSerSerAla 687
 Db 73570 GATTTCAAGCAAGTGAATTAACAGATATCATGATATCTGGGGAATATTCAGCTCGCC 73511
 QY 688 ThrSerLeuArgLeuGlnIleLysArgCysAlaGlyValAlaGlySerLeuSerLeuVal 707
 Db 73510 ACAAGCCTCAGCGTCGCAAAATGAAGATGTCCTGCTGGCTGGAAGCCTCAGTTGGTCTC 73451
 QY 708 LeuSerThrCysLysAsnIleTyrSerLeuMetValGluAlaSerProLeuThrIleGlu 727
 Db 73450 CTCAGACACCTTAAGAACATTTATTTCTCTCTGATGAGAGCAGTCCCTTACCATAGAA 73391
 QY 728 AspGluArgHisIleThrSerValThrAsnLeuLysThrLeuSerIleHisAspLeuGln 747
 Db 73390 GATGAGAGGACATCATCATCTGTAACAACCTGAAACCTTGAGATTCATGACCTACAG 73331
 QY 748 AsnGlnArgLeuProGly 753
 Db 73330 AATCAACGGCTGCGCGGT 73313
 RESULT 10
 AC101793/3
 LOCUS
 DEFINITION Mus musculus clone RP24-178L2, WORKING DRAFT SEQUENCE, 43 unordered
 pieces.
 AC101793 185469 bp DNA linear HTG 21-AUG-2002
 VERSION AC101793.2 GI:22381529
 KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Birren,B., Nusbaum,C. and Lander,E.
 1 (bases 1 to 185469)
 2 (bases 1 to 185469)
 3 (bases 1 to 185469)
 4 (bases 1 to 185469)
 5 (bases 1 to 185469)
 6 (bases 1 to 185469)
 7 (bases 1 to 185469)
 8 (bases 1 to 185469)
 9 (bases 1 to 185469)
 10 (bases 1 to 185469)
 11 (bases 1 to 185469)
 12 (bases 1 to 185469)
 13 (bases 1 to 185469)
 14 (bases 1 to 185469)
 15 (bases 1 to 185469)
 16 (bases 1 to 185469)
 17 (bases 1 to 185469)
 18 (bases 1 to 185469)
 19 (bases 1 to 185469)
 20 (bases 1 to 185469)
 21 (bases 1 to 185469)
 22 (bases 1 to 185469)
 23 (bases 1 to 185469)
 24 (bases 1 to 185469)
 25 (bases 1 to 185469)
 26 (bases 1 to 185469)
 27 (bases 1 to 185469)
 28 (bases 1 to 185469)
 29 (bases 1 to 185469)
 30 (bases 1 to 185469)
 31 (bases 1 to 185469)
 32 (bases 1 to 185469)
 33 (bases 1 to 185469)
 34 (bases 1 to 185469)
 35 (bases 1 to 185469)
 36 (bases 1 to 185469)
 37 (bases 1 to 185469)
 38 (bases 1 to 185469)
 39 (bases 1 to 185469)
 40 (bases 1 to 185469)
 41 (bases 1 to 185469)
 42 (bases 1 to 185469)
 43 (bases 1 to 185469)
 44 (bases 1 to 185469)
 45 (bases 1 to 185469)
 46 (bases 1 to 185469)
 47 (bases 1 to 185469)
 48 (bases 1 to 185469)
 49 (bases 1 to 185469)
 50 (bases 1 to 185469)
 51 (bases 1 to 185469)
 52 (bases 1 to 185469)
 53 (bases 1 to 185469)
 54 (bases 1 to 185469)
 55 (bases 1 to 185469)
 56 (bases 1 to 185469)
 57 (bases 1 to 185469)
 58 (bases 1 to 185469)
 59 (bases 1 to 185469)
 60 (bases 1 to 185469)
 61 (bases 1 to 185469)
 62 (bases 1 to 185469)
 63 (bases 1 to 185469)
 64 (bases 1 to 185469)
 65 (bases 1 to 185469)
 66 (bases 1 to 185469)
 67 (bases 1 to 185469)
 68 (bases 1 to 185469)
 69 (bases 1 to 185469)
 70 (bases 1 to 185469)
 71 (bases 1 to 185469)
 72 (bases 1 to 185469)
 73 (bases 1 to 185469)
 74 (bases 1 to 185469)
 75 (bases 1 to 185469)
 76 (bases 1 to 185469)
 77 (bases 1 to 185469)
 78 (bases 1 to 185469)
 79 (bases 1 to 185469)
 80 (bases 1 to 185469)
 81 (bases 1 to 185469)
 82 (bases 1 to 185469)
 83 (bases 1 to 185469)
 84 (bases 1 to 185469)
 85 (bases 1 to 185469)
 86 (bases 1 to 185469)
 87 (bases 1 to 185469)
 88 (bases 1 to 185469)
 89 (bases 1 to 185469)
 90 (bases 1 to 185469)
 91 (bases 1 to 185469)
 92 (bases 1 to 185469)
 93 (bases 1 to 185469)
 94 (bases 1 to 185469)
 95 (bases 1 to 185469)
 96 (bases 1 to 185469)
 97 (bases 1 to 185469)
 98 (bases 1 to 185469)
 99 (bases 1 to 185469)
 100 (bases 1 to 185469)
 101 (bases 1 to 185469)
 102 (bases 1 to 185469)
 103 (bases 1 to 185469)
 104 (bases 1 to 185469)
 105 (bases 1 to 185469)
 106 (bases 1 to 185469)
 107 (bases 1 to 185469)
 108 (bases 1 to 185469)
 109 (bases 1 to 185469)
 110 (bases 1 to 185469)
 111 (bases 1 to 185469)
 112 (bases 1 to 185469)
 113 (bases 1 to 185469)
 114 (bases 1 to 185469)
 115 (bases 1 to 185469)
 116 (bases 1 to 185469)
 117 (bases 1 to 185469)
 118 (bases 1 to 185469)
 119 (bases 1 to 185469)
 120 (bases 1 to 185469)
 121 (bases 1 to 185469)
 122 (bases 1 to 185469)
 123 (bases 1 to 185469)
 124 (bases 1 to 185469)
 125 (bases 1 to 185469)
 126 (bases 1 to 185469)
 127 (bases 1 to 185469)
 128 (bases 1 to 185469)
 129 (bases 1 to 185469)
 130 (bases 1 to 185469)
 131 (bases 1 to 185469)
 132 (bases 1 to 185469)
 133 (bases 1 to 185469)
 134 (bases 1 to 185469)
 135 (bases 1 to 185469)
 136 (bases 1 to 185469)
 137 (bases 1 to 185469)
 138 (bases 1 to 185469)
 139 (bases 1 to 185469)
 140 (bases 1 to 185469)
 141 (bases 1 to 185469)
 142 (bases 1 to 185469)
 143 (bases 1 to 185469)
 144 (bases 1 to 185469)
 145 (bases 1 to 185469)
 146 (bases 1 to 185469)
 147 (bases 1 to 185469)
 148 (bases 1 to 185469)
 149 (bases 1 to 185469)
 150 (bases 1 to 185469)
 151 (bases 1 to 185469)
 152 (bases 1 to 185469)
 153 (bases 1 to 185469)
 154 (bases 1 to 185469)
 155 (bases 1 to 185469)
 156 (bases 1 to 185469)
 157 (bases 1 to 185469)
 158 (bases 1 to 185469)
 159 (bases 1 to 185469)
 160 (bases 1 to 185469)
 161 (bases 1 to 185469)
 162 (bases 1 to 185469)
 163 (bases 1 to 185469)
 164 (bases 1 to 185469)
 165 (bases 1 to 185469)
 166 (bases 1 to 185469)
 167 (bases 1 to 185469)
 168 (bases 1 to 185469)
 169 (bases 1 to 185469)
 170 (bases 1 to 185469)
 171 (bases 1 to 185469)
 172 (bases 1 to 185469)
 173 (bases 1 to 185469)
 174 (bases 1 to 185469)
 175 (bases 1 to 185469)
 176 (bases 1 to 185469)
 177 (bases 1 to 185469)
 178 (bases 1 to 185469)
 179 (bases 1 to 185469)
 180 (bases 1 to 185469)
 181 (bases 1 to 185469)
 182 (bases 1 to 185469)
 183 (bases 1 to 185469)
 184 (bases 1 to 185469)
 185 (bases 1 to 185469)
 186 (bases 1 to 185469)
 187 (bases 1 to 185469)
 188 (bases 1 to 185469)
 189 (bases 1 to 185469)
 190 (bases 1 to 185469)
 191 (bases 1 to 185469)
 192 (bases 1 to 185469)
 193 (bases 1 to 185469)
 194 (bases 1 to 185469)
 195 (bases 1 to 185469)
 196 (bases 1 to 185469)
 197 (bases 1 to 185469)
 198 (bases 1 to 185469)
 199 (bases 1 to 185469)
 200 (bases 1 to 185469)
 201 (bases 1 to 185469)
 202 (bases 1 to 185469)
 203 (bases 1 to 185469)
 204 (bases 1 to 185469)
 205 (bases 1 to 185469)
 206 (bases 1 to 185469)
 207 (bases 1 to 185469)
 208 (bases 1 to 185469)
 209 (bases 1 to 185469)
 210 (bases 1 to 185469)
 211 (bases 1 to 185469)
 212 (bases 1 to 185469)
 213 (bases 1 to 185469)
 214 (bases 1 to 185469)
 215 (bases 1 to 185469)
 216 (bases 1 to 185469)
 217 (bases 1 to 185469)
 218 (bases 1 to 185469)
 219 (bases 1 to 185469)
 220 (bases 1 to 185469)
 221 (bases 1 to 185469)
 222 (bases 1 to 185469)
 223 (bases 1 to 185469)
 224 (bases 1 to 185469)
 225 (bases 1 to 185469)
 226 (bases 1 to 185469)
 227 (bases 1 to 185469)
 228 (bases 1 to 185469)
 229 (bases 1 to 185469)
 230 (bases 1 to 185469)
 231 (bases 1 to 185469)
 232 (bases 1 to 185469)
 233 (bases 1 to 185469)
 234 (bases 1 to 185469)
 235 (bases 1 to 185469)
 236 (bases 1 to 185469)
 237 (bases 1 to 185469)
 238 (bases 1 to 185469)
 239 (bases 1 to 185469)
 240 (bases 1 to 185469)
 241 (bases 1 to 185469)
 242 (bases 1 to 185469)
 243 (bases 1 to 185469)
 244 (bases 1 to 185469)
 245 (bases 1 to 185469)
 246 (bases 1 to 185469)
 247 (bases 1 to 185469)
 248 (bases 1 to 185469)
 249 (bases 1 to 185469)
 250 (bases 1 to 185469)
 251 (bases 1 to 185469)
 252 (bases 1 to 185469)
 253 (bases 1 to 185469)
 254 (bases 1 to 185469)
 255 (bases 1 to 185469)
 256 (bases 1 to 185469)
 257 (bases 1 to 185469)
 258 (bases 1 to 185469)
 259 (bases 1 to 185469)
 260 (bases 1 to 185469)
 261 (bases 1 to 185469)
 262 (bases 1 to 185469)
 263 (bases 1 to 185469)
 264 (bases 1 to 185469)
 265 (bases 1 to 185469)
 266 (bases 1 to 185469)
 267 (bases 1 to 185469)
 268 (bases 1 to 185469)
 269 (bases 1 to 185469)
 270 (bases 1 to 185469)
 271 (bases 1 to 185469)
 272 (bases 1 to 185469)
 273 (bases 1 to 185469)
 274 (bases 1 to 185469)
 275 (bases 1 to 185469)
 276 (bases 1 to 185469)
 277 (bases 1 to 185469)
 278 (bases 1 to 185469)
 279 (bases 1 to 185469)
 280 (bases 1 to 185469)
 281 (bases 1 to 185469)
 282 (bases 1 to 185469)
 283 (bases 1 to 185469)
 284 (bases 1 to 185469)
 285 (bases 1 to 185469)
 286 (bases 1 to 185469)
 287 (bases 1 to 185469)
 288 (bases 1 to 185469)
 289 (bases 1 to 185469)
 290 (bases 1 to 185469)
 291 (bases 1 to 185469)
 292 (bases 1 to 185469)
 293 (bases 1 to 185469)
 294 (bases 1 to 185469)
 295 (bases 1 to 185469)
 296 (bases 1 to 185469)
 297 (bases 1 to 185469)
 298 (bases 1 to 185469)
 299 (bases 1 to 185469)
 300 (bases 1 to 185469)
 301 (bases 1 to 185469)
 302 (bases 1 to 185469)
 303 (bases 1 to 185469)
 304 (bases 1 to 185469)
 305 (bases 1 to 185469)
 306 (bases 1 to 185469)
 307 (bases 1 to 185469)
 308 (bases 1 to 185469)
 309 (bases 1 to 185469)
 310 (bases 1 to 185469)
 311 (bases 1 to 185469)
 312 (bases 1 to 185469)
 313 (bases 1 to 185469)
 314 (bases 1 to 185469)
 315 (bases 1 to 185469)
 316 (bases 1 to 185469)
 317 (bases 1 to 185469)
 318 (bases 1 to 185469)
 319 (bases 1 to 185469)
 320 (bases 1 to 185469)
 321 (bases 1 to 185469)
 322 (bases 1 to 185469)
 323 (bases 1 to 185469)
 324 (bases 1 to 185469)
 325 (bases 1 to 185469)
 326 (bases 1 to 185469)
 327 (bases 1 to 185469)
 328 (bases 1 to 185469)
 329 (bases 1 to 185469)
 330 (bases 1 to 185469)
 331 (bases 1 to 185469)
 332 (bases 1 to 185469)
 333 (bases 1 to 185469)
 334 (bases 1 to 185469)
 335 (bases 1 to 185469)
 336 (bases 1 to 185469)
 337 (bases 1 to 185469)
 338 (bases 1 to 185469)
 339 (bases 1 to 185469)
 340 (bases 1 to 185469)
 341 (bases 1 to 185469)
 342 (bases 1 to 185469)
 343 (bases 1 to 185469)
 344 (bases 1 to 185469)
 345 (bases 1 to 185469)
 346 (bases 1 to 185469)
 347 (bases 1 to 185469)
 348 (bases 1 to 185469)
 349 (bases 1 to 185469)
 350 (bases 1 to 185469)
 351 (bases 1 to 185469)
 352 (bases 1 to 185469)
 353 (bases 1 to 185469)
 354 (bases 1 to 185469)
 355 (bases 1 to 185469)
 356 (bases 1 to 185469)
 357 (bases 1 to 185469)
 358 (bases 1 to 185469)
 359 (bases 1 to 185469)
 360 (bases 1 to 185469)
 361 (bases 1 to 185469)
 362 (bases 1 to 185469)
 363 (bases 1 to 185469)
 364 (bases 1 to 185469)
 365 (bases 1 to 185469)
 366 (bases 1 to 185469)
 367 (bases 1 to 185469)
 368 (bases 1 to 185469)
 369 (bases 1 to 185469)
 370 (bases 1 to 185469)
 371 (bases 1 to 185469)
 372 (bases 1 to 185469)
 373 (bases 1 to 185469)
 374 (bases 1 to 185469)
 375 (bases 1 to 185469)
 376 (bases 1 to 185469)
 377 (bases 1 to 185469)
 378 (bases 1 to 185469)
 379 (bases 1 to 185469)
 380 (bases 1 to 185469)
 381 (bases 1 to 185469)
 382 (bases 1 to 185469)
 383 (bases 1 to 185469)
 384 (bases 1 to 185469)
 385 (bases 1 to 185469)
 386 (bases 1 to 185469)
 387 (bases 1 to 185469)
 388 (bases 1 to 185469)
 389 (bases 1 to 185469)
 390 (bases 1 to 185469)
 391 (bases 1 to 185469)
 392 (bases 1 to 185469)
 393 (bases 1 to 185469)
 394 (bases 1 to 185469)
 395 (bases 1 to 185469)
 396 (bases 1 to 185469)
 397 (bases 1 to 185469)
 398 (bases 1 to 185469)
 399 (bases 1 to 185469)
 400 (bases 1 to 185469)
 401 (bases 1 to 185469)
 402 (bases 1 to 185469)
 403 (bases 1 to 185469)
 404 (bases 1 to 185469)
 405 (bases 1 to 185469)
 406 (bases 1 to 185469)
 407 (bases 1 to 185469)
 408 (bases 1 to 185469)
 409 (bases 1 to 185469)
 410 (bases 1 to 185469)
 411 (bases 1 to 185469)
 412 (bases 1 to 185469)
 413 (bases 1 to 185469)
 414 (bases 1 to 185469)
 415 (bases 1 to 185469)
 416 (bases 1 to 185469)
 417 (bases 1 to 185469)
 418 (bases 1 to 185469)
 419 (bases 1 to 185469)
 420 (bases 1 to 185469)
 421 (bases 1 to 185469)
 422 (bases 1 to 185469)
 423 (bases 1 to 185469)
 424 (bases 1 to 185469)
 425 (bases 1 to 185469)
 426 (bases 1 to 185469)
 427 (bases 1 to 185469)
 428 (bases 1 to 185469)
 429 (bases 1 to 185469)
 430 (bases 1 to 185469)
 431 (bases 1 to 185469)
 432 (bases 1 to 185469)
 433 (bases 1 to 185469)
 434 (bases 1 to 185469)
 435 (bases 1 to 185469)
 436 (bases 1 to 185469)
 437 (bases 1 to 185469)
 438 (bases 1 to 185469)
 439 (bases 1 to 185469)
 440 (bases 1 to 185469)
 441 (bases 1 to 185469)
 442 (bases 1 to 185469)
 443 (bases 1 to 185469)
 444 (bases 1 to 185469)
 445 (bases 1 to 185469)
 446 (bases 1 to 185469)
 447 (bases 1 to 185469)
 448 (bases 1 to 185469)
 449 (bases 1 to 185469)
 450 (bases 1 to 185469)
 451 (bases 1 to 185469)
 452 (bases 1 to 185469)
 453 (bases 1 to 185469)
 454 (bases 1 to 185469)
 455 (bases 1 to 185469)
 456 (bases 1 to 185469)
 457 (bases 1 to 185469)
 458 (bases 1 to 185469)
 459 (bases 1 to 185469)
 460 (bases 1 to 185469)
 461 (bases 1 to 185469)
 462 (bases 1 to 185469)
 463 (bases 1 to 185469)
 464 (bases 1 to 185469)
 465 (bases 1 to 185469)
 466 (bases 1 to 185469)
 467 (bases 1 to 185469)
 468 (bases 1 to 185469)
 469 (bases 1 to 185469)
 470 (bases 1 to 185469)
 471 (bases 1 to 185469)
 472 (bases 1 to 185469)
 473 (bases 1 to 185469)
 474 (bases 1 to 185469)
 475 (bases 1 to 185469)
 476 (bases 1 to 185469)
 477 (bases 1 to 185469)
 478 (bases 1 to 185469)
 479 (bases 1 to 185469)
 480 (bases 1 to 185469)
 481 (bases 1 to 185469)
 482 (bases 1 to 185469)
 483 (bases 1 to 185469)
 484 (bases 1 to 185469)
 485 (bases 1 to 185469)
 486 (bases 1 to 185469)
 487 (bases 1 to 185469)
 488 (bases 1 to 185469)
 489 (bases 1 to 185469)
 490 (bases 1 to 185469)
 491 (bases 1 to 185469)
 492 (bases 1 to 185469)
 493 (bases 1 to 185469)
 494 (bases 1 to 185469)
 495 (bases 1 to 185469)
 496 (bases 1 to 185469)
 497 (bases 1 to 185469)
 498 (bases 1 to 185469)
 499 (bases 1 to 185469)
 500 (bases 1 to 185469)
 501 (bases 1 to 185469)
 502 (bases 1 to 185469)
 503 (bases 1 to 185469)
 504 (bases 1 to 185469)
 505 (bases 1 to 185469)
 506 (bases 1 to 185469)
 507 (bases 1 to 185469)
 508 (bases 1 to 185469)
 509 (bases 1 to 185469)
 510 (bases 1 to 185469)
 511 (bases 1 to 185469)
 512 (bases 1 to 185469)
 513 (bases 1 to 185469)
 514 (bases 1 to 185469)
 515 (bases 1 to 185469)
 516 (bases 1 to 185469)
 517 (bases 1 to 185469)
 518 (bases 1 to 185469)
 519 (bases 1 to 185469)
 520 (bases 1 to 185469)
 521 (bases 1 to 185469)
 522 (bases 1 to 185469)
 523 (bases 1 to 185469)
 524 (bases 1 to 185469)
 525 (bases 1 to 185469)
 526 (bases 1 to 185469)
 527 (bases 1 to 185469)
 528 (bases 1 to

*	184	1943:	gap of	100	bp
*	1944	2615:	contig of	672	bp in length
*	2616	2715:	gap of	100	bp
*	2716	3318:	contig of	603	bp in length
*	3319	3418:	gap of	100	bp
*	3419	4524:	contig of	1106	bp in length
*	4525	4624:	gap of	100	bp
*	4625	5485:	contig of	861	bp in length
*	5486	5585:	gap of	100	bp
*	5586	6384:	contig of	799	bp in length
*	6385	6484:	gap of	100	bp
*	6485	7162:	contig of	678	bp in length
*	7163	7262:	gap of	100	bp
*	7263	7456:	contig of	194	bp in length
*	7457	7556:	gap of	100	bp
*	7557	8160:	contig of	604	bp in length
*	8161	8260:	gap of	100	bp
*	8261	8941:	contig of	681	bp in length
*	8942	9041:	gap of	100	bp
*	9042	9922:	contig of	881	bp in length
*	9923	10022:	gap of	100	bp
*	10023	11459:	contig of	1437	bp in length
*	11460	11559:	gap of	100	bp
*	11560	12040:	contig of	481	bp in length
*	12041	12140:	gap of	100	bp
*	12141	13305:	contig of	115	bp in length
*	13306	13405:	gap of	100	bp
*	13406	14296:	contig of	891	bp in length
*	14297	14396:	gap of	100	bp
*	14397	15353:	contig of	957	bp in length
*	15394	15455:	gap of	100	bp
*	15454	16520:	contig of	1667	bp in length
*	16521	16620:	gap of	100	bp
*	16621	18291:	contig of	1671	bp in length
*	18292	18391:	gap of	100	bp
*	18392	19794:	contig of	1403	bp in length
*	19795	19894:	gap of	100	bp
*	19895	21659:	contig of	1765	bp in length
*	21660	21759:	gap of	100	bp
*	21760	23729:	contig of	1970	bp in length
*	23730	23829:	gap of	100	bp
*	23830	25103:	contig of	1274	bp in length
*	25104	25205:	gap of	100	bp
*	25204	27230:	contig of	2027	bp in length
*	27231	27330:	gap of	100	bp
*	27331	28923:	contig of	2533	bp in length
*	28924	30023:	gap of	100	bp
*	30024	33248:	contig of	2225	bp in length
*	33249	33348:	gap of	100	bp
*	33349	35145:	contig of	2797	bp in length
*	35146	35245:	gap of	100	bp
*	35246	38595:	contig of	3350	bp in length
*	38596	38695:	gap of	100	bp
*	38696	41857:	contig of	3162	bp in length
*	41858	41957:	gap of	100	bp
*	41958	45734:	contig of	3777	bp in length
*	45735	45834:	gap of	100	bp
*	45835	50585:	contig of	4751	bp in length
*	50586	50685:	gap of	100	bp
*	50686	59553:	contig of	7847	bp in length
*	59563	58632:	gap of	100	bp
*	58633	64513:	contig of	5881	bp in length
*	64514	64613:	gap of	100	bp
*	64614	72116:	contig of	7503	bp in length
*	72117	72216:	gap of	100	bp
*	72217	79497:	contig of	7261	bp in length
*	79498	79597:	gap of	100	bp
*	79598	89233:	contig of	9642	bp in length
*	89240	89339:	gap of	100	bp
*	89340	100740:	contig of	11401	bp in length
*	100741	100840:	gap of	100	bp
*	100841	112859:	contig of	12019	bp in length
*	112860	112959:	gap of	100	bp

[illegible]

Db 152459 GGTTCATGAAATTCACATCCAGAACTGCCAGAAATTTGAACCCCTGATTAAGGAAAC 152400
 Oy 269 HisArgPheIysAsnMetValIleValThrThrThrGluCysLeuArgHisIleArg 288
 Db 152399 CATCCCTTCACAAACATGGTCTATTGTGCACACACACAGGATGGCTTGAGCATATACAGA 152340
 Oy 289 GluPheGlyAlaLeuThrAlaGluValGlyAspMetThrGluAspSerAlaGlnAlaLeu 308
 Db 152339 CATGTGGGGCCCTGACTCTCCAGAGTGGGAGATATGACCGAAGACAGATGCCAAAGATCTC 152280
 Oy 309 IleArgGluValIleLeuGluLeuAlaGluGlyLeuLeuGluGlnIleGlnIysSer 328
 Db 152279 ATCGAGGACGAGTGTGTGCTCTACATGAGTGAACGCTGTGGGCCCAATTCACAGAGTCC 152220
 Oy 329 ArgCysLeuArgAsnLeuMetLysThrProLeuPheValIleIleThrCysAlaIleGln 348
 Db 152219 AGTGCCTGAGAAATCTGTATGAAGACCCCTCTCTGCTGTGATACACGCTGCATTTCCAG 152160
 Oy 349 MetGlyGluSerGluPheHisSerHisThrGlnThrThrLeuPheHisThrPheTyrAsp 368
 Db 152159 ATGGGCAGACAGAAATTCACAACTCACACCAACCATGCTGTCCAAACCTTTCACGAC 152100
 Oy 369 LeuLeuIleGlnIysAsnLysHisLysGlyValAlaIleSerAspPheIleArg 388
 Db 152099 CTCTGATATACAGAAACAGCCACAGATATAGAGGTGAGCTTCAGGTATTTTGGCAGG 152040
 Oy 389 SerLeuAspHisCysGlyAspLeuAlaLeuGluGlyValPheSerHisLysPheAspPhe 408
 Db 152039 AGCCTAGACTACTGTGAGACCTGGCCCTCAGAGGTGTGTTGCCACAAATTTGATTTT 151980
 Oy 409 GluLeuGlnAspValSerSerValAsnGluAspValLeuLeuThrThrGlyLeuLys 428
 Db 151979 GAACCCGAGCATGGGTCCAGCATGAGACGAGCTGTGTCAGATAGGCTCTCTGT 151920
 Oy 429 LysThrThrAlaGluArgPheLysProLysTyrLysPhePheHisLysSerPheGlnGlu 448
 Db 151919 AGTACACAGCTCAGAGGTGAAGCCACGTAATTTTTCATTAATTCATTAATTCATTAATTC 151860
 Oy 449 TyrThrAlaGlyArgArgLeuSerSerLeuLeuThrSerHisGluProGluGluValThr 468
 Db 151859 TACACGGCAGGTGGGAGACTGACAGTTTGCTGACGTCCAAAGACCCAGAGAGGTGAGC 151800
 Oy 469 LysGlyAsnGlyTyrLeuGlnLysMetValSerIleSerAspIleThrSerThrTyrSer 488
 Db 151799 AAAGGACAGCTACTTAACAAATGTGTTTCATCTCTGACATCATCATCCCTATATGTC 151740
 Oy 489 SerLeuLeuArgTyrThrCysGlySerSerValGluAlaThrArgAlaValMetLysHis 508
 Db 151739 AATTCGCTCTCTACACGCTGTGGTCTCCACAGAAACAGGAGGCGCTCATGAGGCAC 151680
 Oy 509 LeuAlaAlaValTyrGlnHisGlyCysLeuLeuGlyLeuSerIleAlaLysArgProLeu 528
 Db 151679 CTTCGAATGTGTTATCAGACGCGACCTCAACAAGACCTTTCAGTCAACAAAGGCTCTTC 151620
 Oy 529 TTPArgGlnGluSerLeuGlnSerValLysAsnThrThrGluGlnGluIleLeuLysAla 548
 Db 151619 TGGAGGACAGAAATTCATCCAGAGTGTGAATAATACACACGACCAAGATGTTTGAAGGC 151560
 Oy 549 IleAsnIleAsnSerPheValGluCysGlyIleHisLeuTyrGlnGluSerThrSerLys 568
 Db 151559 ATCAATGTAAATTCCTCTCTGTAAGTGTGGCATCAATTTGTTCTCAGAGAGTATGCTTAA 151500
 Oy 569 SerAlaLeuSerGlnGluPheGluAlaPhePheGlnGlyLysSerLeuTyrIleAsnSer 588
 Db 151499 TCAGACCTGAGCCAGAAATTTGAAGCTTTCTTCAAGTAAAGTTTATACATCAACTCA 151440
 Oy 589 GlyAsnIleProAspTyrLeuPheAspPhePheGluHisLeuProAsnCysAlaSerAla 608
 Db 151439 GAGAACATCCCTGACTATTATTTACTTCTTGAATCTTGCCTTAATGTTCCAAAGCGCA 151380
 Oy 609 LeuAspPheIleLysLeuAspPheTyrGlyAlaMetAlaSerThrGluLysAlaIle 628
 Db 151379 TTGGACTTCGTGAAGTGGATTTCATATGAAGAGCTACAGACTCACAGGACAAAGGCGAGAA 151320

Oy 629 GluAspThrGlyIleIleHisMetGluGluAlaProGluThrTyrIleProSerArgAla 648
 Db 151319 GAGAAATGCCCTCGAGATTCCACACAGAGGCGCTCAGAAACCTACATTCGCCCCAGGGCT 151260
 Oy 649 ValSerLeuPhePheAsnTrpLysGlnGluPheArgThrLeuGluValThrLeuArgAsp 668
 Db 151259 GTGTCTTGTCTTCCAACTGGAGCAGAAATTCAGAACTCTAGAGTCACTCCGAAAT 151200
 Oy 669 PheSerLysLeuAsnLysGluAspIleThrTyrLeuGlyLysIlePheSerSerAlaThr 688
 Db 151199 ATTAAAGTTGTAATAGCAGATATCAATATCTGGGGAGATATTTAGCTTCCACC 151140
 Oy 689 SerLeuArgLeuGlnIleLysArgCysAlaGlyValAlaGlySerLeuSerLeuValLeu 708
 Db 151139 AACCTCCGGCTCATATCAGAGATGTGAGCATGCGTGGAGAACTCAGCTCACTCTC 151080
 Oy 709 SerThrCysLysAsnIleTyrSerLeuMetValGluAlaSerProLeuThrIleGluAsp 728
 Db 151079 AGAACCTCAGAAACATGCATACCTCATGTGGAGAGCCAGTCCCTCACACGATGAC 151020
 Oy 729 GluArgHisIleThrSerValThrAsnLeuLysThrLeuSerIleHisAspLeuGlnAsn 748
 Db 151019 GAACAGTACATCATCTGTGTGACAGGCTCCAGAACTTAAGTATTCACCGCTTGCACACT 150960
 Oy 749 GlnArgLeuProGly 753
 Db 150959 CAACAGCTGCCAGGT 150945
 RESULT 11
 LOCUS IR2005417 1355 bp mRNA linear PRI 16-JUL-2000
 DEFINITION Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 2005417.
 ACCESSION AL89934
 VERSION AL389934.1 GI:9367839
 KEYWORDS FLI-CDNA.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1355)
 AUTHORS Aufiray,C., Ansoerge,M., Ballabio,A., Estivill,X., Gibson,K.,
 Lehnach,H., Pouska,A. and Lundeberg,J.
 TITLE The European IMAGE consortium for integrated Molecular analysis of
 human gene transcripts
 JOURNAL unpublished
 REFERENCE 2 (bases 1 to 1355)
 AUTHORS Pluvinet,R., Estivill,X., Escarcelier,M. and Sumoy,L.
 TITLE Direct Submission
 JOURNAL Submitted (15-JUL-2000) Dept. Genetica Molecular, Institut de
 Recerca Oncologica (IRO), Hospital Duran i Reynals, Av. Gran Via
 s/n Km 2,7 L'Hospitalet de Llobregat, 08907 Barcelona, Catalunya,
 SPAIN. Tel: ++34-93-260-7775 Fax: ++34-93-260-7776 WWW site:
 http://www.iro.es e-mail enquiries: lsunoy@iro.es
 COMMENT
 EURO-IMAGE Consortium Contact: Aufiray C
 CNRS UPR 420 - Genetique Moleculaire et Biologie du Developpement
 IFR 1221 - Rue Guy Moquet 19, Batiment G - BP 8
 94801 Villejuif Cedex, FRANCE
 Tel: ++33-1-49 58 34 98
 Fax: ++33-1-49 58 35 09
 e-mail: aufiray@infobiogen.fr
 This clone is available royalty-free through IMAGE Consortium
 Distributors.
 IMPORTANT: This sequence represents the full insert of this IMAGE
 cDNA clone. No attempt has been made to verify whether this
 corresponds to the full-length of the original mRNA from which it
 was derived.
 Location/Qualifiers
 1..1355
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="12"
 /map="2p21-p22"

FEATURES

source

/clone="IMAGE cdna clone 2005417"
/clone.lib="NCI_GCAP_Pan1"
<1..1321
/codon_start=2
/product="hypothetical protein, weakly similar to
(AF102871) neuronal apoptosis inhibitory protein 2 [mus
musculus]"
/protein_id="CAB97523.1"
/db_xref="GI:9367840"
/translation="INSGNITPDYLFDFEHLPCNSALIDFTKIDFGGAMASWEKAE
DTGIIHMEAPETIIPRAVSLFNMKQEPFLLEVTLDSEFKLNKQDRIYLGKIFSSA
TSLRIQKRCGAVSGSLVSTCKNITSLVAVSPLTIEDERHITSYNNKTLISD
LONRLPGGLDSGLNKLNTKLTIMDNIKMNEDEAIKLAEGIKNKKMLPFLTSLD
IGEGNDYIVKSLSEPDLEIOLVSCSLSNVYSKIIAONHNLYKSLIDLSERYLE
KQGNDAIHELIDRMNVLEOLTAIIMPCCDYOSKSLKHEEYPOLYKIGKMMRL
TDTERTIIGAFEGFNPKLNPKFOQLNLAGRVSDDGLAMGVFENIKQIVTFDFSTKEF
LPDPALVKLSQVSKLFTLQEARLVGMQFDDDLVITGAFLVTA"

BASE COUNT 416 a 265 c 312 g 362 t
ORIGIN

Alignment Scores:
Pred. No.: 0 Length: 1355
Score: 2300.00 Matches: 438
Percent Similarity: 99.77% Conservative: 0
Best Local Similarity: 99.77% Mismatches: 1
Query Match: 42.13% Indels: 0
DB: 9 Gaps: 0

US-09-697-089-2 (1-1024) x IR2005417 (1-1355)

QY 586 ILEASNSERGLYASNIIEPROASPTRYLEUPHEASPPHEGLNHISLEUPROASNCYS 605
|||||
DB 2 ATCACTCGGAGAACATCCCGCATTAATTGACTTTTGACATTTGCCCAATTTGT 61
QY 606 AIAASERALALEUASPPHEILEYLSLEUASPPHETRYGLYALAMETALASERTPGIU 625
62 GCAGAGCTCTGAGACTTCATTAACATGAGCTTTTATGGGGAGCTATGGCTTCATGGAA 121
QY 626 LYSALALAGLUAAPTHRCILYGLYLHISMETGLUGLUALAPROGLUHTHYRTLEPRO 645
|||||
DB 122 AAGCGTGCAGAGACACAGAGTGAATCCACATGGAAGAGGCCCCAGAAAACCTAACATTTCCC 181
QY 646 SERATGALALAVASERLEUPHEASNTPLYSGLINGLAPHEARTHREUGLUALTHR 665
182 ACAGAGGCGCTATCTTTGTTCTTCACTGGAAGCAGGAATTAAGAGCTTGAGAGCTGACA 241
QY 666 LEUATGASPPHESERLYSLEUASNPYSGLIASPIIERTHYRLEUGLYLSIIEPSESER 685
242 CTCGGGATTTACAGCAAGTTGAATAAGCAAGATATCAGATATCTGGGAAATATTCAAC 301
QY 686 SERALATHSERLEUARYLEUGLNLIELYSARGYSALIGLYVALAGLYSERLEUSER 705
302 TCTGGCACAAAGCTCAGGCTGCAAAATAAAGATGTGCTGCTGGAAGCCCTCACT 361
QY 706 LEUVALLEUSERTHRCYLSYASNIIEYRSEIEMETVALGILALASERPROLEUTHR 725
362 TTGGTCTTCAGCACTCTTAAGACATTTATCTCTCATGCTGGAAGCCAGTCCCTCCAC 421
QY 726 ILEGUASPGLUARGHISILETHSERVALTHRASLEULYSYTHREUSERILEHISASP 745
422 ATAGAAGATGAGAGCACATCATCTGTACAAACCTGAACACCTTGATTTTCATGAC 481
QY 746 LEUGLNASNGLNAIRGLEUPROGLYLYLEUTHRASPSERLEUGLYASNLLEULYSANLEU 765
482 CTACAGAAATCAACGGCTCGCGGTCTGACTGACAGCTTGGAACCTTGGAACACCTT 541
QY 766 THRLYSLEUILEMETASPSNIIELYSMETASNGLUGLUALALLEYLSLEULAGIU 785
542 ACAGAGCTCATATGATATACATTAAGATGAAGATGCTATTAACCTAGCTGAA 601
QY 786 GLYLEULYSANLEULYSLYSMETCYSEUPHENISLEUTHRHISLEUSERASPILEGY 805
602 GGCCTGAAAACCTGAGAAAGATGTGTTATTTCAATTTGACCCACCTTGCTCAGATTTGGA 661

QY 806 GIUGLYMETASPTRYLLEVALLYSSERLEUSERSERGLUPROCYASPIREUGLUILE 825
|||||
DB 662 GAGGGAATGATTACTACTCAAGTCTGTGTAAGGAAGCCCTGATCCCTTAAGAAATTT 721
QY 826 GINLEUVALSERCYSCYSEUSERALASNALAVALLYSILEUVALAGLNASLEUHHIS 845
722 CAATTAGTCTCGTCTGCTGTCTGCAATTCAGATGAAGTAAATCTTACGATCTTCC 781
QY 846 ASNLLEUVALLYSLEUSERILLEUASPLEUSERGLUASNTYRLEUGLULYSASPILYASN 865
782 AATTGGCTCAAACTGAGCATTTCTGTATATCAGAAAATTAACCTGGAAGAAATGGAAT 841
QY 866 GUUALALEHHISGILUULEUASPARGMETASNVALLUGLNULEUTHRALLEUMET 885
842 GAAGCTTCATGAACTGATACGACAGATGAACGTCGTAGAACGCTCACCCGACTGATG 901
QY 886 LEUPROTPRGLYCYASAPVALGNGLYSERLEUSERSERLEUULYSIISLEUGLUGIU 905
902 CTGCCCTGGGGCTGTGACGTGCAAGCAGCCTGAGCAGCCTGTGAAACATTTGGAGGAG 961
QY 906 VALPROGLINLEUVALLYSLEUGLYLEULYSANTPARGLEUTHRASPHRCILUEARG 925
962 GTCCCAACACTGCTCAAGCTTGGAAGAACTGGAGACTCAGATACAGAGATTAGA 1021
QY 926 ILEUUGLYALAPHEPHEGLYLSASNPLOULYSASPHGLINGLINSLEUVALA 945
1022 ATTTAGGTGCTATTTTGGAAAGACCTCTGAAAACCTTCAGCAGATTTGGGCG 1081
QY 946 GLYASNARGVALSERSEASPIGLYTRPLEUALAPHEMGLYVALPHEGLUASNLLEULYS 965
1082 GGAATCGTGTGACGATGATGATGCTTCCCTCATGGGTATTTAGAAATCTTAG 1141
QY 966 GINLEUVALPHEPHEASPPHESERTHYRGLUPHELEUPROASPROALAEUVALARG 985
1142 CAATTAGTGTTTTGGACTTACTATAAGATTTCTACGTGATCCAGCATTAAGCAGA 1201
QY 986 LYSLEUSERGLYVALLEUSERLYSLEUTHRPHLEUGLINGLUALARGLEUVALGITYTP 1005
1202 AACTTACGCCAAGTGTATCCAAAGTTAACTTTTGTGCAAGAGCTAGGCTTGTGGGTGG 1261
QY 1006 GINPHEASPPASPPASPLEUSERVALIETHRGYALAPHELYSLEUVALTHRALA 1024
DB 1262 CAATTGATGATGATGATCTGATTTATACAGGTGCTTTTAACTACTACTGCT 1318

RESULT 12
AX318174 891 bp DNA linear PAT 14-DEC-2001
LOCUS AX318174
DEFINITION Sequence 179 from Patent WO0190156.
ACCESSION AX318174
VERSION AX318174.1 GI:17900865
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Reed,J.C., Plo,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,
Oliveira,Y.A., Hayashi,H. and Pawlowski,K.
CARD domain containing polypeptides, encoding nucleic acids, and
methods of use
JOURNAL Patent: WO 0190156-A 179 29-NOV-2001.
The Burnham Institute (US)
LOCATION/Qualifiers
1..891
/organism="Homo sapiens"
/db_xref="taxon:9606"
<1..>891
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD19350.1"
/db_xref="GI:17900866"
/translation="LQSPCIIEGSESGKSTLLQRIAMWMSGKCAITKRFVFFLR

LSRAOGLFETICDLDIPGTIRKOTFMAMLTKEORVLEFLDGYNEKRONCEIE
ALLREHFRKNMIVTITTEICIRHIFROFGLATAVGMEDESNALREVILKELAG
LLIOIKSRCLRNIMKTPLPVITICAIOMKESSEHSTOTTLPTFPDLIOKRRKH
KGVASDFIRSLDRDLALBGVFSHFDELODVSSVEDVLLTTLCKTYAQRK
PKYFEFKRSQDEYTAGRRSS"

BASE COUNT 237 a 228 c 217 g 209 t
ORIGIN

Alignment Scores:
Pred. No.: 3.77e-234 Length: 891
Score: 1598.00 Matches: 296
Percent Similarity: 99.66% Conservative: 0
Best Local Similarity: 99.66% Mismatches: 1
Query Match: 29.27% Indels: 0
DB: Gaps: 0

US-09-697-089-2 (1-1024) x AX318174 (1-891)

QY 161 LeuGlnSerProCysIleIleGlnGlyuSerGlyGlySerThrLeuGln 180
DB 1 CTTCAGAGCCCTGCATCATTTGAAGGGAACTGGCAAGCAAGTCCACTCTGTCAG 60
QY 181 ArgIleAlaMetLeuThrGlySerGlyCysLysAlaLeuThrLysPheLysVal 200
DB 61 CGCATGGCCATGCTCTGGGGCTCCGAAAGTGCAGGCTCTGACCAAGTCAAAATTCGTC 120
QY 201 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 220
DB 121 TTCTTCCCTCCGCTCAGAGAGGCCAGGGTGACTTTTGAACCCCTCTGTGATCACTC 180
QY 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 240
DB 181 CTGCATATACCTGGCAGCAATCAGCAAGACATTCATGGCCATGCTGTAAGCTGCGG 240
QY 241 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 260
DB 241 CAGAGGGTCTTTTCTTCTTGATGGCTACAAATGAATTCAGAGCCCAAGCTGCCAGAA 300
QY 261 IleGlnAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr 280
DB 301 ATCGAAGCCCGATTAAGAAAGAAACACGCGCTTCAAGAACATGTGATGTCACCACTAC 360
QY 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300
DB 361 ACTGAGTCCCTGAGGACACATACGCGAGTTGTGCTCCAGCTGAGAGTGGGGATATG 420
QY 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGlnGly 320
DB 421 ACAGAAACAGGCGCCAGGCTCTCATCCGAGAGTGTGATCAAGAGCTGTGTAAGGC 480
QY 321 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340
DB 481 TTGTGTGTCCTCAAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGCCCTCTCTT 540
QY 341 ValValIleThrCysAlaIleGlnMetGlyuSerGluPheHisSerHisThrGlnThr 360
DB 541 GTGTCATCAGCTGTGCATCCAGATGGGTGAAGTGAAGTTCACCTCCACACACAACA 600
QY 361 ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGly 380
DB 601 ACGGTGTTCACCTCTTATGATCTGTGATACAGAAACAAACACAAACATTAAGGT 660
QY 381 ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGlnGly 400
DB 661 GTGGGTGCAAGTGAATTCATTCGAGCTGAGCCACCTGGAGAGACTGCTGTGAGGGT 720
QY 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420
DB 721 GTGTTCCTCCACAAAGTTGATTTCGAAGTGCAGATGTGTCAGAGGTGAATGAGATGTC 780
QY 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnAsnArgPheLysProLysTyrLys 440
DB 781 CTGCTGACAACTGGGCTCTCTGTAAATATACAGCTCAAAAGTTCAAGCCAAAGTATAAA 840

QY 441 PhePheHisLysSerPheGlnGluThrThrAlaGlyArgArgLeuSer 457
DB 841 TTCTTCAAGATCATTCACAGAGTACACAGACAGCAAGACTCAGAGT 891

RESULT 13
AX318093 1395 bp DNA Linear PAT 14-DEC-2001
LOCUS
DEFINITION Sequence 98 from Patent WO0190156.
ACCESSION AX318093
VERSION AX318093.1 GI:17900822
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Reed, J.C., Plo, F.F., Godzik, A., Stehlik, C., Damiano, J.S., Lee, S.H.,
Oliveira, V.A., Hayashi, H., and Pawlowski, K.
CARD domain containing polypeptides, encoding nucleic acids, and
methods of use
Patent: WO 0190156-A 98 29-NOV-2001;
The Burnham Institute (US)

JOURNAL
The Burnham Institute (US)
FEATURES
source
1. .1395
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
277-1356
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD19341.1"
/db_xref="GI:17900823"
/translation="MNFIRKDSRALIQRMGVTYIKOTDDLFYNNVLRREVNILCE
KVEDARAGIIHMTIKKGSFSCNLFKSLKEMNYPFLDIDNGSLDSGNLTK
LINDNITKANEDEAKIKLEGLKLNKMLFHLTHSDIGEBMDYVKSLSSEPDDEI
OLVSCISANAVKILAOHLNHLVLTSLDISENLEKGDGALHELIDRNKVLQQLTA
LMLPWGCDVQGSLSLLKHLLEVPQLVKGLKMWRLDTDTIRLGAFGKNPLKNVQ
LNLAGNRVSSDGMWLAEMFVGENLKQLVFPFSTKEFLPDPALVRLKISQVLSKLTFOE
ARLVGMOFDDDDLSVIRGAFKLVYA"

BASE COUNT 436 a 248 c 327 g 384 t
ORIGIN

Alignment Scores:
Pred. No.: 2.88e-207 Length: 1395
Score: 1424.00 Matches: 271
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.63% Mismatches: 0
Query Match: 26.09% Indels: 0
DB: Gaps: 0

US-09-697-089-2 (1-1024) x AX318093 (1-1395)

QY 753 GlyGlyLeuThrAspSerLeuGlyAsnLeuLysAsnLeuThrLysLeuIleMetAspAsn 772
DB 538 AGTGGTCTGACTGACAGCGCTTGGTAACTTGAAGACCTTACAAAGCTCATATGAGATAC 597
QY 773 IleLysMetAsnGluGlnAspAlaIleLysLeuAlaGlnGlyLeuLysAsnLeuLysLys 792
DB 598 ATAAAGATGATGAAAGAGATGCTTAAACTAGCTGAAGGCGCTTAATAAAGCTGAAGAG 657
QY 793 MetCysLeuPheHisLeuThrHisLeuSerAspIleGlyGlnGlyMetAspTyrIleVal 812
DB 658 ATGTGTTATTTCATTTGACCCACTTGTGTCATTTGAGAAGGGAATGATACATAGTTC 717
QY 813 LysSerLeuSerSerGluProCysAspLeuGlnGluIleGlnLeuValSerCysCysLeu 832
DB 718 AAGTCTGTCAAGGAACCCGTGACCTTGAAGAAATTCATTAATGATGCTGCTGCTTG 777
QY 833 SerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuValLysLeuSerIle 852
DB 778 TCTGCAAAATGCAAGTAAATCTTAGCTCAGAAATCTTCAATTTGGTAAAGTGAAGCTT 837
QY 853 LeuAspLeuSerGluAsnTyrLeuGlnLysAspGlyAsnGlnAlaLeuHisGluLeuIle 872

|||||
Db 838 CTTGATTTATCAGAAATTTACTCGAAAAAGATGAAATGAAGCTCTTCATGACATGCATC 897
QY 873 ASPARGMETASNVALLLEUGLNLNLEUTHRALALEUMETLEUPROTPGLCYCASPVAL 892
Db 898 GACAGGATGAAAGCTCTGAGAACAGCTCACCGCAGTGCCTCGGGGCTGTGACGTG 957
QY 893 GINGLYSERLEUSERSERLEULEUYSHSLEUGLNUVALPROGLINLEUVALLYSLEU 912
Db 958 CAAGGACGCTGAGCAGCCTGTGAAACATTTGGAGAGAGTCCCACTGCTCAAGCTT 1017
QY 913 GLYLEULYSASNTRPARGLEUTHRASPTHRLGUILLEARGILEULEUGLYALAPHEPHEGLY 932
Db 1018 GGGTTGAAAAAAGCTGAGACTACAGATACAGAGATTAGAAATTTTAGTTCATTTTGGGA 1077
QY 933 LYSASNPROLEULYSASNPHENGLINLEUASNLEUALAGLYASNARYVALSERSERASP 952
Db 1078 AAGAACCCCTGCGAAAAACTTCCAGCAGTTGGAATTTGGCGGGAATCGTCTGAGCAGTGAT 1137
QY 953 GLYTRPLEUALAPHEMETGLYVALPHEGUASNLEULYSGLINLEUVALPHEPHEASPHPE 972
Db 1138 GGATGGCTTGCCCTTCATGGGTATTTGAGAACTTAAACCAATTAAGTGTTTTGAAGCTT 1197
QY 973 SERTHRLYSGLUPHELEUPROASPPROALALEUVALARGLYSLEUSERGLINALLEUSER 992
Db 1198 AGTACTAAAGAATTTCTACTGATCCAGCATAGTCAGAAAACTTAGCCAACTGTTATCC 1257
QY 993 LYSLEUTHRPHLEUGLNUALARGLEUVALGLYTPGLINPHEASPPASPSAPSPLEU 1012
Db 1258 AAGTTAACTTTCTGCAAGAACCTGAGGCTTGTGGTGCAATTTGATGATGATGATCTC 1317
QY 1013 SERTVALLETHRGLYALAPHELYSLEUVALTHRALA 1024
Db 1318 AGTGTTATTACAGGTCTTTTAACTAGTAACTGCT 1353
RESULT 14
AY027788
LOCUS Homo sapiens CLANB (CLANL) mRNA, complete cds.
DEFINITION
ACCESSION AY027788
VERSION AY027788.1 GI:14324114
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1395)
AUTHORS Damiano,J.S., Stehlik,C., Plo,F., Godzik,A. and Reed,J.C.
TITLE Clan, a novel human ced-4-like gene
JOURNAL Genomics 75 (1-3), 77-83 (2001)
MEDLINE 21365712
PUBMED 11472070
REFERENCE 2 (bases 1 to 1395)
AUTHORS Stehlik,C., Damiano,J.S., Plo,F., Godzik,A. and Reed,J.C.
TITLE Direct Submision
JOURNAL Submitted (21-FEB-2001) Program on Apoptosis and Cell Death
Research, The Burnham Institute, 10901 North Torrey Pines Road, La
Jolla, CA 92037, USA
FEATURES
source
1..1395
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/map="2p22-p21"
/tissue_type="lung"
1..1395
/gene="CLANL"
/gene="CLANL"
277..1356
/note="alternatively spliced; similar to Ced-4"
/codon_start=1
/product="CLANB"
/protein_id="AAK14777.1"

/db_xref="GI:14324115"
/translation="MNFKIDMSRLIOMGNTVIKOITDLEFVNVLNREVNITICE
KVEDDAARGITIHMLIKKSESQNFLEKRWNYPIKODLNGSGIDPISGLNLIK
LIMNDIKNEDAIKLAGLKNLKKMCFHETHSHDISEGNDIYKSLSSPCDIEI
OLVSCSLANAVKILIAONLHNLVKLSITLIDSENYLEKGNLEHLIDRWVLDQTA
LMLPGCDVOGSLSLKHELEVPOLVGLKGMNLTETRIILGAFGKNPLKRFQ
LNLGNRVSDGWLAFMGVFENLKOIVFEFDSFEFLDPALVRKLSOVLKTFIQE
ARLVGMODDDDLVITGAFKLVTN"
BASE COUNT 436 a 248 c 327 g 384 t
ORIGIN
Alignment Scores:
Pred. No.: 2,88e-207 Length: 1395
Score: 1424.00 Matches: 271
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.63% Mismatches: 0
Query Match: 26.09% Indels: 0
Gaps: 0
US-09-697-089-2 (1-1024) x AY027788 (1-1395)
QY 753 GLYGLYLEUTHRASPSERLEUGLYASNLEULYSASNLEUTHRLYSLEUILMECLASPAN 772
Db 538 AGTGGCTGACTGACAGAGCTTGGGTAACTTGAAGAACCTTACAAAGCTCATATGATGAAC 597
QY 773 ILEYSMETASNGLUGLNASPALAILEYLSLEUALAGLUGLYLEULYSASNLEULYSYS 792
Db 598 ATAAAGATGAATGAAGAAATCTATAAACAGCTGAAGGCTGAAACCTGGAAGAAAG 657
QY 793 METCYLSLEUPHEHISLEUTHRHISLEUSERASPILEGLYGLYMETASPTYRILEVAL 812
Db 658 ATGTGTTATTTCATTTTGAACCCACTTGTCTGACATTGGAGAGGAATGGATTACATAGTC 717
QY 813 LYSSEUSERSERGLUPROCYSAPSPLEUGLNUILEGLINLEUVALSERCYSLEU 832
Db 718 AAGTCTGTCTCAAGTGAACCCCTGTGACCTTGAAGAAATCAATTAAGTCTGCTGCTTG 777
QY 833 SERTALAASNLVALLYSLEULEUALAGINASNLEUHSASNLEUVALLYSLEUSERILE 852
Db 778 TCTGCAAAATGCAAGTAAAACTCTACCTGAAATCTTCAAAATTTGGTCAAACTGAGCAAT 837
QY 853 LEUASPLEUSERSERGLUASNTRYRLEUGLULYSASPGLYASNGUALALEUHSGLULEUILE 872
Db 838 CTTGATTTATCAGAAATTTACTGGAAGAAAGATGGAAGATGAGCTTTCATGATCACTGATC 897
QY 873 ASPARGMETASNVALLLEUGLNLNLEUTHRALALEUMETLEUPROTPGLCYCASPVAL 892
Db 898 GACAGGATGAAAGCTCTGAGAACAGCTCACCGCAGTGCCTCGGGGCTGTGACGTG 957
QY 893 GINGLYSERLEUSERSERLEULEUYSHSLEUGLNUVALPROGLINLEUVALLYSLEU 912
Db 958 CAAGGACGCTGAGCAGCCTGTGAAACATTTGGAGAGAGTCCCACTGCTCAAGCTT 1017
QY 913 GLYLEULYSASNTRPARGLEUTHRASPTHRLGUILLEARGILEULEUGLYALAPHEPHEGLY 932
Db 1018 GGGTTGAAAAAAGCTGAGACTACAGATACAGAGATTAGAAATTTTAGTTCATTTTGGGA 1077
QY 933 LYSASNPROLEULYSASNPHENGLINLEUASNLEUALAGLYASNARYVALSERSERASP 952
Db 1078 AAGAACCCCTGCGAAAAACTTCCAGCAGTTGGAATTTGGCGGGAATCGTCTGAGCAGTGAT 1137
QY 953 GLYTRPLEUALAPHEMETGLYVALPHEGUASNLEULYSGLINLEUVALPHEPHEASPHPE 972
Db 1138 GGATGGCTTGCCCTTCATGGGTATTTGAGAACTTAAACCAATTAAGTGTTTTGAAGCTT 1197
QY 973 SERTHRLYSGLUPHELEUPROASPPROALALEUVALARGLYSLEUSERGLINALLEUSER 992
Db 1198 AGTACTAAAGAATTTCTACTGATCCAGCATAGTCAGAAAACTTAGCCAACTGTTATCC 1257
QY 993 LYSLEUTHRPHLEUGLNUALARGLEUVALGLYTPGLINPHEASPPASPSAPSPLEU 1012
Db 1258 AAGTTAACTTTCTGCAAGAACCTGAGGCTTGTGGTGCAATTTGATGATGATGATCTC 1317

QY 1013 SerValIleThrGlyAlaPheLysLeuValThrAla 1024
|||||
Db 1318 AGTGTATTACAGGTGCTTTAACTAGTACTGCT 1353
RESULT 15
AX318176
LOCUS AX318176 618 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 181 from Patent WO0190156.
ACCESSION AX318176
VERSION AX318176.1 GI:17900867
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
AUTHORS 1
TITLE Reed, J.C., Plo, F.F., Godzik, A., Stehlik, C., Damiano, J.S., Lee, S.H.,
Oliveira, V.A., Haysash, H. and Pawlowski, K.
Card domain containing polypeptides, encoding nucleic acids, and
methods of use
JOURNAL Patent: WO 0190156-A 181 29-NOV-2001;
The Burnham Institute (US)
FEATURES
source
1..618
location/Qualifiers
CDS
/organism="Homo sapiens"
/db_xref="taxon:9606"
<1..>618
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD19351.1"
/db_xref="GI:17900868"
/translation="GNLKNLTKLIMDNINKNEBAIKLAEGLKNKKMCLFHLTHLSLSD
IGGMDYIVKSLSEPDLEIQLVSCCLSNANVKILAQNLHNLVKLSDLSNLYLE
KDGNEALHELDIDRMNVLEQLTALMLPWGCGVQGSLSILKHEVLPOLVTKLKNMRL
TDEIRIGAFEFKKNPLKNEQNLNAGNRVSDQWLAFMGVFENLK"
BASE COUNT 194 a 113 c 148 g 163 t
ORIGIN
Alignment Scores:
Pred. No.: 1.69e-155 Length: 618
Score: 1084.00 Matches: 206
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 19.86% Indels: 0
Gaps: 0
US-09-697-089-2 (1-1024) x AX318176 (1-618)
QY 760 GlyAsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAsp 779
|||||
Db 1 GGTAACTTGAAGAACCTTACAAAGCTCATATGATTAACATAAAGATGAATGAAGAAGAT 60
QY 780 AlaIleLysLeuAlaGluGlyLeuLysAsnLeuLysMetCysLeuPheHisLeuThr 799
|||||
Db 61 GCTATAAACTAGCTGAAGGCTGAAAAACCTGAAGAAGATGTGTTATTTTCATTGAC 120
QY 800 HisLeuSerAspIleGlyGlyMetAspTyrIleValLysSerLeuSerSerGluAspPro 819
|||||
Db 121 CACTTGTCTGACATTCGAGAGGAAATGATTAAGTCAAGTCTCTCTCAAGTCAACCC 180
QY 820 CysAspLeuGluGluIleGlnLeuValSerCysLeuSerAlaAsnAlaValLysIle 839
|||||
Db 181 TGTGACCTTGAAGAATTCATTAAGTCTGCTGCTGCAAAATGACAGTGAATTC 240
QY 840 LeuAlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyr 859
|||||
Db 241 CTACTCGAATCTTCAACAATTTGTCAACTGAGCATTCTTGATTATCAGAAAAATTAC 300
QY 860 LeuGluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGlu 879
|||||
Db 301 CTGAAAAAAGATGGAATGAAAGCTTCTTCATGACATGACAGATGACAGCTGCTAGAA 360
QY 880 GlnLeuThrAlaLeuMetLeuProTropGlyCysAspValGlnGlySerLeuSerSerLeu 899

|||||
Db 361 CAGCTCACCCGACATGATGCTCCCTGGGGCTGTGACGTGCAAGGCAGCCTGAGACCTG 420
QY 900 LeuLysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeu 919
|||||
Db 421 TTGAACAATTTGGAGAGAGTCCCAACACTGCTCAAGCTTGGGTGGAAAAACTGGAGACTC 480
QY 920 ThrAspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPhe 939
|||||
Db 481 ACAGATACAGAGATTAGAAATTTAGTGTCATTTTGGAAAGAACCTCTGAAAAACTTC 540
QY 940 GlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPleuAlaPheMetGly 959
|||||
Db 541 CAGCAGTTGAATTTGGCGGGAATCGTGTGACAGTGAATGATGATGCTTGCCTCATGGGT 600
QY 960 ValPheGluAsnLeuLys 965
|||||
Db 601 GTATTGGAATCTTAAAG 618

Search completed: January 31, 2003, 10:48:55
Job time : 6830 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_p2n model

Run on: January 31, 2003, 07:11:06 ; Search time 487 Seconds
(without alignments)
4735.208 Million cell updates/sec

Title: US-09-697-089-2

Perfect score: 5459
Sequence: 1 MNFKDNRRLIQLMGMTVI.....MQFDDDLSTVTGFKLVTA 1024

Scoring table:

PAM120	4.0 ,	Xgapext 12.0
Xgapop	4.0 ,	Xgapext 12.0
Fgapop	6.0 ,	Fgapext 7.0
Delop	6.0 ,	Delext 7.0

Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-O=/cgn2.1/USPFO.spool/US09697089/unsat_29012003_092504_19148/app_query.fasta.1.1223
-DB=N_Geneseq.101002-QEFT-FASTAP-SUFFIX=p2n.rng-MINMATCH=0.1-LOOPCL=0-
-LOOPEXT=0-UNITIS-bits-START=1-END=-1-MATRIX=pam120-TRANS-human40.cdi
-LIST=45-DOCCALIGN=200-THR.SCORE=pct-THR.MAX=100-THR.MIN=0-ALIGN=15
-MODE=LOCAL-OUTFMT=ptc-NORM=ext-HEAPSIZE=500-MIMLEN=0-MAXLEN=2000000000
-USER=US09697089_GCGN.L1.344_@unsat_29012003_092504_19148-NCPU=6-ICPU=3
-NO_XLUPX-NO_MMAR-LARGEQUERY-NEG_SCORES=0-WAIT-LOGGLOG-DEV.TIMEOUT=120
-WANT_TIMEOUT=30-THREADS=1-XGAPOP=4-XGAPEXT=12-FGAPOP=6-FGAPEXT=7
-YGAPOP=4-YGAPEXT=12-DELOP=6-DELEXT=7

Database :

N_Geneseq.101002:*
1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	5459	100.0	3133	22	AA03945	Human caspase rec
2	5448	99.8	3213	22	AAH78219	Nucleotide sequenc
3	5438	99.6	3396	24	ABK22731	Human cDNA encodin
4	5438	99.6	3545	22	AAH98254	Murine EST-derived
5	5188	95.0	3615	22	AA03946	Human caspase recr
6	3950	72.4	2215	22	AAH78218	Nucleotide sequenc
7	3346	61.3	2950	22	AAH99581	Human protein enco
8	1598	29.3	891	24	ABK22766	Human cDNA encodin
9	1424	26.1	1395	24	ABK22732	Human cDNA encodin
10	1084	19.9	618	24	ABK22767	Human cDNA encodin
11	1005	18.4	608	22	AA526160	Human cDNA encodin
12	954	17.5	2735	22	AAH34171	Human colon cancer
13	853	15.6	768	24	ABK22734	Human cDNA encodin
14	725	13.3	522	22	AA526575	Human cDNA encodin
15	493	9.0	578	24	ABK22735	Human cDNA encodin
16	485	8.9	261	24	ABK22765	Human cDNA encodin
17	435	8.0	421	22	ABA56112	Human breast cell
18	435	8.0	421	22	ABA56119	Human foetal liver
19	435	8.0	421	22	ABA52770	Probe #4236 for ge
20	435	8.0	421	22	AAK04305	Human brain expres
21	435	8.0	421	22	AAK29801	Human bone marrow
22	435	8.0	421	22	AAI14389	Probe #4322 for ge
23	435	8.0	421	22	AAI35764	Probe #4450 used t
24	435	8.0	421	22	AAI04213	Probe #4204 used t
25	435	8.0	421	24	AB504362	Human genome-deriv
26	391	7.2	220	22	ABA50734	Human breast cell
27	391	7.2	220	22	ABA68704	Human foetal liver
28	391	7.2	220	22	ABA35668	Probe #4134 for g
29	391	7.2	220	22	AAK17044	Human brain expres
30	391	7.2	220	22	AAK42828	Human bone marrow
31	391	7.2	220	22	AAI23590	Probe #13523 for g
32	391	7.2	220	22	AAI48904	Probe #17590 used
33	391	7.2	220	22	AAI09206	Probe #1979 used t
34	391	7.2	220	24	AB516884	Human genome-deriv
35	287	5.3	165	24	ABK22768	Human cDNA encodin
36	279	5.1	5366	20	AAK58001	Gonadotropic hormo
37	279	5.1	5502	17	AA556273	Human apoptosis in
38	279	5.1	5502	17	AA530092	Neuronal apoptosis
39	279	5.1	5502	18	AAAT71263	Neuronal apoptosis
40	279	5.1	5984	20	AAK58000	Gonadotropic hormo
41	279	5.1	5984	20	AAK56272	Human apoptosis in
42	279	5.1	5984	21	AAA39808	Human MAP cDNA.
43	279	5.1	6124	18	AAAT71265	Neuronal apoptosis
44	279	5.1	6124	24	ABL67992	Ovary cancer relat
45	279	5.1	6133	18	AAAT71264	Neuronal apoptosis

ALIGNMENTS

RESULT 1
AA03945
ID AA03945 standard; cDNA: 3133 BP.
AA03945;
12-SEP-2001 (first entry)
Human caspase recruitment domain 12 (CARD-12) cDNA.
Caspase recruitment domain; CARD-12; apoptosis; stress-related pathway;
cancer; viral infection; poxvirus; adenovirus; autoimmune disorder;
Kw systemic lupus erythematosus; arthritis; neurological disorder; stroke;
Kw Alzheimer's disease; amyotrophic lateral sclerosis; haematologic disease;
Kw aplastic anaemia; myocardial infarction; inflammatory disorder;
Kw Crohn's disease; insulin-dependent diabetes; contact dermatitis;
Kw psoriasis; graft rejection; bacterial infection; lepromatous leprosy;
Kw tuberculosis; ischaemic brain injury; hypoxic brain injury; ss;

kidney ischaemia; reperfusion injury; acute bacterial meningitis;
excitotoxic brain damage; liver disease.

Homo sapiens.

Key Location/Qualifiers
FH 36..3110
FM /*tag= a
CD5 /product= "Human CARD-12"

WO200130971-A2.
XX PN
XX PD 03-MAY-2001.
XX PF 26-OCT-2000; 2000WO-US29643.
XX PR 27-OCT-1999; 99US-0161822.
XX (MILL-) MILLERNIUM PHARM INC.
XX PA
XX PT Berlin J, Robison KE;
XX DR WPI: 2001-308628/32.
DR P-PSDB: AAU02860.
XX
XX Isolated caspase recruitment domain-12 polypeptide and nucleic acids
PT encoding them, useful for treating and diagnosing disorders associated
PT with abnormal apoptosis such as cancer, arthritis and Alzheimer's
PT disease -
XX
XX Claim 2; Fig 1; 93pp; English.
XX PS

The sequence represents a cDNA which encodes the human caspase
CC recruitment domain 12 (CARD-12) polypeptide. CARD domains are found in a
CC number of proteins that transmit signals that activate apoptosis and
CC inflammatory pathways in response to stress and other stimuli. Therefore
CC CARD-12 and its corresponding nucleic acid may be used in treatment and
CC diagnosis of patients suffering from disorders associated with an
CC abnormal level (an increase or a decrease) of apoptotic cell death or
CC abnormal activity of stress-related pathways. The disorders include
CC cancer, viral infections (e.g. caused by poxviruses, adenoviruses),
CC autoimmune disorders (e.g. systemic lupus erythematosus, arthritis),
CC neurological disorders (e.g. Alzheimer's disease, amyotrophic lateral
CC sclerosis), haematologic diseases (e.g. aplastic anaemia, myocardial
CC infarction, stroke), inflammatory and immune system disorders (e.g.
CC Crohn's disease, insulin-dependent diabetes, contact dermatitis,
CC psoriasis, graft rejection), bacterial infections (e.g. tuberculosis,
CC lepromatous leprosy), ischaemic and hypoxic brain injury, kidney
CC ischaemia/reperfusion injury, excitotoxic brain damage, acute bacterial
CC meningitis and liver disease.
XX
XX SQ Sequence 3133 BP; 903 A; 691 C; 729 G; 810 T; 0 other;

Alignment Scores:

Pred. No.:	Score:	Length:
0	5459.00	3133

Percent Similarity:	Matches:
100.00%	1024

Best Local Similarity:	Conservative:
100.00%	0

Query Match:	Mismatches:
100.00%	0

DB:	Gaps:
22	0

OS-09-697-089-2 (1-1024) x AAS03945 (1-3133)

OY 1 MetAsnPhelIeLyASPAsnSerARgAlaLeuIllegInArMetGlyMeThrValIle 20
Db 36 ATGAATTTCATTAAGACCAATAAGCCCGACCCTTATTAAAGAATGGCAATGACTGTATA 95
OY 21 LysGlnIleThrAsPAsPleuPheValITrPAsnVaILeuAsnaRrgIugluVaLaSnIle 40
Db 96 AAGCAAAATCACAGATGACCTATTGTATGGAATGTCTTGATGCCAAGAAAGTAACATC 155
OY 41 IlecYcSgLUlYsVvalGlUGlnAsPaLaIAlaRgclYlleIleHisMetLleLeuLYs 60
|||||

D	b	156	ATTGCTGCAGAAAGTGAGGAGCAGGATGCGTACGAGGGGATCATTCACATGATTTTGAA	215
O	y	61	LysGlySerGlnSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTrpProLeu	80
D	b	216	AAGGTTTCAGAGTCCTGCTAACCTCTTCTTAAATCCCTTAAAGATGGAACTACATCTCTA	275
O	y	81	PheGlnAspLeuAsnGlnGlyInSerLeuPheHisGlnThrSerGlnGlyAspLeuAsp	100
D	b	276	TTTTCAGGACTTGAATGGACAAGCTCTTTTTCATCAACATCAAGAAAGGAGACTTGACAT	335
O	y	101	LeuAlaGlnAspLeuLysAspLeuTrpHisThrProSerPheLeuAsnPheTrpProLeu	120
D	b	336	TTGGCTCAGAGATTAAAGAGCTGTACATACCACCTCTTTCTGACTTTATCCCTT	395
O	y	121	GlyGlnAspLysAspLysLeilePheAsnLeuLysSerThrPheThrGluProValLeuTrp	140
D	b	396	GGTGAAGATATGTACATTATTTTAACTTGAAAGACCTTCACAGAACTGTCTCTGG	455
O	y	141	ArgLysAspGlnHisHisSarGluGluGlnLeuThrLeuAsnGlyLeuGlnAla	160
D	b	456	AGGAGAGCCCAACCCATCAACCCGCGGAGACACTGACCTTAAGGGCTCTCTGACGCT	515
O	y	161	LeuGlnSerProCysLysLeileGlnGlyGlnSerGlyLysGlyLysSerThrLeuGln	180
D	b	516	CTTCAGAGCCCTTCATCATATTGAAGGGGAACTTCGCAAAAGCAAGTCCACTGTCTGAG	575
O	y	181	ArgLysAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal	200
D	b	576	CGCATTTGCCATGCTCTGGGGCTCCGGAAAGTGCAGAGCTGTGCCAAGTTCAATTTCTGC	635
O	y	201	PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu	220
D	b	636	TTTCTTCCTCCGTCACACAGGGCCGAGGGGTGACTTTTGAACCCCTGTGTATCACTC	695
O	y	221	LeuAspLysProGlyThrThrLeuArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg	240
D	b	696	CTGATTTATCTGGCAACAATCAGAAAGCAACACTTGTATGCGCATGTGTGAAGCTGGGG	755
O	y	241	GlnArgValLeuPheLeuLeuAspGlyTrpAsnGlnPheLysProGlnAsnCyProGlu	260
D	b	756	CAGAGGGTCTTTTCCCTTTGATGGGTACAATGATTCAGCCCAAGACTGGCCAGAA	815
O	y	261	IleGluAlaLeuLysGlyGlnAsnHisArgPheLysAsnMetValIleValThrThrThr	280
D	b	816	ATCCAGAGCCCTGATTAAGAAAGAAACCAACCGCTTCAGAACATGTCATGTCCACCTACC	875
O	y	281	ThrGlnCysLeuArgHisIleLeuArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet	300
D	b	876	ACTGAGTGCCTGAGGCACTACGCGAGTTTGGTGGCTTACTGCTGAGGTGGGGCATATG	935
O	y	301	ThrGlnAspSerAlaGlnAlaLeuLysArgGluValLeuLysGlyLeuAlaGluGly	320
D	b	936	ACAGAGACAGCGGCCGAGGCTCTCATCCGAGAAAGTGTATCAAGAGGTTGTCTGAAGGC	995
O	y	321	LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe	340
D	b	996	TTTGTGCTCCAAATTCAGAAATCCAGATGCTTTGAGGAATCATATAGAGCCCTCTCTTT	1055
O	y	341	ValValIleThrCysAlaIleGlnMetGlyGlnSerGluPheHisSerHisThrGlnThr	360
D	b	1056	GTGGTCATCACTTGTGCATTCAGATGGAGTGGGAAGTGAATTCACCTCTCACACACAAACA	1115
O	y	361	ThrLeuPheHisThrPheTrpAspLeuLeuLysGlyAsnLysHisIleLysGly	380
D	b	1116	ACCGCTTCCATACCTCTTATGATCTGTGTATACAAAAAACAACACAAACATATAAGT	1175
O	y	381	ValAlaAlaSerAspPheIleLeuArgSerLeuAspHisCysGlyAspLeuAlaLeuGlnGly	400
D	b	1176	GTGGCTGCAAGTGCATTCATTCGAGAGCTGTGACCACTGTGAGACCTTACTGTGAAGGCT	1235
O	y	401	ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGlnAspAla	420
D	b	1236	GTGTTCCTCCCAAGTTTGATTTTCGAATCTCAGAGATGTGTCCAGCGTGATATAGGATGTCT	1295

QY 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440
 |||||||
 Db 1296 CTGTGCAACTGGGCTCCCTCTGTAATATACACTCAAGGTTCAAGCCAAATATATAA 1335
 QY 441 PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgLysSerSerLeuLeuThr 460
 |||||||
 Db 1356 TTCTTTCACAAGTCATTCACAGAGATACACAGACAGAGAACTCAGACAGTTTATGACG 1415
 QY 461 SerHisGlnProGlnGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerLle 480
 |||||||
 Db 1416 TCTCATAGCCAGAGGAGGAGGACCAAGGAAATGTTACTTGCAAAATGTTTCATT 1475
 QY 481 SerAspLleHisSerThrTyrSerSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500
 |||||||
 Db 1476 TCGGACATTACATCCACTTATAGAGGCTGCTCGGTACACCTTGGGTATCTGTGGAA 1535
 QY 501 AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly 520
 |||||||
 Db 1536 GCCACCGGGCTGTATGAAAGCACCTCGACAGTGTATCAACACGGGCTGCTTCGGA 1595
 QY 521 LeuSerLleAlaLysArgProLeuTyrArgGlnGlnSerLeuGlnSerValLysAsnThr 540
 |||||||
 Db 1596 CTTTCCATCGCCAAAGAGGCTCTCTGAGACAGGAATCTTTCGCAAACTGTGAAAAACACC 1655
 QY 541 ThrGlnGlnGluLleLeuLysAlaAlaAsnLleAsnSerPheValGlyCysGlyLleHis 560
 |||||||
 Db 1656 ACTGACGAGAAATTTGAAAGCCATTAACATCAATTCCTTGTAGAGTGGGATCATCAT 1715
 QY 561 LeuTyrGlnGlnSerThrSerLysSerAlaLeuSerGlnGlnPheGlnAlaPheGln 580
 |||||||
 Db 1716 TTAATATACAGAGTACATCCAAATACAGCCCTGAGCCAAAGATTTGAAAGCTTCTTCAA 1775
 QY 581 GlyLysSerLeuTyrLleAsnSerGlyAsnLleProAspTyrLeuPheAspPheGln 600
 |||||||
 Db 1776 GGTAAAGCTTATATATACATCAGGAAACATCCCGATTTACTTATTTGAACTTTTGAA 1835
 QY 601 HisLeuProAsnCysAlaSerAlaLeuAspPheLleLysLeuAspPheTyrGlyGlyAla 620
 |||||||
 Db 1836 CATTTGCCCAATGTGCAAGTCTCTGACTTCATTAACGTGAGCTTTATGGGGAGCT 1895
 QY 621 MetLaserTrpGlyLysAlaAlaGlnAspThrGlyLleHisMetGlnGluAlaPro 640
 |||||||
 Db 1896 ATGGCTTCAATGGAAGGCTGCAAGAGACACAGGTGAATCCACATGGAAGAGGCCCA 1955
 QY 641 GlnThrTyrLleProSerArgAlaValSerLeuPhePheAsnTyrPlyGlnGluPheArg 660
 |||||||
 Db 1956 GAAACCTACATCCACAGAGGCTGTATCTTTGTTTCAACTGGAAGCAAGGAATTCAGG 2015
 QY 661 ThrLeuGlnValThrLeuAlaGAspPheSerLysLeuAsnLysGlnAspLleThrTyrLeu 680
 |||||||
 Db 2016 ACTGTGAGGTGACACATCCGGGATTTTCAGCAAGTTGAATGAAGCAAGATACACATATCTG 2075
 QY 681 GlyLysLlePheSerSerAlaThrSerLeuArgLeuGlnLleLysArgCysAlaGlyVal 700
 |||||||
 Db 2076 GGGAAATATTCAGCTCTGCCACAAAGCTCAGGCTCAAAATAAAGAAATGGCTGTGTG 2135
 QY 701 AlaglySerLeuSerLeuValLeuSerThrCysLysAsnLleTyrSerLleMetValGlu 720
 |||||||
 Db 2136 GCTGGAAGCTCAGTTGGTCTCTCAGACCTGTAAAGAACTTATTTCTCATAGTGTGAA 2195
 QY 721 AlaSerProLeuThrLleGlnAspGlnArgHisLleThrSerValThrAsnLeuLysThr 740
 |||||||
 Db 2196 GCGAGTCCCTCAACCATAGAAGATGAGAGACATCATCTGTAAACAAACCTCAAAACC 2255
 QY 741 LeuSerLleHisAspLeuGlnAsnGlnArgLeuProGlyLysLeuThrAspSerLeuGly 760
 |||||||
 Db 2256 TTGAGTTCATGATGATCAAGAAATCAACGCTGCCGGGTGTGATGATGACACCTGGGT 2315
 QY 761 AsnLeuLysAsnLeuThrLysLeuLleMetAspAsnLleLysMetAsnGlnGluAspAla 780
 |||||||
 Db 2316 AACTTGAAGAACTTACAAAGCTCATATATGATTAACATTAAGATGAAGAAAGATGCT 2375

QY 781 IleLysLeuAlaGlnGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800
 |||||||
 Db 2376 ATAAAACTAGCTGAAGGCTGCAAAACCTGAAGAAGATGTGTTTATTTTCATTTCACCCAC 2435
 QY 801 LeuSerAspLleGlyGlnGlyMetAspTyrLleValLysSerLysSerSerGlnProCys 820
 |||||||
 Db 2436 TTGCTGACATTTGAGAGGGAATGATGATACATAGTCAAGTCTCTGTCAAGTGAACCTGT 2495
 QY 821 AspLeuGlnGlnLleGlnLeuValSerCysSerSerSerAlaAsnAlaValLysLleLeu 840
 |||||||
 Db 2496 GACCTGAAGAAATTCATTAATAGTCTCTGCTGTGTCTGCAAAATGAGTGAATATCCTA 2555
 QY 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerLleLeuAspLeuSerGlnAsnTyrLeu 860
 |||||||
 Db 2556 GCTGAGAACTCTCCATTTTGGTCAAACTGACATTTCTGATTTATCAGAAAAATTTACTG 2615
 QY 861 GlnLysAspGlyAsnGlnAlaLeuHisGlnLeuLleAspArgMetAsnValLeuGln 880
 |||||||
 Db 2616 GAAAAAGATGGAATGGAAGCTCTTCATGAACTGATCGACAGAGATGAACGTGCTGAAACAG 2675
 QY 881 LeuThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlnSerLeuSerSerLeu 900
 |||||||
 Db 2676 CTCACCGACTGATGCTGCCCTGGGCTGTGACGTGCAAGGACGCTGACAGCTGTG 2735
 QY 901 LysHisLeuGlnGlnValProGlnLeuValLysLeuGlyLeuLysAsnTyrParGleuThr 920
 |||||||
 Db 2736 AAACATTTGGAGAGGATGCCCAAACTGCTCAGCTTGGTTGAAAACTGAGAGCTCACA 2795
 QY 921 AspThrGlnLleArgLleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940
 |||||||
 Db 2796 GATACAGAGATTTGAATTTTGAAGTGTGCAATTTTGGAAAGAACCTCTGAAAAAATTCCAG 2855
 QY 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrThrAlaPheMetGlyVal 960
 |||||||
 Db 2856 CAGTTGAATTTGGCGGGAATTCGTGACAGATGATGATGGCTGCTTCATAGGGGTGA 2915
 QY 961 PheGlnAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGlnPheLeuProAsp 980
 |||||||
 Db 2916 TTTCAGAACTTTAAGCAATTAAGTGTGTTTTCGACTTGTGATCAAAAGAAATTTCTACATCAT 2975
 QY 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla 1000
 |||||||
 Db 2976 CCAGCATTAATGCAAGAAACCTTACCAAGTGTATACCAAGTTAACTTTTCGCAAGAGCT 3035
 QY 1001 ArgLeuValGlyTyrGlnPheAspAspAspAspLeuSerValLleThrGlyAlaPheLys 1020
 |||||||
 Db 3036 AGGCTTGTGGTGGCAATTTGATGATGATGATCTCAGTGTATTAACAGGTGCTTTAAA 3095
 QY 1021 LeuValThrAla 1024
 |||||||
 Db 3096 CTAACTACTGCT 3107
 RESULT 2
 AAH78219
 ID AAH78219 standard; DNA: 3213 BP.
 XX
 AC AAH78219:
 XX
 DT 26-NOV-2001 (first entry)
 XX
 DE Nucleotide sequence of a human secreted polypeptide.
 XX
 KW Human: secreted polypeptide; nervous disease; muscular disease; tumour;
 KW gastrointestinal ulceration; spinal cord disease; trachea disease;
 KW thyroid gland disease; ovary disease; prostate disease; heart disease;
 KW renal gland disease; small intestine disease; thymus disease;
 KW lymph node disease; muscular system disease; colon disease;
 KW lipase deficiency; cystic fibrosis; pancreatitis; clot formation;
 KW myocardial infarction; angioplasty; liver disease; coagulation disorder;
 KW microbial disease; immune disorder; inflammation; transplant rejection;
 KW bone thickness; bone density; ferroxidase loss; apoptosis;
 KW vascular smooth cell proliferation; vaccine; ss.
 XX

|||||
Db 1399 CTGCTGACAACTGGGCTCTCTGTAATAATATACAGCTCAAGGCTCAAGCCAAAGTATATAA 1458
OY 441 PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuThr 460
Db 1459 TTCTTTCAACAAGTCAATTCAGAGATACACAGACGAGACGAACTGACAGCTTATTTAGAG 1518
OY 461 SerHisGluProGlnGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480
Db 1519 TCTCATGAGCCGAGAGAGAGTGCACAGGGGAATGGTTACTTCCAGAAAATGGTTTCCATT 1578
OY 481 SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500
Db 1579 TCGGCAATTACATCCACTTATGAGCCAGCTCCGCTACACCTGGGTCATCTGGGA 1638
OY 501 AlaThrArgAlaValMetLysHisLeuValAlaValTyrGlnHisGlyCysLeuLeuGly 520
Db 1639 GCCACCAAGGGCTGTATGAGACCTCCGACAGTGTATCAACACAGCGCTCTTCGGA 1698
OY 521 LeuSerIleAlaLysArgProLeuThrArgGlnGlnSerLeuGlnSerValLysAsnThr 540
Db 1699 CTTTCCATCCGCCAAGAGGCTCTCTGAGACAGAGATCTTTCACAAAGTGTGAAAAACAC 1758
OY 541 ThrGlnGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560
Db 1759 ACTGAGCAAGAAATCTGAAAGCCATAAACATCAATTCCTTGTAGAGTGGCATCCAT 1818
OY 561 LeuTyrGlnGlnSerThrSerLysSerAlaLeuSerGlnGlnLysPheGln 580
Db 1819 TTATATCAAGAGATACATCCAAATCAGCCCTGACCCAAAGAAATTTGAACCTTCTTTCAA 1878
OY 581 GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPheGlu 600
Db 1879 GGTAAAGCTTATATATCATCACTCAGGAAACATCCCGATTAATTGACTTCTTTGAA 1938
OY 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyAla 620
Db 1939 CATTTGCCCAATTTGCAAGTCCCTCGCATTCATTAACCTGAGATTATATGGGGAGCT 1998
OY 621 MetAlaSerTrpGlnLysAlaAlaGlnAspThrGlyGlyIleHisMetGlnLysLysPro 640
Db 1999 AGCGTTTCATGGGAAAGGCTGCACAGACACAGGTGAGTCCACATGGAAAGGCCCA 2058
OY 641 GluThrTyrIleProSerArgAlaValSerLeuPheAsnTrpLysGlnLysPheArg 660
Db 2059 GAAACCTACATTCACAGCAGGCTATCTTTGTTCTTCACTGGAAGCAGGAATTCACG 2118
OY 661 ThrLeuGlnValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu 680
Db 2119 ACTCTGAGAGTCACTCCGGGATTTCAGCAAGTTGAATTAACAGATATACAGATATCG 2178
OY 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700
Db 2179 GGGAAAAATATTCAGCTCTGCCACAGCTCAGGCTCAAAATTAAGATGTCTGCTGTGTG 2238
OY 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu 720
Db 2239 GCTGGAAGCCTCAGTTTGGTCTCAGACCTGTAAAGACATTATCTCTCAATGGTGGAA 2298
OY 721 AlaSerProLeuThrIleGlnAspGlnArgHisIleThrSerValThrAsnLeuLysThr 740
Db 2299 GCCAATCCCTCCACATAGAGATAGAGGCAATCACAATCGTAAACAACTGAAAC 2358
OY 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 760
Db 2359 TTGATATATTCATGACCTCAGATCAACAGCGCTGGGTGGTCTGACACAGCTTGGGT 2418
OY 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAspGlnGlnAspAla 780
Db 2419 AACTTGAAGAACCTTACAAAGCTCATTAATGGATTAACATTAAGATGAAGAAATGCT 2478
OY 781 IleLysLeuAlaGlnGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800
|||||

Db 2479 ATMAAACTAGCTGAAGGCTCGTAAAAACCTGAAGAGATGTGTTATTTCAATTGACCCAC 2538
OY 801 LeuSerAspIleGlyGlnGlyMetAspTyrIleValLysSerLeuSerSerGluProCys 820
Db 2539 TTGTCTGACATTGGAGAGGAGGATGATTAACATAGCAATGATCTCTGTCAAGTGAACCTGT 2598
OY 821 AspLeuGlnGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840
Db 2599 GACCTTGAAGAAATTCATTAATGTCCTGCTGCTGTCTGCGAAATGCAAGTGAATCCCTA 2658
OY 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860
Db 2659 GCTCAGAAATCTTCAACAATTTGGTCAACCTGACACTTCTGATTATTCAGAAAAATTAACCTG 2718
OY 861 GluLysAspGlyAsnGlnAlaLeuHisGlnGluLeuIleAspArgMetAsnValLeuGlnGln 880
Db 2719 GAAAGATGGAATGAAAGCTTCTCATGACACTGATCGACAGGATGACGCTGCTAAGACAG 2778
OY 881 LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900
Db 2779 CTCACCGCACATGATGCTGCTCGGGGCTGTGACGTGCAAGGCAAGGCTGACGACCTGTTG 2838
OY 901 LysHisLeuGlnGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThr 920
Db 2839 AAACATTTGGAGAGGCTCCACACACTGTCAGACTTGGGTTGAAAAACTGGAGACTCACA 2898
OY 921 AspThrGluIleArgIleLeuGlnLysAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940
Db 2899 GATACAGAGATTAGAAATTTAGTGCATTTTGGAAAAAGAACCTCTGAAAAAATCTTCAG 2958
OY 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrTrpLeuAlaPheMetGlyVal 960
Db 2959 CAGTTGAATTTGGCGGGAATGCTGTGACACTGATGATGATGCTTCCCTTCAATGGCTGTA 3018
OY 961 PheGlnAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980
Db 3019 TTTCAGAAATCTTAAACAATTAAGTGTTTTGTGACTTAAGTAAAGAAATTTCTACCTGAT 3078
OY 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGlnLys 1000
Db 3079 CCAGCATTTAGTCAGAAACTTATAGCCAAAGTGTATCAAGTTAACTTCTCGCAAAACCT 3138
OY 1001 ArgLeuValGlyTyrGlnPheAspAspAspAspLeuSerValIleThrGlyAlaPheLys 1020
Db 3139 AGCTTGTGGTGGCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3198
OY 1021 LeuValThrAla 1024
Db 3199 CTAGTAACGTCT 3210
RESULT 3
ABK22731
ID ABK22731 standard; cDNA: 3396 BP.
XX ABK22731;
AC 26-MAR-2002 (first entry)
XX
DE Human cDNA encoding CLAN A.
XX Caspase recruitment domain; CARD; ss: NB-ARC; ANGTO-R; LRR; SAM;
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
KW autoimmune disease; inflammation; keratinocyte hyperplasia;
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
KW leukon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;
KW Crohn's disease; graft-versus-host disease; stroke;
KW myocardial infarction; heart failure; neurodegenerative disease;
KW Parkinson's disease; Alzheimer's disease; HIV;
KW human immunodeficiency virus infection.
XX Homo sapiens.
XX

QY 441 PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgLeuSerSerLeuThr 460
|||||
Db 1597 TTCTTCACAGATCATTCACAGGAGTACACAGCGAGACGAACTCATGCACTTATTATGACG 1656
QY 461 SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480
|||||
Db 1657 TCTCAAGAGCGACAGAGGAGGACCAAGGGAAATGGTTACTTGCAGAAAATGGTTCCATT 1716
QY 481 SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500
|||||
Db 1717 TCGGACATTACATCCACTTATACACGCTCGCTCCGGTACACCTGTGGTATCTGTGGAA 1776
QY 501 AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuGlu 520
|||||
Db 1777 GCCACAGGGCTGTATGAAAGCACCTCGACAGCATATCAACACGGCTCCCTTCGGA 1836
QY 521 LeuSerIleAlaLysArgProLeuTyrParGlnGluSerLeuGlnSerValLysAsnThr 540
|||||
Db 1837 CTTTCCATCGCCCAAGAGCGCTCTGTGAGACAGCAATCTTTCGCAAGTGGAAAAACACC 1896
QY 541 ThrGlnGlnGlnIleLeuLysAlaIleAsnIleAsnSerPheValGlyCysGlyIleHis 560
|||||
Db 1897 ACTGACCAAGAAATTCGAAAGCCATTAACATCAATTCCTTGTAGAGTGTGGCATCCAT 1956
QY 561 LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln 580
|||||
Db 1957 TTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCAAAGAAATTTAGACTTCTTTCAA 2016
QY 581 GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhePheGlu 600
|||||
Db 2017 GGTAAGAGCTTATATATCAACTCAGAGGAACATCCCGATTACTTATTTGACTCTTTGAA 2076
QY 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyGlyAla 620
|||||
Db 2077 CATTTCCCAATTTGTCCAAAGTGCCTGCACTTCAATTAACGTGACCTTTATGGGGAGCT 2136
QY 621 MetaLaserTyrPgluLysAlaIleGluAspThrGlyGlyIleHisMetGlnGluAlaPro 640
|||||
Db 2137 ATGGCTTCATGGGAAAGAGCTCGAGAGACACAGGTGCAATCCACATCGAGAGGCCCA 2196
QY 641 GluThrTyrIleProSerArgAlaValSerLeuPhePheAsnTyrPylsGlnLupheArg 660
|||||
Db 2197 GAAACCTACATTCGCCAGAGGGCTGTATCTTGTCTTCACTGGAAGCAGAAATTCAG 2256
QY 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu 680
|||||
Db 2257 ACTCTGGAGGTCAACCTCGGGATTCACAGCAAGTTGAATGAAGCAAGATATCACATATCTG 2316
QY 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700
|||||
Db 2317 GGGAAAAATTCAGCTCTCCACACAGCTCAGAGCTCAAAATTAAGATGTGGTGTG 2376
QY 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu 720
|||||
Db 2377 GCTGGAGAGCTCAGTTGGTCTCTCAGCACCTGTAAAGAAATTTATCTCTCAATGGTGA 2436
QY 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740
|||||
Db 2437 GCCAGTCCCTCCACATTAAGATGAGAGGACATACATCTGTAAACCAACCTGGAACACC 2496
QY 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 760
|||||
Db 2497 TTGAGATTCATGACATACAGAAATCAAGGCTCGCGGTCTGTGATACAGACTTGGGT 2556
QY 761 AsnLeuLysAsnLeuThrTyrLeuIleMetAspAsnIleLysMetAsnGluGluAspAla 780
|||||
Db 2557 AACTTGAAGAACCTTCAAAAGCTCATTAATGAATGAATGAATGAATGAAGAGATGCT 2616
QY 781 IleLysLeuAlaGlnGlyLeuLysAsnLeuLysMetCysLeuPheHisLeuThrHis 800
|||||
Db 2617 ATTAACCTAGCTGAGAGGCTGAAAAACCTGAAGAGATGTGTTTATTTGATTTGACCCAC 2676

QY 801 LeuSerAspIleGlyGlnGlyMetAspTyrIleValLysSerLeuSerGluProCys 820
|||||
Db 2677 TTGTCTGACATTGGAGGGAAATGATTTACATGTCATGATGTCAGTCTGTGCAAGTGAACCTGT 2736
QY 821 AspLeuGlnGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840
|||||
Db 2737 GACCTTGAAGAAATTCATTAATAGTCTCTGCTGCTTCTGTGCAAAATCAGAGAAATCTTA 2796
QY 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860
|||||
Db 2797 GCTCAGAAATCTTCACATTTGGTCAAACTGAGCATTCCTGTGATTTATCAGAAAATTAACCTG 2856
QY 861 GluLysAspGlyAsnGlnAlaLeuHisGluLeuIleAspArgMetAsnValLeuGlnGln 880
|||||
Db 2857 GAAAAAGATGGAATATAGCTTTCATGAACATATGACAGATGAACGTGCTAGAACAG 2916
QY 881 LeuThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900
|||||
Db 2917 CTCACCGCACTGATGCTGCCCTGGGCTGTGACGTGCAGAGGACGCTGAGACAGCTGTG 2976
QY 901 LysHisLeuGlnGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrParGluThr 920
|||||
Db 2977 AAACATTTGGAGGAGGTCCACAACTGTCMAAGCTTGGGTGAAAAACGAGACATCACA 3036
QY 921 AspThrGluIleArgIleLeuGlnGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940
|||||
Db 3037 GATACAGAGATTGAAATTTTAGTGCATTTTGGAAAGAACCTCTGAAAAAATCTCCAG 3096
QY 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPheAlaPheMetGlyVal 960
|||||
Db 3097 CAGTTGAATTTGGCGGGAATCTGTGACAGAGATGATGATGGCTTGCCTCATGGGTGTA 3156
QY 961 PheGlnAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980
|||||
Db 3157 TTTGAGAAATCTTAAGCAATTAAGTGTGTTTGTGACTTGAATAAGAAATTTCACTGAT 3216
QY 981 ProAlaLeuValArgLysLeuSerGlnValIleSerLysLeuThrPheLeuGlnGluAla 1000
|||||
Db 3217 CCAGCATTTAGTCGAAAACTTAGCCAAAGTGTATCCAAAGTTAACTTTTGTGCAAGAGCT 3276
QY 1001 ArgLeuValGlyTyrPgluPheAspAspAspLeuSerValIleThrGlyAlaPheLys 1020
|||||
Db 3277 AGGCTTGTGGGGGCAATTTGATGATGATGATCAGTGTATATACAGTGTCTTTAA 3336
QY 1021 LeuValThrAla 1024
|||||
Db 3337 CTAGTAAGTGTCT 3348
RESULT 4
AAH98254
ID AAH98254 standard; cDNA: 3545 BP.
XX
AC AAH98254;
XX
DT 12-OCT-2001 (first entry)
XX
DE Murine EST-derived coding sequence SEQ ID NO: 111.
XX
KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition; ss.
OS Mus musculus.
XX
PN WO200154477-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US02687.
XX
PR 25-JAN-2000; 2000US-0491404.
PR 17-JUL-2000; 2000US-0617746.

PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663870.
XX
XX
XX (HXSE-) HXSEQ INC.
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi Y;
PI Cao Y, Dmanac RA, Zhang J, Wehrman T;
XX WPI: 2001-476164/51.
DR P-PSDB: AAM23595.
XX
XX Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
XX
XX Claim 1; Page 250-251; 1275bp; English.
XX
XX The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a cDNA
CC of the invention.
XX
XX
SQ Sequence 3545 BP; 1038 A; 755 C; 816 G; 936 T; 0 other;

Alignment Scores:

Pred. No.:	0	Length:	3545
Score:	5438.00	Matches:	1021
Percent Similarity:	99.71%	Conservative:	0
Best Local Similarity:	99.71%	Mismatches:	3
Query Match:	99.62%	Indels:	0
DB:	22	Gaps:	0

US-09-697-089-2 (1-1024) x AAH98254 (1-3545)

QY 1 MetAspHeiLeuLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
Db 232 ATGATTTTCATTAAGACAAATAGCCGAGCCCTTATTCAAGAAATGGAAATGACTGTATA 291
QY 21 LysGlnIleThrAspAspLeuPheValITrpaAsnValLeuAsnArgGluValAsnIle 40
Db 292 AAGCAAAATCACAGATGACCTATTGTATGAAATGTTCTGAATCGCGAAACATAAACAATC 351
QY 41 IleCysCysGluLysValGlnGlnAspAlaIleArgGlyIleIleHisMetIleLeuLys 60
Db 352 ATTTCCTCGAGAAAGGTGAGAGATGCTGCTAGAGGATATTCACACTGATTTTGAAA 411
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluITrpaAsnITrProLeu 80
Db 412 AAGGTTTCAGAGTCTGTAACCTTTTCTTAATCCCTTAAGAGAGGAAATATCCTCTA 471
QY 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnITrSerGlyGlyAspLeuAspAsp 100
Db 472 TTTTCGAGACTTGAATGGAACAAAGCTTTTTCATCAGACATCGAAGGAGAACTTGGACGAT 531
QY 101 LeuAlaGlnAspLeuLysAspLeuITrHisITrProSerPheLeuAsnPheITrProLeu 120
Db 532 TTGGCTCAGGATTTAAAGACTTGTACCATACCCCACTTTTCTGAACCTTTATCCCTT 591
QY 121 GlyIleAspIleAspIleIlePheAsnLeuLysSerITrPheITrGluITrValLeuITrP 140
Db 592 GGTGAAGATATTGACATATTATTTTAACTTGAAGAAACACACTTCACAGAACTCTCTGTGG 651
QY 141 ArgLysAspGlnHisHisArgValGlnGlnLeuITrHisITrLeuAsnGlyLeuLeuGlnAla 160
Db 652 AGGAAGAGCAACACATCACCGCGTGGAGAGCTGACCTGAATGGCCTCTGACAGGT 711
QY 161 LeuGlnSerProCysIleIleGlnGluGlyGluSerGlyLysGlyLysSerITrLeuLeuGln 180
Db 712 CTTCAGAGCCCTGCATCATTTGAAGGGAAATCTGGCAAAAGGCAATGCCACTCTGCTGAG 771

QY 161 ArgIleAlaMetLeuITrPGLysSerGlyLysCysLysAlaLeuITrLysPheLysPheVal 200
Db 772 CGCATTCGCATCTCTGGGGGCTCCGAAAGTCAAGGCTCTGACCAAGTTCAAAATTCCTGC 831
QY 201 PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGlnITrLysCysAspGlnLeu 220
Db 832 TTTCTTCCTCCGCTCAGAGGGCCAGGGGTGACTTTTGAAGCCCTGTGATCACTC 891
QY 221 LeuAspIleProGlyITrHisArgLysGlnITrPheMetAlaMetLeuLysLeuArg 240
Db 892 CTGATATACCTGGACACATCGAAGCAGACATTCATGCGCATCTGCTGAGAGTGGGG 951
QY 241 GlnArgValLeuPheLeuLeuAspGlyITrHisGlnITrPheLysProGlnAsnCysProGlu 260
Db 952 CAGAGGGTCTTTTCTTCTTGATGCTACATGAATCAAGCCCAAGAACGCCACAGAA 1011
QY 261 IleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValITrThrITr 280
Db 1012 ATCGAAGCCCTGATTAAGAAACCAACCGCTTCAAGAACATGTCATGTCACCACTACC 1071
QY 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuITrAlaGluValGlyAspMet 300
Db 1072 ACTGAGTGCCTGAGGCACATACGAGCATTTGGTGCCTGACCTGACCTGAGGTGGGATATG 1131
QY 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValIleLysGluLeuAlaGluGly 320
Db 1132 ACAGAGACAGCCGCCAGGCTCTCATCCGAGAACTGATCAAGACCAAGACCTGCTGAAGGC 1191
QY 321 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysITrProLeuPhe 340
Db 1192 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGAAGAAATCTCATAAACCCCTCTCTTT 1251
QY 341 ValValIleITrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisITrGlnITr 360
Db 1252 GTGCTGATCATTGTGCAATCCAGATGGGTGAAGTGAATGATTCATCTCACACCAAAACA 1311
QY 361 ThrLeuPheHisITrPheITrAspLeuLeuIleGlnLysAsnLysHisLysGly 380
Db 1312 ACGCTGTTCCATACCTTCTATGATCTGTGAATACAGAAACCAACCAACATTAAGGT 1371
QY 381 ValAlaIleAspAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGlnGly 400
Db 1372 GTGGCTGCAAGTACTTCAATTCGAGCTGCAACCTGTGATACCTGATGACTCTGGAAGGT 1431
QY 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420
Db 1432 GTGTTCTCCCAACAATTTGATTTCGAACTGCAAGATGCTGTCAGGCTGAATGAGGATGTC 1491
QY 421 LeuLeuITrThrGlyLeuLeuCysLysITrITrAlaGlnArgPheLysProLysITrLys 440
Db 1492 CTGCTGACAACTGGGCTCCTCTGTAATATACAGCTCAAGGTTCAAGCCAAAGTATAA 1551
QY 441 PhePheHisLysSerPheGlnGluITrITrHisArgAlaGlyGluSerSerLeuLeuITr 460
Db 1552 TTTCTTTCACAACTCAATTCAGAGATACACAGAGGACGAAGCTCAGAGTTTATTTGACG 1611
QY 461 SerHisGluProGlnGluValITrLysGlyAsnGlyITrLysGlnITrLysMetValSerIle 480
Db 1612 TCTCATGACCCAGAGAGAGTACCAAGGGGAATGTTACTTTCGACAAATAGTTTCCATT 1671
QY 481 SerAspIleITrSerITrLysSerSerLeuLeuArgITrITrCysGlySerSerValGlu 500
Db 1672 TCGGACATATACCATCACTTATAGAGCTGCTCGCGGTACACTGCGGTCAATCTGTGAA 1731
QY 501 AlaITrArgAlaValMetLysHisLeuAlaValITrGlnHisGlyCysLeuLeuGly 520
Db 1732 GCCACCAAGGGGTATTATGAAGCACCTCCAGACAGTGTATCAACAGGCTGCTTCGGA 1791
QY 521 LeuSerITrAlaLysArgProLeuITrParGlnGlnGlnSerLeuGlnSerValLysAsnITr 540
Db 1792 CTTCATCTGCGCAAGAGGCTCTCTGAGACAGGATCTTTCGAAGTGTGAAAGAACACC 1851
QY 541 ThrGlnGlnIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyITrHis 560


```

|||||
Db 1852 ACTGAGCAGAAATTCGTAAGAACCATTAACATCAATTCCTTTGTAGAGTGGCATCCAT 1911
QY 561 LeuTYrGInGluSerThrSerLySerAlaLeuSerGInGluPheGluAlaPheGln 580
Db 1912 TTATATTCAGAGATACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAACCTTCTTCAA 1971
QY 581 GLYrSerLeuTYrIleAsnSerGlyAsnIleProAspTYrLeuPheAspPheGln 600
Db 1972 GGTAAAGCTTATATATCACTCAGAGAACATCCCGATTACTTATTTGACTTTTGAA 2031
QY 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleTyLeuAspPheTYrGlyAla 620
Db 2032 CATTTGCCCAATTTGTCAGAGTGCTCTGGACTTCATTAACCTGGCTTTATAGGGAGCT 2091
QY 621 MetAlaSerTPripGluLysAlaAlaGluAspThrGlyGlyIleHisMetGInGluAlaPro 640
Db 2092 ATGGCTTCATGGGAAAGGCTGCAGAGACACAGGTGGATCCACATGCAAGAGGCCCA 2151
QY 641 GluThrTYrIleProSerArgAlaValSerLeuPheAsnTPripLysGInGluPheArg 660
Db 2152 GAACCTACATTTCCACAGCGGCTGTATCTTGTCTTCACTGGAGCAGGAATTCAGG 2211
QY 661 ThrLeuGluValThrLeuArgAspPheSerLyLeuAsnLysGInAspIleThrTYrLeu 680
Db 2212 ACTGTGAGAGTCACACCTCGGATTTACAGCAAGTTGAATACAGATATCAGATATCTG 2271
QY 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGInIleLysArgCysAlaGlyVal 700
Db 2272 GGGAAATATTCAGCTCTGCCACAAAGCCCTCAGCTGCATTAAGATGATGCTGTGTG 2331
QY 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTYrSerLeuMetValGlu 720
Db 2332 GTGGAGGCTCAGTTGGTCTCTCAGACCTGTAAAGATTAATTCCTCATGGGGAA 2391
QY 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740
Db 2392 GGCAGTCCCTCACCATGAGAGATGAGAGGCATCAGATCTGTAAACAACTGAAACCC 2451
QY 741 LeuSerIleHisAspLeuGInAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 760
Db 2452 TTGAATATTCAGACCTTCAGATCAAGGCTCGCGGGGTCTACTGACGCTTGCGGT 2511
QY 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluLysAla 780
Db 2512 AACTTGAGGAACCTTACAAAGCTCATANTGATTAACATTAATGATTAACAAAGATGCT 2571
QY 781 IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800
Db 2572 ATAAAACTAGCTGAGAGGCTGAAAAAAGCTGAAGAGATGTGTTTATTCATTTGACCCAC 2631
QY 801 LeuSerAspIleGlyGluGlyMetAspTYrIleValLysSerLeuSerSerGluProCys 820
Db 2632 TTGTCTGACATTTGAGAGGAAATGATTAACATAGTCAATCTCTCTCAAGTAAACCTCT 2691
QY 821 AspLeuGluGluIleGlnLeuValSerCysLysSerAlaAsnAlaValLysIleLeu 840
Db 2692 GACCTTGAAGAAATTCATTAAGTCTCTCTCTCTCTCTGCGCAAAATGCAAGTAAATCTCA 2751
QY 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTYrLeu 860
Db 2752 GCTCAGAAATCTTCACAAATTTGGTCAAACTGAGCATTTCTGATTTATCAAGAAATTAACCTG 2811
QY 861 GluLysAspArgLysAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGln 880
Db 2812 GAAAAAGATGAATGAAGCTCTTCATGAATCGATCGAAGGATGAACCTGCTTAACACG 2871
QY 881 LeuThrAlaLeuMetLeuProTPripLysCysAspValGInGlySerLeuSerSerLeuLeu 900
Db 2872 CTCACCGCAGCATGCTGCGCTGGGGCTGTGACGTGCAAGGAGGCTGAGCGAGCTGTGG 2931
QY 901 LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTPripArgLeuThr 920
|||||

```

```

Db 2932 AAACATTTGGAGAGAGTCCCAACACTGTCAGACTTTGGGTTGAAAAAAGCTGAGACTCACA 2991
QY 921 AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940
Db 2992 GATACAGAGATTAAGAAATTTAGTGCATTTTGGAAAAAGAACCTCTGAAAAACTTCAG 3051
QY 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTPripLeuAlaPheMetGlyVal 960
Db 3052 CAGTTGCAATTTGGCGGAAATGCTGTGAGCAGATGATGATGCTTCCCTTCATGGGTGTA 3111
QY 961 PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980
Db 3112 TTGAGAAATCTTAACCAATTAAGTGTTTTGTGACTTATAGACTAAAGAAATTTCTACCTGAT 3171
QY 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGInGluAla 1000
Db 3172 CCAGCATTAAGTGAAGAAATTAAGTGAAGGTTATCCAAATTAAGCTTTCTGCAAGAGCT 3231
QY 1001 ArgLeuValGlyTPripGluPheAspAspAspLeuSerValIleThrGlyAlaPheLys 1020
Db 3232 AGCTTTGTTGGGTGGCAATTTGATGATGATGATCTCAGTGTTATTTACAGGTCTTTTAA 3291
QY 1021 LeuValThrAla 1024
Db 3292 CTAGTAAGTGT 3303

RESULT 5
AAS03946
ID AAS03946 standard; DNA; 3615 BP.
XX
AC AAS03946;
XX
DT 12-SEP-2001 (first entry)
XX
DE Human caspase recruitment domain 12 (CARD-12) genomic DNA.
XX
KW Caspase recruitment domain; CARD-12; apoptosis; stress-related pathway;
KW cancer; viral infection; poxvirus; adenovirus; autoimmune disorder;
KW systemic lupus erythematosus; arthritis; neurological disorder; stroke;
KW Alzheimer's disease; amyotrophic lateral sclerosis; hematologic disease;
KW aplastic anaemia; myocardial infarction; inflammatory disorder;
KW Crohn's disease; insulin-dependent diabetes; contact dermatitis;
KW psoriasis; graft rejection; bacterial infection; lepromatous leprosy;
KW tuberculosis; ischaemic brain injury; hypoxic brain injury; ds;
KW kidney ischaemia; reperfusion injury; acute bacterial meningitis;
KW excitotoxic brain damage; liver disease.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
FH 1.3615
FT CDS /*tag= a
FT /product= "Human CARD-12"
FT
XX
PN WO200130971-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US29643.
XX
PR 27-OCT-1999; 99US-0161822.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Bertin J, Robison KE;
XX
DR WPI; 2001-308628/32.
XX
P-PSDB; AAU02881.
XX
PT Isolated caspase recruitment domain-12 polypeptide and nucleic acids
PT encoding them, useful for treating and diagnosing disorders associated
PT with abnormal apoptosis such as cancer, arthritis and Alzheimer's
PT disease -

```

XX Disclosure; Fig 2; 93pp; English.
PS
XX The sequence represents a genomic DNA which encodes the human caspase
CC recruitment domain 12 (CARD-12) polypeptide. CARD domains are found in a
CC number of proteins that transmit signals that activate apoptosis and
CC inflammatory pathways in response to stress and other stimuli. Therefore,
CC CARD-12 and its corresponding nucleic acid may be used in treatment and
CC diagnosis of patients suffering from disorders associated with an
CC abnormal level (an increase or a decrease) of apoptotic cell death or
CC abnormal activity of stress-related pathways. The disorders include
CC cancer, viral infections (e.g. caused by poxviruses, adenoviruses),
CC autoimmune disorders (e.g. systemic lupus erythematosus, arthritis),
CC neurological disorders (e.g. Alzheimer's disease, amyotrophic lateral
CC sclerosis), haematologic diseases (e.g. aplastic anaemia, myocardial
CC infarction, stroke), inflammatory and immune system disorders (e.g.
CC Crohn's disease, insulin-dependent diabetes, contact dermatitis,
CC psoriasis, graft rejection), bacterial infections (e.g. tuberculosis,
CC leptomatous leprosy), ischaemic and hypoxic brain injury, kidney
CC ischaemia/reperfusion injury, excitotoxic brain damage, acute bacterial
CC meningitis and liver disease.
XX

SQ Sequence 3615 BP; 1041 A; 811 C; 845 G; 918 T; 0 other;

Alignment Scores:

Pred. No.:	Length:	3615
Score:	5188.00	Matches: 1014
Percent Similarity:	98.16%	Conservative: 1
Best Local Similarity:	98.07%	Mismatches: 18
Query Match:	95.04%	Indels: 1
DB:	22	Gaps: 1

US-09-697-089-2 (1-1024) x AAS03946 (1-3615)

QY 1 MetLsnPheIleIysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThValIle 20
Db 418 GTGATTTTCATTAAGGACAAATAGCCGACCTTATTCATAAAGTGGATGACCTGTTTA 477
QY 21 LysGlnIleThrAspAspLeuPheValTyrPsnValIleuAsnArgGluGluValAsnIle 40
Db 478 AAGCAATACAGATGACCTTTTGTATGAAATGTTTCGAATCCGAAAGAACTAAACATC 537
QY 41 IleCysCysGluIysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuIys 60
Db 538 ATTGCTGCGAGAGAGGTGAGCAGATGCTGCTAGAGGATCATTCATGATTTTGA 597
QY 61 LysGlySerGluSerCysAsnLeuPheLeuIysSerLeuIysGluTTPAsnTyrProleu 80
Db 598 AAGGATTCAGAGTCCCTGTAACCTCTTCTTAATCCCTTAAGGATGAACTATCCCTCA 657
QY 81 PheGlnAspLeuAsnGlyGlnSer----- 88
Db 658 TTTCAAGCACTTGATGCAAAAGTTTTCAGAGACACAGAAATTTGGGCTTCTTTAACATC 717
QY 89 -----LeuPheHisGlnThrSerGluGlnIysAspLeuAspAspLeuAla 102
Db 718 ACCTCTCTCTAATAGAGCTTTTTCATCAGACATCAGAAAGAGACTTGAGATTTGGCT 777
QY 103 GlnAspLeuIysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProleuGluIu 122
Db 778 CAGATTTTAAAGACTGTGTACCATACCCATCTTTTCGAACCTTTTATCCCTTGGTAA 837
QY 123 AspIleAspIleIlePheAsnLeuIysSerThrPheThrGluProValLeuTyrArgIys 142
Db 838 GATTTGATCATTTATTTAACTTGAAGAAACACCTTCACAGAAACCTGCTCTGGAGAG 897
QY 143 AspGlnHisHisIleArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuGln 162
Db 898 GACCAACACCATCACCGGTGAGACGCTGACCTGATGCGCTCCCTCAGAGCTCTCAG 957
QY 163 SerProCysIleIleGluGlyGluSerGlyIysGlyIysSerThrLeuLeuGlnArgIle 182
Db 958 AGCCCTGCAATCATTTGAAGGGGAATCTGGCAAAAGCAAGTCACCTCTCTGAGGAAAT 1017

QY 183 AlaMetLeuTyrGlySerGlyIysCysIysAlaLeuThrIysPheIysPheValPhePhe 202
Db 1018 GCCATGCTCTGGGCTCCCGGAAAGTGCAGAGCCTGTACCAAGTTCAATTCGTTCTTTC 1077
QY 203 LeuArgLeuSerArgAlaGlnGlyIleGlyLeuPheIleThrLeuIysAspGlnLeuAsp 222
Db 1078 CTCGGCTCACAGAGGCCCGAGGGTGGACTTTTAAACCCCTGTGTATCAACTCTGTGAT 1137
QY 223 IleProGlyThrIleArgIysGlnThrPheMetAlaMetLeuLeuIysLeuArgGlnArg 242
Db 1138 ATACCTGGCACAAATCAGAGAACACACATTCATGGCCATGCTGCTGAAGCTCGGCAAGG 1197
QY 243 ValLeuPheLeuLeuAspGlyTyrAsnGluPheIysProGlnAsnCysProGluIleGlu 262
Db 1198 GTCTTTTCCCTCTTGATGCTGTACAAATTCAGGCCCGCAAGCTCGCCAGAAATCGAA 1257
QY 263 AlaLeuIleIysGluAsnHisArgPheIysAsnMetValIleValIleThrThrGlu 282
Db 1258 GCCCTGATTAAGGAAACACACCGCTTCAGAAACATGTGTCATCCACCTACACCTGAG 1317
QY 283 CysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMetThrGlu 302
Db 1318 TGCCTGAGGACATACGCGAGTTGTGCTGCTGCTGCTGAGGTGGGATATATACAGAA 1377
QY 303 AspSerAlaGlnAlaLeuIleArgGluValLeuIleIysGluLeuAlaGluGlyLeuLeu 322
Db 1378 GACAGCGGCCAGGCTCTCATCCGAAAGTGTGATCAAGAGAGCTTGCTGAAGGCTTGTTG 1437
QY 323 LeuGlnIleGlnIysSerArgCysLeuArgAsnLeuMetIysThrProleuPheValAla 342
Db 1438 CTCCAAAATTCAGAAATCCAGGTGCTTGGAGATCTCATGAAAGACCCCTCTCTTGTGTGTC 1497
QY 343 IleThrCysAlaIleGlnIleMetGlyGluSerGluPheHisSerHisThrGlnThrLeu 362
Db 1498 ATCATCTGTGCATTCACGATGAGTGAAGTGAAGTTCACCTTCACACACAAACACGCTG 1557
QY 363 PheHisThrPheTyrAspLeuLeuIleGlnIysAsnIysHisIysGlyValAla 382
Db 1558 TTCCATACCTCTGTATGATCTGTGTATCAGAAACAAACAAACATTAAGGTGTGCT 1617
QY 383 AlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGlyValPhe 402
Db 1618 GCAAGTCACTTCATTCGAGAGCTGTGACACATGTGAGACCTTACGCTGAGAGGTGTGTC 1677
QY 403 SerHisIysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspValLeuLeu 422
Db 1678 TCCCAACAAGTTGATTTGAACTGCGAGATGTTCACGCTGAATGAGAGATGCTCTGCTG 1737
QY 423 ThrThrGlyLeuLeuCysIysTyrThrAlaGlnArgPheIysProIysTyrIysPhePhe 442
Db 1738 ACAACTGGGCTCTCTGTAAATATACAGCTCAAGGTTCAAGCCAAAGTATAAATTCCTT 1797
QY 443 HisIysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuThrSerHis 462
Db 1798 CACAAGTATTTCCAGGAATTCACAGACAGCAAGAACTCACACAGTTTATATACCTTCAT 1857
QY 463 GluProGluGluValThrIysGlyAsnGlyTyrLeuGlnIysMetValSerIleSerAsp 482
Db 1858 GAGCCAGAGAGGTGACCAAGGGGAATGTACTTCGAGAAATGCTTCCATTTCCGAC 1917
QY 483 IleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGluAlaThr 502
Db 1918 ATTACATCTCATATAGACAGCTGCTCGGTACACCTGTGGGTATCTGTGAAGCCAC 1977
QY 503 ArgAlaValMetIysHisLeuAlaAlaValIysGlnHisGlyCysIleLeuGlyLeuSer 522
Db 1978 AGGGCTGTTATGAAGCACCTGCGACAGATGTATCAACCGCTGCTCTGGACTTTC 2037
QY 523 IleAlaIysArgProleuTyrArgGlnIysSerLeuGlnSerValIysAsnThrThrGlu 542
Db 2038 ATCGCAAGAGGCTCTCTGTGAGACAGAAATCTTTGCAAAAGTGTGAATAAACACCACTGAG 2097

QY 543 GINGLIIleLeuLYsAlaIleasnIleasnSerPheValGluCysGlyIleHisLeuTyr 562
 DB 2098 CAGAGAAATTCGTAAGCCATAACATCAATTCCTTGTAGAGTGTGGCATTCATTTATAT 2157
 QY 563 GINGIuSerThrSerLYsSerAlaLeuSerGInguPheGluAlaPhePheGInguLYs 582
 DB 2158 CAGAGAGACATCCAAATACACCCCTGAGCCCAAGAAATTTGAAGCTTTCTTCAAGTAA 2217
 QY 583 SerLeuTyrIleasnSerGlyasnIleProAspTyrIleuPheAspPheHeuHisLeu 602
 DB 2218 ACCCTATATATCACTCAGGGAACATCCCGATTAATTTGACTTCTTTAAACAATTTG 2277
 QY 603 ProAsnCysAlaSerAlaLeuAspPheIleLYsLeuAspPheTyrGlyValaIleAla 622
 DB 2278 CCCAATTTGTGCAAGTCCCTGGACTTCATTAACAGGACTTTTATGGGGAGCTATGGCT 2337
 QY 623 SerTPGILuLYsAlaGluAspThrGlyIleHisMetGluGluAlaProGluThr 642
 DB 2338 TCATGGGAAAGGCTGCAGAAACACAGGTGGAAATCCACATGGAAAGAGCCCCAGAAACC 2397
 QY 643 TyrIleProSerArgAlaValSerLeuPheAsnTrpLYsGInguPheArgThrLeu 662
 DB 2398 TACATTCCTCCAGGAGGCTGTATCTTGTCTTCACTGGAAACAGAAATTCAGACTCTG 2457
 QY 663 GluValIThrLeuArgAspPheSerLYsLeuAsnLYsGInAspIleThrTyrLeuGlyLYs 682
 DB 2458 GAGGTACACACTCCGGGATTTCCAGCAAGTTGAATTAAGCAAGATATCAGATATCTGGGGAAA 2517
 QY 683 IlePheSerSerAlaThrSerLeuArgLeuGInIleLYsArgCysAlaGlyValaIleGly 702
 DB 2518 AATATCAGCTCTGCCACAAGCTCAGGCTGCAAAATAAAGATGTCGTGGCTGGTGA 2577
 QY 703 SerLeuSerLeuValLeuSerThrCysLYsAsnIleTyrSerLeuMetValaIleAsp 722
 DB 2578 ACCCTCAGTGTGCTCTCAGCCCTGTAAACAATTTCTCTCATGTGTGAACCCACT 2637
 QY 723 ProLeuThrIleGluAspGluArgHisIleThrSerValIThrAsnLeuYsThrLeuSer 742
 DB 2638 CCCCTCACCATGAAAGATGAGAGCACATCATCTGTATACAACTGAAACCTTGAT 2697
 QY 743 IleHisAspLeuGInAsnGInArgLeuProGlyGlyLeuThrAspSerLeuGInLYsLeu 762
 DB 2698 AATTCATGACCTACAAATCAACAGGCTGCCGTGTCTGACAGACAGCTTGCTAACTTG 2757
 QY 763 LysAsnLeuThrLYsLeuIleMetAspAsnIleLYsMetAsnGluGluAspAlaIleLYs 782
 DB 2758 AAGAACCTTACAAAGCTCTAATAGATACATAAAGATGAATGAAGAAATGCTATAAA 2817
 QY 783 LeuAlaGluGlyLeuLYsAsnLeuLYsLYsMetCysLeuPheHisLeuThrHisLeuSer 802
 DB 2818 CTAGCTGAAGGCTGAAAAACCTGAAGAAGATGTGTTTATTTTCATTGTGACCCACTGTGT 2877
 QY 803 AspIleGlyGlyIleMetAspTyrIleValLYsSerLeuSerSerGluProCysAspLeu 822
 DB 2878 GACATTTGGAGAGGAGATGATTACATAGTCAAGTCTCTGTCAAGTGAACCTGTGACTT 2937
 QY 823 GluGluIleGInLeuValSerCysCysLeuSerAlaAsnAlaValLYsIleLeuAlaGIn 842
 DB 2938 GAAAGAAATTCATATAGTCTCTGCTGCTGTCTGCAAAAGCAGTGAATAATCTAGCTCAG 2997
 QY 843 AsnLeuHisAsnLeuValLYsLeuSerIleLeuAspLeuSerGluAsnTyrLeuGluLYs 862
 DB 2998 AATCTTCACAAATTTGTGCAAACTGAGCATTTTGATTTATCGAAATAATTAACCTGAAAAA 3057
 QY 863 AspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGInLeuThr 882
 DB 3058 GATGAAATGAAGCTCTTCATGAATCAGACAGATGAACGCTGTAGAACAGCTCAGC 3117
 QY 883 AlaLeuMetLeuProTrpGlyCysAspValGInguLYsSerLeuSerSerLeuLeuLYsHis 902
 DB 3118 GCACGTGATGCTCCCTGGGGCTGTGACGTGCAAGGACAGCTGTGTTGTTGAAACAT 3177
 QY 903 LeuGluGluValProGInLeuValLYsLeuGlyLeuLYsAsnTrpArgLeuThrAspThr 922

DB 3178 TTGGAGAGAGTCCCAACACTGCTCAAGCTTGGGTTGAAAAACTGGAGACTCAACATACA 3237
 QY 923 GIuIIeArgIleLeuGInLYaIaPhePheGlyLYsAsnProLeuLYsAsnPheGInguLeu 942
 DB 3238 GAGATTAGAAATTTGTGTCATATTTTGGAAAGAACCCCTGAAAAACTTCCAGCAGTTG 3297
 QY 943 AsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyValaPheGlu 962
 DB 3298 AATTTGGCGGGAATCGTGTGAGCAGTGAATGATGGCTTGCTTCATGGGGTATTTTGAG 3357
 QY 963 AsnLeuLYsGInLeuValaPhePheAspPheSerThrLYsGInuPheLeuProAspProAla 982
 DB 3358 AATCTTAAGCAATTTAGTGTTTTGTGACTTGTACTAGTAAAGAAATTTCTACTGATCCAGCA 3417
 QY 983 LeuValArgLYsLeuSerGInValLeuSerLYsLeuThrPheLeuGInguAlaArgLeu 1002
 DB 3418 TTAGTCAGAAAACTTAGCCCAAGTGTATCCCAAGTTAACTTTCTGCAGAAAGCTAGGCTT 3477
 QY 1003 ValGlyTrpGInPheAspAspAspAspLeuSerValIleThr 1016
 DB 3478 GTTGGGTGGCAATTTGATGATGATGATCTCAGTGTATTACA 3519
 RESULT 6
 AAH78218
 ID AAH78218 standard; DNA; 2215 BP.
 AC AAH78218;
 XX
 DT 26-NOV-2001 (first entry)
 DE Nucleotide sequence of a human secreted polypeptide.
 KW Human; secreted polypeptide; nervous disease; muscular disease; tumour;
 KW gastrointestinal ulceration; spinal cord disease; trachea disease;
 KW thyroid gland disease; ovary disease; prostate disease; heart disease;
 KW renal gland disease; small intestine disease; thymus disease;
 KW lymph node disease; muscular system disease; colon disease;
 KW lipase deficiency; cystic fibrosis; pancreatitis; clot formation;
 KW myocardial infarction; angioplasty; liver disease; coagulation disorder;
 KW microbial disease; immune disorder; inflammation; transplant rejection;
 KW bone thickness; bone density; ferroxidase loss; apoptosis;
 KW vascular smooth cell proliferation; vaccine; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..2214
 FT /*tag= a
 FT /product= "secreted polypeptide"
 FT /note= "no termination codon given"
 XX
 PN WO200166690-A2.
 PD 13-SEP-2001.
 XX
 PE 05-MAR-2001; 2001WO-US07143.
 XX
 PR 06-MAR-2000; 2000US-0187107.
 PR 13-MAR-2000; 2000US-0188916.
 PR 03-OCT-2000; 2000US-0236874.
 PR 03-OCT-2000; 2000US-0237846.
 XX
 PA (SMK) SMITHKLINE BEECHAM CORP.
 PA (SMK) SMITHKLINE BEECHAM PLC.
 XX
 PI Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;
 XX
 DR WPT. 2001-570768/64.
 DR P-PSDB; AAG67526.
 XX
 PT Novel isolated secreted polypeptide useful for treating nervous and
 PT muscular diseases, gastrointestinal ulceration, coagulation and immune

PT disorders, microbial diseases, inflammation and transplant rejection -
XX
PS Claim 2; Page 52-53; 102pp; English.
XX
CC The present sequence encodes a human secreted polypeptide. The
CC secreted polypeptides and polynucleotides are useful for treating
CC nervous and muscular diseases, for inhibiting tumor formation and
CC metastasis, for treating gastrointestinal ulceration, for preventing
CC and treating diseases in spinal cord, thyroid gland, ovary, prostate,
CC renal gland, small intestine, heart, trachea, thymus, lymph node,
CC muscular system and colon, for treating lipase deficiency in cystic
CC fibrosis and pancreaticitis, for treating undrizable clot formation
CC such as myocardial infarction, during angioplasty and all surgical
CC procedures that require decreased blood clot formation, for treating
CC liver diseases, coagulation disorders and microbial diseases, for
CC treating immune disorders, for treating inflammation and transplant
CC rejection, for enhancing bone thickness and increasing bone density,
CC for reducing the loss of essential ferroxiases, for suppressing
CC apoptosis, and for regulating vascular smooth cell proliferation. They
CC may also be used as vaccines.
XX

US-09-697-089-2 (1-1024) x AAH78218 (1-2215)

Alignment Scores:
Pred. No.: 0 Length: 2215
Score: 3950.00 Matches: 737
Percent Similarity: 99.86% Conservative: 0
Best Local Similarity: 99.86% Mismatches: 1
Query Match: 72.36% Indels: 0
DB: 22 Gaps: 0

15 MetcylmethrValileysGlnIlethrAspAspleuPheValITrPasnValleuasn 34
1 ATGGGAAATGACTGTATTAAGCAATACAGATGACCATTTGTATGGAATGTTCTGAT 60
35 ArgcgluGluValAsnIleIleCysCysGluValGluGlnAspAlaAlaArgGlyIle 54
61 CGCAAGAGATTAACATCATTTGCTGCGAGAGGTGAGCAGATGCTGTAAGAGGATC 120
55 IleHisMetIleLeuIleuIleGlySerGluSerCysAsnIleuPheLeuIleuSerLeu 74
121 ATTACATGATTTTGAAGAGGTTTCAAGTCCGTAACTCTTTTAAATCCCTTAAG 180
75 GluITrPasnIleuPheGlnAspleuAsnGlyGlnSerIleuPheHisGlnThrSer 94
181 GAGTGGAACTATCCTCATTTTCAGACTGTGATGACAAATCTTTTTCATCAGACATCA 240
95 GluGlyAspleuAspAspleuAlaGlnAspleuIleuIleuIleuIleuIleuIleu 114
241 GAAGGAGACTTGGAGATTGCTCAGGATTTAAAGCACTGTACATACCCCATCTTTT 300
115 LeuAsnIleuPheIleuGlyAspleuIleuIleuIleuIleuIleuIleuIleuIleu 134
301 CTGACATTTTATCCCTTGGAGATATGACATTTATTTTAACTTGAAGAGCACTTC 360
135 ThrGluProValleuITrPargLysAspGlnHisHisIleuIleuIleuIleuIleu 154
361 ACAGAACTGTCCTGTGGAGAGAGACCAACATCCGCGTGGAGACTGACCTG 420
155 AsnGlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGlyGlyIleuSerGlyIle 174
421 AATGGCTCTCGAGGCTCTTCAAGAGCCCTGCATCATTTGAAGGGGATTCGGAAGGC 480
175 LysSerThrLeuLeuGlnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 194
481 AAGTCCACTGCTGCGAGCGAATGCAATGCTCTGGGGCTCCGGAAGATGCAAGGCTTG 540
195 ThrIlePheIleuPheValIleuPheLeuArgLeuSerArgAlaGlnIleuIleuPheGln 214
541 ACAGAGTTCAATTCGCTTCTTCTCCGCTCAGCAAGGCCCAAGGGGAGCTTTTGA 600

215 ThrIleCysAspGlnLeuLeuAspIleProGlyThrIleArgGlyGlnThrPheMetAla 234
601 ACCCTCTGTATCAACTCTCGATATACCTGGACAAATCAGAGAGCAACATTCATGCGC 660
235 MetLeuLeuIleuIleuArgGlnArgValLeuPheLeuLeuAspGlyIleuIleuIleu 254
661 ATGCTGCTGAAGCTCGGGCAGAGGGTCTTTTCTCTTGTGATGCTCAATGAATTCAG 720
255 ProGlnAsnCysProGluIleGlnAlaLeuIleuIleuIleuIleuIleuIleuIleu 274
721 CCCAGAACTGCCCAAGATATGAAAGCTGTATTAAGGAAACCAACCGCTTAAAGACTG 780
275 ValIleValIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 294
781 GTCATCTGCACACACTACACATGAGAGGCTGAGGACATACGCGAGTTGGCGCTGACT 840
295 AlaGluValIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 314
841 GCTGAGGTGGGGATATACAGAAAGACAGCCCGAGGCTCTCATCCGGAAGTCTGTATC 900
315 LysGluLeuAlaGluGlyLeuLeuLeuGlnIleuIleuIleuIleuIleuIleuIleu 334
901 AAGGAGCTTGTCTGAAGGCTTGTCTGCTCAATTCAGAAATCCAGTGTAGGAAATTC 960
335 MetIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 354
961 ATGAAGACCCCTCTCTTGTGTGATCATCTGTGCAATCCAGATGGGGAAGTGAAGTTC 1020
355 HisSerHisIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 374
1021 CACTCTCACACAAACCAACCTCTTCCATACCTTCTATGATCTGTGATACACAAAC 1080
375 LysHisIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 394
1081 AAACACAAACATTAAGAGTGTGCTGCAAGTACATTCATTCGAGACCTGGACATGAGGA 1140
395 AspleuAlaLeuGluGlyValIleuPheSerHisIleuPheAspPheGluLeuGlnAspValSer 414
1141 GACCTAGCTCTGAGAGGCTGTCTCCACAAAGTTTGAATTCGAATCCAGAGATGTCTCC 1200
415 SerValAsnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 434
1201 AGCGTGAATGAGATGCTCTCTGACACATGGGCTCTCTTAATATACAGCTCAAGG 1260
435 PheIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 454
1261 TTCAAGCAAAAGTATTAATTTCTTCAAGATCATTCAGAGGTACAGAGGAGCAAGA 1320
455 LeuSerSerLeuLeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 474
1321 CTCAGAGATTATTTGACGCTCTCATGAGCCAGAGAGGTGACCAAGGGGAAATGTTACTTG 1380
475 GlnIleuMetValSerIleuSerAspIleuIleuIleuIleuIleuIleuIleuIleu 494
1381 CAGAAATATGTTTTCATTTTCGACATTTTCATTCCTTATGACAGCTCTCTCGGTACACC 1440
495 CysGlySerSerValIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 514
1441 TGTGGGTCATGTGTGGAAGCCACAGGCGTGTATGAAGCACTGCGAGAGGTATCAAA 1500
515 HisGlyCysLeuLeuGlyLeuSerIleuAlaIleuIleuIleuIleuIleuIleu 534
1501 CACGGCTGCCCTTCTCGGACTTTCATTCAGCCCAAGAGGCTCTCTGAGACAGAAATCTT 1560
535 GlnSerValIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 554
1561 CAAGGTGTGAAGAAACACACCTGAGCAGAAATTTGTGAAGCCATTAATATTCCTTT 1620
555 ValIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 574
1621 GTAGAGGTGTGCATTCATTTATTCAGAGAGTATCATCAATCAGCCCTGAGCAAGAA 1680
575 PheGluAlaIleuPheGlnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 594

|||||
Db 1681 TTGAAGCTTCTTCAAGAGTAAAGCTTATATATCAACTCAGGGAACATCCCGATTAC 1740
QY 595 LeuphAspPheGluHisLeuProAsnCysAlaSerAlaLeuAspHelleuLeu 614
Db 1741 TTATTTGACTTCTTTGACATTGTGCCAATGTGCAGTGCCCTGGACTTCTTTAAACG 1800
QY 615 AspPheTYrGlyAlaMetAlaSerTPGluYsAlaAlaGluAspThrAlaGly 634
Db 1801 GACTTTTATGGGGAGCATATGCTTCATGGGAAAAGGCTGCAGAAACACACAGTGAATC 1860
QY 635 HisMetGluGluAlaProGluThrTYrIleProSerArgAlaValSerLeuPheAsn 654
Db 1861 CACATGGAAGAGGCCCAAAACCTACATTCACAGAGGCTGTATCTTTCTTCAAC 1920
QY 655 TrpYsGluGluPheArgThrLeuGluValThrLeuArgAspPheSerLysLeuAsn 674
Db 1921 TGGAAAGCAGAAATTCAGACTCTGGAGGTCACACTCCGGATTTGACAAATGAATAG 1980
QY 675 GluAspIleThrTYrLeuGlyLysIlePheSerSerAlaThrSerLeuArgLeuGln 694
Db 1981 CAAAGTATCAGATATCTGGGGAAATATTCAGCTCTGCCACAGCCTCAGGCTGCAATA 2040
QY 695 LysArgCysAlaGlyValAlaGlySerLeuSerLeuValLeuSerThrCysLysAsn 714
Db 2041 AAGAGATGCTGCTGTGGCTGGAAGCCTCAGTTGTGCTCAGACCTGTAAGAACAT 2100
QY 715 TyrSerLeuMetValGluAlaSerProLeuThrIleGluAspGluArgHisIleThr 734
Db 2101 TATTTCTCATGTGTGAAGCCAGTCCCTCACATAGAAAGACAGGACATCTCATCT 2160
QY 735 ValThrAsnLeuLysThrLeuSerIleHisAspLeuGluAsnGluArgLeuPro 752
Db 2161 GTAAACAACCTGAAACCTTGAGTATCTGACTACAGATCAACGGCTGCCG 2214
RESULT 7
AAH99581
ID AAH99581 standard; cDNA; 2950 BP.
XX
AC AAH99581;
XX
DT 16-OCT-2001 (first entry)
XX
DE Human protein encoding cDNA sequence SEQ ID NO:416.
XX
KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
KW antibacterial; endocrine; cardiant; central nervous system; virucide;
KW anti-HIV; fungicide; antitumagen; cardiovascular; antianaemic; anaemia;
KW dermatological; haemostatic; vulnary; antileuc; osteopathic; eczema;
KW neuroprotective; antidiabetic; antidiabetic; cytostatic;
KW immunostimulant; gene therapy; antiparkinsonian; infection;
KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
KW thrombocytopenia; osteoporosis; severe combined immunodeficiency;
KW allergic rhinitis; diabetes; multiple sclerosis; depression;
KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
KW neurological disorder; ss.
OS Homo sapiens.
XX
XX WO200153455-A2.
PM
PD 26-JUL-2001.
XX
XX 22-DEC-2000; 2000MO-US35017.
PF
XX 23-DEC-1999; 99US-0471275.
PR 21-JAN-2000; 2000US-0486725.
PR 25-APR-2000; 2000US-0552317.
XX

PA (HYSE-) HYSEQ INC.
XX
XX Tang YF, Liu C, Drmanac RT;
PI
XX WPI: 2001-457603/49.
DR
XX P-PSDB: AAM25640.
PT Isolated human polynucleotides encoding polypeptides, useful for the
PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
XX
XX Claim 1; Page 511-512; 1217pp; English.
PS
XX
XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
CC AAM25963. The proteins can have activities based on the tissues and
CC cells they are expressed in, such as: antiinflammatory; antirheumatic;
CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
CC central nervous system; virucide; anti-HIV; fungicide; antitumagen;
CC cardiovascular; antianaemic; antidiabetic; haemostatic; vulnary;
CC antileuc; osteopathic; dermatological; antiallergic; antidiabetic;
CC antidiabetic; cytostatic; neuroprotective; antidiabetic; antidiabetic;
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
CC encoding them can be used in gene therapy, antisense therapy and vaccine
CC production. The proteins and polynucleotides are useful for screening for
CC agonists or antagonists of a protein and for the treatment and diagnosis
CC of disorders associated with the activity of a protein e.g. inflammation,
CC rheumatoid arthritis, arthritis, pancreatitis, cardiac dysfunction,
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
CC anaemia, platelet disorders, thrombocytopenia, wounds, burns, ulcers,
CC osteoporosis, severe combined immunodeficiency, eczema, allergic
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
CC neurological disorders.
SQ Sequence 2950 BP; 915 A; 592 C; 628 G; 815 T; 0 other;
XX
Alignment Scores:
Pred. No.: 0 Length: 2950
Score: 3346.00 Matches: 638
Percent Similarity: 99.53% Conservative: 1
Best Local Similarity: 99.38% Mismatches: 3
Query Match: 61.29% Indels: 0
DB: 22 Gaps: 0
US-09-697-089-2 (1-1024) x AAH99581 (1-2950)
QY 383 AlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluValAlaPhe 402
Db 2 GCAAGTGAATTCATTCCGAGGCTGGACCACTGTGATACCTATCTGTGAGGCTGTTC 61
QY 403 SerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspValLeuLeu 422
Db 62 TCCCAAGATTGATTTGCACATGCAAGATGTGTCACAGCTGAATGAGCATCTCTGCG 121
QY 423 ThrThrGlyLeuLeuCysLysTYrThrAlaGlnArgPheLysProLysTYrLysPhePhe 442
Db 122 ACACTGGGCTCTCTGTAATATACAGCTCAAAGTTTCACCCAAAGTATATATCTTT 181
QY 443 HisLysSerPheGluGluTYrThrAlaGlyArgLeuSerSerLeuLeuThrSerHis 462
Db 182 CACAAGTCAATTCAGAGATGACACAGCAGCAACACACAGAGTTTATGACGTCATC 241
QY 463 GluProGluGluValThrLysGlyAsnGlyTYrLeuGlnLysMetValSerLysSerAsp 482
Db 242 GAGCCAGAGAGATGACCAAGGGGAATGTTACTTGCAAAATGTTTCCATTTCCGAGC 301
QY 483 IleThrSerThrTYrSerSerLeuLeuArgTYrThrCysGlySerSerValGluAlaThr 502
Db 302 ATTACATCACTTATAGACAGCTGCTCCGATACACTTGTGGTCAATCTGTGAACCCACC 361
QY 503 ArgAlaValMetLysHisLeuAlaAlaValTYrGlnHisGlyCysLeuLeuGlyLeuSer 522
Db 362 AGGCTGTATAGACACCTCGACACAGATGATCAACACAGGCTGCTCTCGGACTTTC 421

QY 523 ILeaIaIyArGProLeuTrPaRgInGInuSerLeuGInSerValIyAsnThrThGInu 542
 |||||||
 Db 422 ATGCCAAGAGCCTCTCTGGAGACAGAACTTTGCCAAATGTGCAAAACACCACTAG 481
 QY 543 GInGInuIleuLySaIaIleAsnIleAsnSerPheValGInGInuIleHisLeuTr 562
 |||||||
 Db 482 CAAAGAAATTCGAAAGCCATTAATCCCTTTGTAGAGTGGCATCATTTATAT 541
 QY 563 GInGInuSerTrSerLySerValLeuSerGInGInuPheGInuAlaPhePheGInGInu 582
 |||||||
 Db 542 CAAGAGATATCATCAATTCAGCCCTGAGCCAGAAATTTGAAGCTTTCTTCAGAGTAA 601
 QY 583 SerLeuTrYrIleAsnSerGInyAsnIleProAspTrYrLeuPheAspPheGInuHisLeu 602
 |||||||
 Db 602 AGCTATATATCACTCACTGAGAACATCCCGATTACTATTGACTCTTTGAACATTTG 661
 QY 603 ProAsnCySaIaSerAlaLeuAsPheIleLyLeuAsPheTrYrGInyAlaMetAla 622
 |||||||
 Db 662 CCCAATGTGTGCAAGTCTGTGACTCAWTAACTGGGCTTTATGGGGAGCATGTGCT 721
 QY 623 SerTrpGInuLySaIaIaIaGInAsPheTrGInyIleHisMetGInGInuAlaProGInuTr 642
 |||||||
 Db 722 TCATGGGAAAGGCTGCGAAGACAGAGTGGAATCCCATGGAGAGAGGCCCAAGAAC 781
 QY 643 TyrIleProSerArGaIaValSerLeuPhePheAsnTrpLySInGInuPheArGTrLeu 662
 |||||||
 Db 782 TACATTCGCCACAGGGGCTGTCTTTGTTCTTCAACTGGAAGAGGAATTCAGGACTGTG 841
 QY 663 GluValAlrLeuArGAsPheSerLySerLySInuLySInuAlaPheTrYrLeuGInyLyS 682
 |||||||
 Db 842 GAGGTCACACTCCGGGATTTGAGCAAGTTGAATAGCAAGATATTCAGATTCGGGGAA 901
 QY 683 IlePheSerSerAlaThrSerLeuArGInuIleLySArGySaIaGInyValaIaGIny 702
 |||||||
 Db 902 ATATTACACTCTGCCACAGACCTCAGGCTGCAATTAAGAATATGTGCTGTGCTGA 961
 QY 703 SerLeuSerLeuValLeuSerThrCysLySAsnIleYrSerLeuMetValGInuAlaSer 722
 |||||||
 Db 962 AGCTCAGATTGTCCTCAGCAGCCTGTMAACAATTTATCTCTCATGTGTGGAAGCCAGT 1021
 QY 723 ProLeuTrIleGInuAsPheGInuArGHisIleThrSerValThrAsnLeuLyThLeuSer 742
 |||||||
 Db 1022 CCCCTCACCATAAGAGAGAGGACACATCTGTAAACCTGAAACCTGTGCTG 1081
 QY 743 IleHisAsPheGInuAsnGInArGLeuProGInyLeuTrAsPheSerLeuGInyAsnLeu 762
 |||||||
 Db 1082 ATTCATGACCTACAGAAATCAACGGGTGCGGTGCTGACTGACAGCTTGGTAACTTG 1141
 QY 763 LysAsnLeuThrLySLeuIleMetAsPAsnIleLySMeLAsnGInuAlaPheAlaIleLyS 782
 |||||||
 Db 1142 AAGAACCTTACAAAGCTCATATGATTAACATTAAGATGAATGAAGATGCTATAAA 1201
 QY 783 LeuAlaGInuGInuLySAsnLeuLySMeLysMeLysPheHisLeuThrHisLeuSer 802
 |||||||
 Db 1202 CTAGCTGAAGGCTGAAAGAACTGAGAGAGATGTGTTATTTCAATTTACCCACTGTCT 1261
 QY 803 AspIleGInyGInuLyMetAsPTrYrIleValLySerLeuSerSerGInuProCysAsPhe 822
 |||||||
 Db 1262 GACATTTGAGAGGGAATGATTAATCATAGTCTCTGTCAGAGGAAGCCCTGTGACTTT 1321
 QY 823 GluGInuIleGInuLeuValSerCysCysLeuSerAlaAsnAlaValLySileuAlaGIn 842
 |||||||
 Db 1322 GAAGAAATTCATATAGTCTCTGCTGCTTGTCTCAATTCAGAGGAATCTAGCTAG 1381
 QY 843 AsnLeuHisAsnLeuValLySLeuSerIleLeuAsPheSerGInuAsTrYrLeuGInuLyS 862
 |||||||
 Db 1382 AATCTTCACAAATTTGGTCAAACTGAGCATCTTGTATTTATAGAAATTAACCTGAAAAA 1441
 QY 863 AspGInyAsnGInuAlaLeuHisGInuLeuIleAsPArGMeLAsnValLeuGInuLeuThr 882
 |||||||
 Db 1442 GATGGAATGAAGCTTTTCATGAACGTATGCACAGGATGAAGCTGTAGAAACGCTCACC 1501

QY 883 AlaLeuMetLeuProTrpGInyCysAsPValGInGInySerLeuSerSerLeuLeuLyHis 902
 |||||||
 Db 1502 GCACGTAGTCCCTCGGCGCTGTGAGCTGCAAGGACGCCCTGAGACAGCTGTGAACAT 1561
 QY 903 LeuGInuGInuAlProGInuLeuValLySLeuGInyLeuLySAsnTrpArGLeuThrAsPThr 922
 |||||||
 Db 1562 TTGGAGAGGAGGCCCAACCTGTCAGCTTGCGTTGAAAACTGGAACCTCACAGATACA 1621
 QY 923 GluIleArGInuLeuGInyAlaPhePheGInyLySAsnProLeuLySAsnPheGInuLeu 942
 |||||||
 Db 1622 GAGATTGAATTTTATAGTGCATTTTGGAGAAAGAACCTTCGAAAACTTCACAGACTTG 1681
 QY 943 AsnLeuAlaGInyAsnArGValSerSerAsPGLyTrPheuAlaPheMetGInyValPheGIn 962
 |||||||
 Db 1682 AATTTGGGGGAAATGCGTGCAGCAGATGATGATGCTTGCTTCATGGGGTATTTGAG 1741
 QY 963 AsnLeuLySInuLeuValPhePheAsPheSerThrLySGLuPheLeuProAsPProAla 982
 |||||||
 Db 1742 AATCTTAAGCAATTAAGTGTGTTTGTGACTTAACTAAAGAAATTCATCTGATCCAGCA 1801
 QY 983 LeuValArGInyLeuSerGInValLeuSerLySLeuThrPheLeuGInuAlaArGLeu 1002
 |||||||
 Db 1802 TTAGTCAGAAACCTTAGCCAGAGTGTATCCAAAGTTAACTTTTCGCAAGAAAGTAAAGCTT 1861
 QY 1003 ValGlyTrpGInuPheAsPAsPAsPLeuSerValIleThrGInyAlaPheLySLeuVal 1022
 |||||||
 Db 1862 GTTGGGTGGCAATTTGATGATGATGATCATCAGTGTATTAACAGTGTCTTTAACTAGTA 1921
 QY 1023 ThrAla 1024
 |||||||
 Db 1922 ACTGCT 1927
 RESULT 8
 ABRK22766
 ID ABRK22766 standard; cDNA; 891 BP.
 AC ABRK22766;
 XX 26-MAR-2002 (first entry)
 DT XX
 DE Human cDNA encoding CLAN NACHT.
 XX
 KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
 KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
 KW autoimmune disease; inflammation; keratinocyte hyperplasia;
 KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
 KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
 KW leukemia; allergy; arthritis; lupus; Crohn's syndrome;
 KW Crohn's disease; graft-versus-host disease; stroke;
 KW myocardial infarction; heart failure; neurodegenerative disease;
 KW Parkinson's disease; Alzheimer's disease; HIV;
 KW human immunodeficiency virus infection.
 XX
 OS Homo sapiens.
 XX
 PN W0200190156-A2.
 XX
 PD 29-NOV-2001.
 XX
 PE 24-MAY-2001; 2001MO-US17158.
 XX
 PR 24-MAY-2000; 2000US-0579240.
 PR 10-OCT-2000; 2000US-0686347.
 PR 14-MAR-2001; 2001US-275980P.
 PR 23-MAY-2001; 2001US-0864921.
 XX
 PA (BURN-) BURNHAM INST.
 XX
 PI Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
 PI Oliveira VAM, Hayashi H, Pawlowski K;
 XX
 DR WPI: 2002-083086/11.
 DR P-PSDB: AAU80872.

XX New caspase recruitment domain (CARD)-containing polypeptides and
 PT encoding nucleic acids, useful for treating abnormal cell proliferation
 PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
 PT arthritis or stroke

XX Claim 1: Page 200-201; 216pp; English.

XX The invention relates to an isolated caspase recruitment domain (CARD)
 CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
 CC from it, and the polynucleotides encoding them. Also included are a
 CC recombinant vector comprising the polynucleotide, recombinant cells
 CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
 CC and insect cells) and an anti-CARD antibody. The CARD-containing
 CC polypeptide and CARD-encoding nucleic acid are useful for treating a
 CC pathology characterised by abnormal cell proliferation (e.g. cancer). In
 CC abnormal cell death (apoptosis), autoimmune diseases or inflammation.
 CC Particular, the polypeptide and nucleic acid are useful for treating
 CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
 CC muscle cell proliferation in arteries following balloon angioplasty
 CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,
 CC allergies, arthritis, lupus, Schogen's syndrome, Crohn's disease,
 CC graft-versus-host disease, stroke, myocardial infarction, heart failure,
 CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
 CC disease) or immunodeficiency associated disease (e.g. human
 CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
 CC in a variety of diagnostic applications. The present sequence is a
 CC cDNA encoding a CARD domain containing protein.

XX Sequence 891 BP; 237 A; 228 C; 217 G; 209 T; 0 other;

Alignment Scores:

Pred. No.:	3-21e-228	Length:	891
Score:	1598.00	Matches:	296
Percent Similarity:	99.66%	Conservative:	0
Best Local Similarity:	99.66%	Mismatches:	1
Query Match:	29.27%	Indels:	0
DB:	24	Gaps:	0

US-09-697-089-2 (1-1024) x ABR227266 (1-891)

QY 161 LeuGlnSerProCysIleIleGlnGlyGlnSerGlyGlySerThrLeuLeuGln 180
 DB 1 CTTCAAGAGCCCTGCATCTTGAAGGGAAATCTGGCAAGGACGTCCTGCGCAG 60
 QY 181 ArgIleAlaMetLeuTrpGlySerGlyGlyCysLysAlaLeuThrLysPheLysPheVal 200
 DB 61 CGCATTCGCATGCTCTGGGGCTCCGGAAGTCAAGGCTCTGACCAAGTCAAAATCCGTC 120
 QY 201 PhePheLeuArgLeuSerArgAlaGlnGlyLysLeuPheGluThrLeuLysAspGlnLeu 220
 DB 121 TTCCTCTCCGCTCGACGAGGGCCAGGGGTGACTTTTGAAGCCCTGTCATCAACTC 180
 QY 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 240
 DB 181 CTGGATATACCTGGACATATCGAAGCAGACATTCATGCGCATGCTGTGAAGCTGCGG 240
 QY 241 GlnArgValLeuPheLeuLeuAspGlyTyraGlnLysPheLysProGlnAsnGlyProGln 260
 DB 241 CAGAGGGTCTTTCCTTCCTTCATGCTACATGTAATCAACCCAGAGAGTCCAGAA 300
 QY 261 IleGlnAlaLeuIleLysGlnLysAsnHisArgPheLysAsnMetValIleValThrThrThr 280
 DB 301 ATCGAAGCCCTATTAAGGAAACACCCCTTCAGAAACATGTCATCTCCACCTACC 360
 QY 281 ThrGlnCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300
 DB 361 ACTGAGTGCCTAGGACACATACGAGTTGTGCTGCTGACGAGAGTGGGGATAG 420
 QY 301 ThrGlnAspSerArgGlnAlaLeuIleArgGluValLeuIleLysGlnLeuAlaGluGly 320
 DB 421 ACAGAGACAGGCCAGGCTCTCATCGAAGAGTCTGATCAAGAGAGCTTCTGTAAGGC 480

QY 321 LeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340
 DB 481 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGGAGAAATCTCATGAACCCCTCTTT 540
 QY 341 ValIleIleThrCysAlaIleGlnMetGlyGlnSerGluPheHisSerHisThrGlnThr 360
 DB 541 GTGGTCATCATCTTGTCATTCAGATCGAGATGGGTGAAGTGAAGTTCACCTCCACACACAA 600
 QY 361 ThrLeuPheHisThrPheTyraPheLeuLeuIleGlnLysAsnLysHisLysGly 380
 DB 601 AGCGTTCATTAACCTTCATATATCTGTGATACGAAACAAACAAACATTAAGT 660
 QY 381 ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly 400
 DB 661 GTGGCTGCAAGTACTTCTTTCGAGCCCTGGACACCGTGGAGACCTTGGAGGCT 720
 QY 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGlnAspVal 420
 DB 721 GTGTTCTCCACACAGTTGATTTTCGAACTCGAGATGTGTCAGGCTGAATGAGATGTC 780
 QY 421 LeuLeuThrThrGlyLeuLeuCysLysTyraThrAlaGlnArgPheLysProLysTyraLys 440
 DB 781 CTGCTGACAACTGGGCTCTCTGTAAATATACAGCTCAAAAGGTTCAAGCCAAAGTATAAA 840
 QY 441 PhePheHisLysSerPheGlnGlnIleThrThrAlaGluArgArgLeuSerSer 457
 DB 841 TTCCTTCACAGTCAATTCAGAGATGACACGACGAGGACGAAGACTCAGCAGT 891

RESULT 9
 ABR22732
 ID ABR22732 standard; cDNA; 1395 BP.
 AC ABR22732;
 DT 26-MAR-2002 (first entry)
 XX Human cDNA encoding CLAN B.
 DE
 XX
 KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
 KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
 KW autoimmune disease; inflammation; keratinocyte hyperplasia;
 KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
 KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
 KW leukaemia; allergy; arthritis; lupus; Schogen's syndrome;
 KW Crohn's disease; graft-versus-host disease; stroke;
 KW myocardial infarction; heart failure; neurodegenerative disease;
 KW Parkinson's disease; Alzheimer's disease; HIV;
 KW human immunodeficiency virus infection.
 XX
 OS Homo sapiens.
 XX
 PN WO200190156-A2.
 XX
 PD 29-NOV-2001.
 XX
 PE 24-MAY-2001; 2001WO-US17158.
 XX
 PR 24-MAY-2000; 2000US-0579240.
 PR 10-OCT-2000; 2000US-0686347.
 PR 14-MAR-2001; 2001US-275980P.
 PR 23-MAY-2001; 2001US-0864921.
 XX
 PA (BURN-) BURNHAM INST.
 XX
 PI Reed JC, Plo FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
 PI Oliveira VAM, Hayashi H, Pawlowski K;
 DR WPI: 2002-083086/11.
 DR P-PSDB: AAU80862.
 XX
 PT New caspase recruitment domain (CARD)-containing polypeptides and
 PT encoding nucleic acids, useful for treating abnormal cell proliferation
 PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,

PT arthritis or stroke -
XX
PS Claim 1; Page 174-176; 216pp; English.
XX
CC The invention relates to an isolated caspase recruitment domain (CARD)
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
CC from it, and the polynucleotides encoding them. Also included are a
CC recombinant vector comprising the polynucleotide, recombinant cells
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
CC and insect cells) and an anti-CARD antibody. The CARD-containing
CC polypeptide and CARD-encoding nucleic acid are useful for treating a
CC pathology characterised by abnormal cell proliferation (e.g. cancer),
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In
CC particular, the polypeptide and nucleic acid are useful for treating
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
CC muscle cell proliferation in arteries following balloon angioplasty
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukemias,
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
CC disease) or immunodeficiency associated disease (e.g. human
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
CC in a variety of diagnostic applications. The present sequence is a
CC cDNA encoding a CARD domain containing protein.
XX
SQ Sequence 1395 BP; 436 A; 248 C; 327 G; 384 T; 0 other;

Alignment Scores:
Pred. No.: 6,28e-202 Length: 1395
Score: 1424.00 Matches: 271
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.63% Mismatches: 0
Query Match: 26.09% Indels: 0
DB: Gaps: 0

US-09-697-089-2 (1-1024) x ABR22732 (1-1395)

QY 753 GlycylLeuThrAspSerLeuGlyAsnLeuLysAsnLeuThrLysLeuIleMetAspAsn 772
DB 538 AGTGGTCTGACTGACAGCTGGTGAACCTTACAAAGCTCATATGATGATAC 597
QY 773 IleLysMetAsnGluGluAspAlaIleLysLeuAlaGluGluLysAsnLysLys 792
DB 598 ATAAAGATGAATGAAGAAGATGCTATTAACCTGAAAGCCGTAAGAACTGAAGAG 657
QY 793 MetCysLeuPheHisLeuThrHisLeuSerAspIleGlyGluGlyMetAspTyrIleVal 812
DB 658 ATGTGTTTATTCATTTCACCCACTGTCTGACANTGAGAGGGAATGATTAATGATC 717
QY 813 LysSerLeuSerSerGluProCysAspLeuGluGluIleGluLeuValSerCysCysLeu 832
DB 718 AAGTCTCTGTCAGTGAACCTGTGACCTGAAAGAAATTCATATGCTCTGCTGCTTG 777
QY 833 SerIlaAsnAlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuValLysLeuSerIle 852
DB 778 TCTGGAATGAGAGTGAATAATCCTAGACTCAGAAATCTTCAAACTGAGCAATT 837
QY 853 LeuAspLeuSerGluAsnTyrLeuGluIuLysAspGlyAsnGluAlaLeuHisGluLeuIle 872
DB 838 CTTGATTTATCAGAAAAATTTACTGTGAAAAAATGAAATGAACTCTTCATGAACTGATC 897
QY 873 AspArgMetAsnValLeuGluGlnLeuThrAlaLeuMetLeuProTyrPglyCysAspVal 892
DB 898 GACAGAGATGAACGTGTGAGAACAGCTACCGCACTGATGCTGCCCTGGCGCTGAGAGCTG 957
QY 893 GlnGlySerLeuSerSerLeuLeuLysHisLeuGluGluValProGlnLeuValLysLeu 912
DB 958 CAAGGAGCCCTGACAGCTCTTGAACATTTGGAGGAGGCTCCACACAACCTGCTCAAGCTT 1017
QY 913 GlyLeuLysAsnTrpArgLeuThrAspThrGluIleArgGluIleGluGlyAlaPhePheGly 932
DB 1018 GGGTTGAAAAAAGCTGAGAGCTCAGATACAGAGATTAAGAAATTTTAAAGGTGATTTTGTGGA 1077

QY 933 LysAsnProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAsp 952
DB 1078 AAGAAGCCCTCGAAAAAAGCTTCACAGCTGATTTGGCGGGAATTCGTGAGCAGTATC 1137
QY 953 GlyThrPheAlaPheMetGlyValPheGluAsnLeuLysGlnLeuValPhePheAspPhe 972
DB 1138 GGATGGCTGCTTCATCAGGCTGGTATTTGAGAACTTAAAGCAATTAAGTGTGTTGACTTT 1197
QY 973 SerThrLysGluPheLeuProAspProAlaLeuValArgLysLeuSerGlnValLeuSer 992
DB 1198 AGTACTAAGAATTTCTATCAGATCCAGATCAGATAGCAGAAAACTAGCAGAGTGTATTC 1257
QY 993 LysLeuThrPheLeuGlnGluAlaArgLeuValGlyTyrGlnPheAspAspAspLeu 1012
DB 1258 AAGTTAACTTTCTGCAAGAGCTAGAGCTGTGTGGGTGGCAATTTGATGATGATGATCTC 1317
QY 1013 SerValIleThrGlyAlaPheLysLeuValPheAla 1024
DB 1318 AGTGTATTACAGGTGCTTTTAACTACTACTGCT 1353

RESULT 10

ABK22767
ID ABR22767 standard; cDNA; 618 BP.

XX ABR22767;

XX 26-MAR-2002 (first entry)

DE Human cDNA encoding CLAN LRR.

XX Caspase recruitment domain; CARD; SS; NB-ARC; ANGIO-R; LRR; SAM;
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
KW autoimmune disease; inflammation; keratinocyte hyperplasia;
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;
KW Crohn's disease; graft-versus-host disease; stroke;
KW myocardial infarction; heart failure; neurodegenerative disease;
KW Parkinson's disease; Alzheimer's disease; HIV;
KW human immunodeficiency virus infection.

XX Homo sapiens.

XX WO200190156-A2.

XX 29-NOV-2001.

XX 24-MAY-2001; 2001MO-US17158.

XX 24-MAY-2000; 2000US-0579240.

XX 10-OCT-2000; 2000US-0686347.

XX 14-MAR-2001; 2001US-275980P.

XX 23-MAY-2001; 2001US-0664921.

XX (BURN-) BURNHAM INST.

XX Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
PI Oliveira VAM, Hayashi H, Pawlowski K;

XX WPI; 2002-083086/11.

XX P-PSDS; AA080873.

XX New caspase recruitment domain (CARD)-containing polypeptides and
PT encoding nucleic acids, useful for treating abnormal cell proliferation
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
PT arthritis or stroke -

XX Claim 1; Page 202-203; 216pp; English.

CC The invention relates to an isolated caspase recruitment domain (CARD)
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
CC from it, and the polynucleotides encoding them. Also included are a
CC recombinant vector comprising the polynucleotide, recombinant cells

CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
CC and insect cells) and an anti-CARD antibody. The CARD-containing
CC polypeptide and CARD-encoding nucleic acid are useful for treating a
CC pathology characterised by abnormal cell proliferation (e.g. cancer),
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In
CC particular, the polypeptide and nucleic acid are useful for treating
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
CC muscle cell proliferation in arteries following balloon angioplasty
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,
CC allergies, arthritis, lupus, Schriegen's syndrome, Crohn's disease,
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
CC disease) or immunodeficiency associated disease (e.g. human
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
CC in a variety of diagnostic applications. The present sequence is a
CC cDNA encoding a CARD domain containing protein.

XX Sequence 618 BP; 194 A; 113 C; 148 G; 163 T; 0 other;

Alignment Scores:

Pred. No.:	1 5e-151	Length:	618
Score:	1084.00	Matches:	206
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	19.86%	Indels:	0
DB:	24	Gaps:	0

US-09-697-089-2 (1-1024) x ABR22767 (1-618)

QY	760	GlyAsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluLysAsp	779
DB	1	GGTAACTTGAAGAACCTTACAAAGCTCATATGATTAACATAAGATGAAGTGAAGAT	60
QY	780	AlaIleLysLeuAlaGluGlyLeuLysAsnLeuLysMetCysLeuPheHisLeuThr	799
DB	61	GCTATAAACTACTGAGAGGCTGCAAAACCTGAAGAGATGCTTATTTCATTGACC	120
QY	800	HisLeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluPro	819
DB	121	CACTGTCTACATTTGGAGAGGGAATGATTAATAGTCAAGTCTCTGTAAGTGAACCC	180
QY	820	CysAspLeuGluGluIleGluLeuValSerCysCysLeuSerAlaAsnAlaValLysIle	839
DB	181	TGTGACCTTGAAGAAATTCATTAGTCTCTGCTGCTTGTCTGCAAAATGACGTGAATC	240
QY	840	LeuAlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyr	859
DB	241	CTAGCTCAGAACTTTCACAAATTTGGTCAAACTGAGCATTCCTTATTCAGAAAATTAC	300
QY	860	LeuGluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGlu	879
DB	301	CTGGAAAAAGATGGAATGAAGCTCTTCATGAACCTGATCCAGAGATGAACGTGCTAGAA	360
QY	880	GlnLeuThrAlaLeuMetLeuProTyrPglyCysAspValGlnGlySerLeuSerSerLeu	899
DB	361	CAGCTCACCCACTGAGAGTGCCTGGGGCTGTGACCTGCAAGGACCTGAGAGGCTTG	420
QY	900	LeuLysHisLeuGluValIleProGlnLeuValLysLeuGlyLeuLysAsnTyrPargLeu	919
DB	421	TTGAAACATTTGGAGGGGCTCCACAACTGTCAAAGCTGGGTTGAAAACTGGAGACTC	480
QY	920	ThrAspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPhe	939
DB	481	ACAGATTCACAGATTAAGATTTTAAAGTGCATTTTGGAAAGAACCTCTGAAAAACTTC	540
QY	940	GlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPheLeuAlaPheMetGly	959
DB	541	CACAGAGTTGAATTTGGCGGGAATCGTGTGACAGATGATGATGGCTTGCTTCATGGGT	600
QY	960	ValPheGluAsnLeuLys 965	
DB	601	GTATTGTGAATCTTAAG 618	

RESULT 11
ID AAS26160
AAS26160 standard; cDNA; 608 BP.
AC AAS26160;
XX 07-NOV-2001 (first entry)
DE Human cDNA encoding a novel secreted protein, Seq ID 339.
XX
XX Human: immunosuppressive; antiarthritic; ss; antiinflammatory;
XX cytotoxic; cardiant; vasotropic; cerebroprotective; nootropic;
XX neuroprotective; antibacterial; virucide; fungicide; ophtalmological;
XX vulnary; secreted protein; rheumatoid arthritis;
XX hyperproliferative disorder; cardiovascular disorder; cardiac arrest;
XX cerebrovascular disorder; cerebral ischaemia; angiogenesis;
XX nervous system disorder; Alzheimer's disease; infection; ocular disorder;
XX corneal infection; wound healing; epithelial cell proliferation;
XX skin ageing; food additive; preservative; antiproliferative.
XX
OS Homo sapiens.
PN WO200155322-A2.
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01341.
XX
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
XX 24-FEB-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0189874.
XX 17-MAR-2000; 2000US-0190076.
XX 18-APR-2000; 2000US-0198123.
XX 19-MAY-2000; 2000US-0205515.
XX 07-JUN-2000; 2000US-0209467.
XX 28-JUN-2000; 2000US-0214886.
XX 30-JUN-2000; 2000US-0215135.
XX 07-JUL-2000; 2000US-0216647.
XX 07-JUL-2000; 2000US-0216880.
XX 11-JUL-2000; 2000US-0217487.
XX 11-JUL-2000; 2000US-0217496.
XX 14-JUL-2000; 2000US-0218290.
XX 26-JUL-2000; 2000US-0220963.
XX 26-JUL-2000; 2000US-0220964.
XX 14-AUG-2000; 2000US-0224518.
XX 14-AUG-2000; 2000US-0224519.
XX 14-AUG-2000; 2000US-0225213.
XX 14-AUG-2000; 2000US-0225214.
XX 14-AUG-2000; 2000US-0225266.
XX 14-AUG-2000; 2000US-0225267.
XX 14-AUG-2000; 2000US-0225268.
XX 14-AUG-2000; 2000US-0225270.
XX 14-AUG-2000; 2000US-0225447.
XX 14-AUG-2000; 2000US-0225757.
XX 14-AUG-2000; 2000US-0225758.
XX 14-AUG-2000; 2000US-0225759.
XX 18-AUG-2000; 2000US-0226279.
XX 22-AUG-2000; 2000US-0226681.
XX 22-AUG-2000; 2000US-0226688.
XX 23-AUG-2000; 2000US-0227182.
XX 23-AUG-2000; 2000US-0227009.
XX 30-AUG-2000; 2000US-0228924.
XX 01-SEP-2000; 2000US-0229287.
XX 01-SEP-2000; 2000US-0229343.
XX 01-SEP-2000; 2000US-0229344.
XX 01-SEP-2000; 2000US-0229345.
XX 05-SEP-2000; 2000US-0229509.
XX 05-SEP-2000; 2000US-0229513.
XX 06-SEP-2000; 2000US-0230437.
XX 06-SEP-2000; 2000US-0230438.
XX 08-SEP-2000; 2000US-0231242.

```
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 12-SEP-2000; 2000US-0232081.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239335.
PR 13-OCT-2000; 2000US-0239337.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0244674.
PR 08-NOV-2000; 2000US-0244675.
PR 08-NOV-2000; 2000US-0244676.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.

PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0251988.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPI: 2001-488783/53.
P-PSDB: AA016173.

New nucleic acid molecules encoding 461 human secreted proteins for
diagnosing, preventing, treating or ameliorating medical conditions and
used as food additives or preservatives -
Claim 1; SEQ ID NO 339; 980pp; English.

The invention relates to isolated nucleic acid molecules and their
encoded secreted proteins. The nucleic acids and proteins are used to
prevent, treat or ameliorate a medical condition in e.g. humans, mice,
rabbits, goats, horses, cats, dogs, chickens or sheep. They
are also used in diagnosing a pathological condition or susceptibility
to a pathological condition. Antibodies to the proteins can also
be used in alleviating symptoms associated with the disorders and in
diagnostic immunoassays e.g. radioimmunoassays or enzyme linked
immunosorbent assays (ELISA). Disorders which are diagnosed or treated
include autoimmune diseases e.g. rheumatoid arthritis,
hyperproliferative disorders e.g. neoplasms of the breast or liver,
cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.
Alzheimer's disease, infections caused by bacteria, viruses and fungi
and ocular disorders e.g. corneal infection, and many other
disorders listed in the specification. The polypeptides can also
be used to aid wound healing and epithelial cell proliferation, to
prevent skin aging due to sunburn, to maintain organs before
transplantation, for supporting cell culture of primary tissues, to
regenerate tissues and in chemotaxis. The polypeptides can also be used
as a food additive or preservative to increase or decrease storage
capabilities, fat content, lipid, protein, carbohydrate, vitamins,
minerals, cofactors and other nutritional components. The present
sequence encodes a novel secreted protein of the invention.

Alignment Scores:
Pred. No.: 9,63e-140 Length: 608
Score: 1005.00 Matches: 189
Percent Similarity: 98.45% Conservative: 1
Best Local Similarity: 97.93% Mismatches: 3
Query Match: 18.41% Indels: 0
DB: 22 Gaps: 0

US-09-697-089-2 (1-1024) x AAS26160 (1-608)

QY 479 SerTIEserPIIerThSerThTyriserSerIeulauAgyTYrThCysGlyserSer 498
:::||||| |||||||||
Db 28 GCCATTTCGCCCATTCACCTACTATAGCAGCCGCTCCGCTACACCTGTGGTCATNT 87
QY 499 ValGluAlaThArgAlaValMetLysHisLeuAlaAlaValTYrGlnHisGlyCysLeu 518
|||||||||
```


DE Human cDNA encoding CLAN D.
XX
XX Caspase recruitment domain; CARD; ss: NB-ARC; ANGIO-R; LRR; SAM;
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
KW autoimmune disease; inflammation; keratinocyte hyperplasia;
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
KW leukemia; allergy; arthritis; lupus; Schrogen's syndrome;
KW Crohn's disease; graft-versus-host disease; stroke;
KW myocardial infarction; heart failure; neurodegenerative disease;
KW Parkinson's disease; Alzheimer's disease; HIV;
KW human immunodeficiency virus infection.
XX
XX Homo sapiens.
OS
XX
XX WC0200190156-A2.
PN
XX
XX 29-NOV-2001.
PD
XX
XX 24-MAY-2001; 2001WO-US17158.
PF
XX
XX 24-MAY-2000; 2000US-0579240.
PR 10-OCT-2000; 2000US-0686347.
PR 14-MAR-2001; 2001US-275960P.
PR 23-MAY-2001; 2001US-0864921.
XX
XX (BURN-) BURHAM INST.
PA
XX
XX Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
PI Oliveira VAM, Hayashl H, Pawlowski K;
PI
XX
XX MPI; 2002-083086/11.
DR P-PSDB; AAU80864.
XX
XX New caspase recruitment domain (CARD)-containing polypeptides and
PT encoding nucleic acids, useful for treating abnormal cell proliferation
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
PT arthritis or stroke
XX
XX Claim 1; Page 178-179; 216pp; English.
PS
XX
XX The invention relates to an isolated caspase recruitment domain (CARD)
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
CC from it, and the polynucleotides encoding them. Also included are a
CC recombinant vector comprising the polynucleotide, recombinant cells
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
CC and insect cells) and an anti-CARD antibody. The CARD-containing
CC polypeptide and CARD-encoding nucleic acid are useful for treating a
CC pathology characterised by abnormal cell proliferation (e.g. cancer),
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In
CC particular, the polypeptide and nucleic acid are useful for treating
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
CC muscle cell proliferation in arteries following balloon angioplasty
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
CC disease) or immunodeficiency associated disease (e.g. human
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
CC in a variety of diagnostic applications. The present sequence is a
CC cDNA encoding a CARD domain containing protein.
XX
XX Sequence 768 BP; 218 A; 157 C; 180 G; 213 T; 0 other;
SQ
XX
XX Alignment Scores:
Pred. No.: 7.2e-117 Length: 768
Score: 853.00 Matches: 154
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 15.63% Indels: 0
DB: 24 Gaps: 0
US-09-697-089-2 (1-1024) x ABR22734 (1-768)

QY 1 MetasphelleielysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
DB 277 ATGATTTTCATTAAGGACATATAGCCGACCTTTTAAAGATGGAAATGACCTGTATA 336
QY 21 LysGlnIleThrAspAspLeuPheValITrpAsnValLeuAsnArgGluGluValAsnIle 40
DB 337 AAGCAATTCACAGATGACCTATTGTATGGAATGTCTGAAATGCCGAAGAATTAACATC 396
QY 41 IleGlySerGluGlyValAlaGluGlnAspAlaAlaArgGlyIleIleIleHisMetIleLeuLys 60
DB 397 ATTTGCTGCAGAGAGAGGAGGACAGATGCTGTAGAGGATCATTCATGATTTTGAAA 456
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluITrpAsnITrpProLeu 80
DB 457 AAGGTTTCAGAGTCTTACCTTTTCTTAATCCCTTAAGAGGTGAGACTATCCCTTA 516
QY 81 PheGlnAspLeuAsnGlnGlnSerLeuPheHisGlnIThrSerGluGlyAspLeuAspAsp 100
DB 517 TTTCAGACCTTGAAATGACAAAGCTTTTTCATCAGACATCAGAAAGAGACTTGAGAGAT 576
QY 101 LeuAlaGlnAspLeuLysAspLeuITyrHisIThrProSerPheLeuAsnPheITyrProLeu 120
DB 577 TTGGCTCAGGATTTTAAAGACTGTGTACCATACCCCATCTTTTGAACTTTTATCCCTT 636
QY 121 GlyGluAspIleAspIleIlePheAsnLeuLysSerIThrPheITrGluITrProValLeuITrp 140
DB 637 GGTCAAGATATATGACATATATTTTAACTTGAAAAGCACTTCACAGAACTGTCTGTGG 696
QY 141 ArgLysAspGlnHisHisArgValGluGlnLeuIThrLeu 154
DB 697 AGGAAAGCAACACATCACCGCGGTGAGACAGCTGACCTTA 738
RESULT 14
AAS26575
ID AAS26575 standard; cDNA; 522 BP.
XX
AC AAS26575;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human cDNA encoding a novel secreted protein, Seq ID 754.
XX
XX Human; immunosuppressive; antiarthritic; ss; antirheumatic;
KW cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;
KW neuroprotective; antibacterial; virucide; fungicide; optalmalogical;
KW vulnary; secreted protein; rheumatoid arthritis;
KW hyperproliferative disorder; cardiovascular disorder; cardiac arrest;
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; infection; ocular disorder;
KW corneal infection; wound healing; epithelial cell proliferation;
KW skin ageing; food additive; preservative; antiproliferative.
XX
OS Homo sapiens.
XX
XX WC0200155322-A2.
PN
XX
XX 02-AUG-2001.
PD
XX
XX 17-JAN-2001; 2001WO-US01341.
PF
XX
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.

PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225470.
PR 14-AUG-2000; 2000US-0225477.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 23-AUG-2000; 2000US-0227182.
PR 30-AUG-2000; 2000US-0227009.
PR 01-SEP-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229309.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 08-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0233397.
PR 14-SEP-2000; 2000US-0233398.
PR 14-SEP-2000; 2000US-0233399.
PR 14-SEP-2000; 2000US-0233400.
PR 14-SEP-2000; 2000US-0233401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 21-SEP-2000; 2000US-0234265.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239335.
PR 13-OCT-2000; 2000US-0239337.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.

PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
(HUMA -) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPI. 2001-488783/53.
P-PSDB; AA016588.

New nucleic acid molecules encoding 461 human secreted proteins for
diagnosing, preventing, treating or ameliorating medical conditions and
used as food additives or preservatives -

Claim 1; SEQ ID No 754; 980pp; English.

The invention relates to isolated nucleic acid molecules and their
encoded secreted proteins. The nucleic acids and proteins are used to
prevent, treat or ameliorate a medical condition in e.g. humans, mice,
rabbits, goats, horses, cats, dogs, chickens or sheep. They
are also used in diagnosing a pathological condition or susceptibility
to a pathological condition. Antibodies to the proteins can also
be used in alleviating symptoms associated with the disorders and in
diagnostic immunoassays e.g. radioimmunoassays or enzyme linked

CC immunosorbant assays (ELISA). Disorders which are diagnosed or treated
CC include autoimmune diseases e.g. rheumatoid arthritis,
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC e.g. cerebral ischaemia, angiodenesis, nervous system disorders e.g.
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi
CC and ocular disorders e.g. corneal infection, and many other
CC disorders listed in the specification. The polypeptides can also
CC be used to aid wound healing and epithelial cell proliferation, to
CC prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors and other nutritional components. The present
CC sequence encodes a novel secreted protein of the invention.

Alignment Scores:

Pred. No.:	5.97e-98	Length:	522
Score:	725.00	Matches:	150
Percent Similarity:	89.47%	Conservative:	3
Best Local Similarity:	87.72%	Mismatches:	14
Query Match:	13.28%	Indels:	6
DB:	22	Gaps:	1

US-09-697-089-2 (1-1024) x AAS26575 (1-522)

QY 80 LEUPHEGINASPLEUASNGLYGINSERLEUPHEHISGINTHRSERGLIYASPLEUASP 99
DB 3 CTATTTGAGGACTTGAAAGGACAAAGCTTTTTCATCAGACATCAGGAAGAACCTTGAGC 62
QY 100 ASPLEUAGINASPLEUASPLEUTYRHSRPROSERPHELEUASNPHERYPRO 119
DB 63 GATTGGGTGAGGATTAAAGACTGTACCATACCCATCTTTCTGAACTTTATGCC 122
QY 120 LEUGLYIUSAPLIEAPLIELEPHEASNULEYSSERTHRPHERTHGLUPVALLEU 139
DB 123 CTGGTGAAAGATATGACATATTTTAACTTGAAGAACACCTTCACAGAACCTGCTCG 182
QY 140 TRPATGLVASPGINHSHISHTARVAGLUGINSLEUTHLEUASNGLYLEUENGIN 159
DB 183 TGGAGGAAGACCAACACCATCACCCTGGAGCAGCTGACCTGAATGAGCCTCTGCA 242
QY 160 ALALEUGINSERPROCYSLIELEGLUGLYUSERSGLYLYSERTHRLEUEN 179
DB 243 GCTCTTCAGAGCCCTGCATCATTTGAGGGGAAATCGGAAAGCAATCCATCTGCG 302
QY 180 GINATGIIIEALMETLEUTRPGYISERGLYSCYLSAIALEUTHRLYSPHELYS-PH 199
DB 303 CAGCCCATTCGATCCTCTGGGGCTCCGAAAGTCCAGAGGCTCTGACCAAGTTTCAANT 362
QY 199 EVALPHE-PHELEUARGYSEARARGALAGLNGLY-GLYLEUPHEGLUTHRLYUCYAS 218
DB 363 GCTCTTCTTTCTCTCTGTTTCAGCAGAGGCCAGGGGGGCTTTTGAACCCCTGTGTAT 422
QY 219 GINLEUENASPLIEPROGLYTHRLIARGLYSGINTHRPHEMETALAMETLEUEN 238
DB 423 CAATTCGCG-GGTATACGGGACA-TTCAGGAGCAGACATTTAGGCCNCGT---GCTGAG 477
QY 239 LEUATGGINARGVALLEUPHELEUEN 247
DB 478 GTGCGCAGAGGGTCTTTTCTTCTTGTG 504

RESULT 15

ABK22733 standard; CDNA; 578 BP.

AC ABK22733:

DT 26-MAR-2002 (first entry)

DE Human cDNA encoding CLAN C.

XX

KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
KW autoimmune disease; inflammation; keratinocyte hyperplasia;
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;
KW Crohn's disease; graft-versus-host disease; stroke;
KW myocardial infarction; heart failure; neurodegenerative disease;
KW Parkinson's disease; Alzheimer's disease; HIV;
KW human immunodeficiency virus infection.

Homo sapiens.

WO200190156-A2.

29-NOV-2001.

24-MAY-2001; 2001WO-US17158.

24-MAY-2000; 2000US-0579240.

10-OCT-2000; 2000US-0686347.

14-MAR-2001; 2001US-275980P.

23-MAR-2001; 2001US-0864921.

(BURN-) BURNHAM INST.

Reed JC, Plo FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
Oliveira VAM, Hayashi H, Pawlowski K;
WPI; 2002-083086/11.
P-PSDB; AAU80863.

PT New caspase recruitment domain (CARD)-containing polypeptides and
PT encoding nucleic acids, useful for treating abnormal cell proliferation
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
PT arthritis or stroke

Claim 1; Page 177; 216pp; English.

XX The invention relates to an isolated caspase recruitment domain (CARD)
XX -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
XX from it, and the polynucleotides encoding them. Also included are a
XX recombinant vector comprising the polynucleotide, recombinant cells
XX containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
XX and insect cells) and an anti-CARD antibody. The CARD-containing
XX polypeptide and CARD-encoding nucleic acid are useful for treating a
XX pathology characterised by abnormal cell proliferation (e.g. cancer),
XX abnormal cell death (apoptosis), autoimmune diseases or inflammation. In
XX particular, the polypeptide and nucleic acid are useful for treating
XX keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
XX muscle cell proliferation in arteries following balloon angioplasty
XX (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukemias,
XX allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
XX graft-versus-host disease, stroke, myocardial infarction, heart failure,
XX neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
XX disease) or immunodeficiency associated disease (e.g. human
XX immunodeficiency virus (HIV) infection). The nucleic acids are useful
XX in a variety of diagnostic applications. The present sequence is a
XX cDNA encoding a CARD domain containing protein.

Sequence 578 BP; 172 A; 106 C; 143 G; 157 T; 0 other;

Alignment Scores:

Pred. No.:	3.46e-63	Length:	578
Score:	493.00	Matches:	89
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	9.03%	Indels:	0
DB:	24	Gaps:	0

US-09-697-089-2 (1-1024) x ABK22733 (1-578)

QY 1 Metasphelelelyaspanserargalaleuileglnargmetcglymerthvalle 20


```
Db 277 ATGATTTTCATAAGCACAATAGCCGAGCCCTTATTCAAGAATGGGAATGACTGTTATA 336
QY 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle 40
Db 337 AAGCAATACACAGATGACCTATTGTATGGAATGTTCTGAAATCGCGAAGAACTAAACATC 396
QY 41 IleCysCysGluIuysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
Db 397 ATTGCTGCGAGAGAGTGAGCAGATGCTGCTAGAGGAGATCATTCACATGATTTGAAA 456
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu 80
Db 457 AAGGTTTCAGAGTCCCTGTAACCTCTTCTTAATCCCTTAAGGAGTGGAACATATCCTCTA 516
QY 81 PheGlnAspLeuAsnGlyGlnSerLeu 89
Db 517 TTTCAGGACTTGAAATGGACAAAGTCTT 543
```

Search completed: January 31, 2003, 08:55:35
Job time : 532 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 31, 2003, 08:44:56 ; Search time 3285 Seconds
(without alignments)
5048.456 Million cell updates/sec

```

Title: US-09-697-089-2
Perfect score: 5459
Sequence: 1 MNFTKIDNSRALIQRMGTVI.....WQFDDDDSVITGAFKLVTA 1024

```

Scoring table:	
PAM120	
Xgapop	4.0 , Xgapext 12.0
Ygapop	4.0 , Ygapext 12.0
Fgapop	6.0 , Fgapext 7.0
Delop	6.0 , Delext 7.0

```
Searched:      16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters:  32308132
```

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

```

-MODEL-frame+52n.model -DEV-xlh
-o-/cgn2.1/USPPO.spool/US096697089/crunat.29012003.092505.19166/app_query.fasta.1.1222
-DB-EST -QEMT-fastcap -SUFFIX-p2n.rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=1 -MATRIX-pam120 -TRANS-human40.cdi -LIST=5
-DOCALLIN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFM=ptc -NORM-ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US096697089.cgn2.1.12475.crunat.29012003.092505.19166 -NCPU=6
-NO_XLPHY -NO_MMAR -LARGSCORE -NEG_SCORES=0 -WAIT -LONLOG -DEV_TIMEOUT=120
-MARK_TIMEOUT=30 -THREADS=1 -XGAPOP=4 -XGAPEXT=12 -FCAPOP=6 -FCAPEXT=7
-YGAPOP=4 -YGAPEXT=12 -DELOP=6 -DELEXT=7

```

```
Database :

EST.*
1: em_estba.*
2: em_estchum.*
3: em_estlin.*
4: em_estmu.*
5: em_estrov.*
6: em_estrpl.*
7: em_estro.*
8: em_hlc.*
9: gb_est1.*
10: gb_est2.*
11: gb_hlc.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: gb_gss.*
18: em_gss_hum.*
19: em_gss_inv.*
20: em_gss_pln.*
21: em_gss_vrt.*
22: em_gss_fun.*
23: em_gss_mam.*
24: em_gss_mus.*
25: em_gss_other.*
26: em_gss_pro.*
27: em_gss_rpd.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query				ID	Description
	Score	Match	Length	DB		
1	976	18.2	697	17	BH293386	BH293386 CTRB-44G
2	994	17.8	552	17	AQ309404	AQ309404 CTRB-EI-
3	872	16.0	650	10	BB627584	BB627584 B8627584
4	853	15.6	741	13	B1824482	B1824482 603038854
5	837	15.3	480	10	AV719179	AV719179 AV719179
6	826	15.1	748	13	B1908869	B1908869 603066455
7	824	15.1	602	17	A2360053	A2360053 IM0103H11
8	793	13.5	518	17	BH348412	BH348412 CH230-42F
9	644	11.8	619	17	BH267158	BH267158 CH230-19B
10	628	11.5	775	13	B1854236	B1854236 603381263
11	613	11.2	817	17	BH358172	BH358172 CH230-18E
12	609	11.2	364	9	A1263294	A1263294 qxf5P01..x
13	586	10.7	371	10	AV656315	AV656315 AV656315
14	547	10.0	719	14	BQ204082	BQ204082 UI-R-DNL-
15	522	9.6	637	9	AL639997	AL639997 AL639997
16	500	9.2	728	9	AL652549	AL652549 AL652549
17	485	8.9	476	12	BG210375	BG210375 RST92913
18	446	8.2	470	17	AO624020	AO624020 HS-5378.B
19	398	7.3	261	10	AW337918	AW337918 hel2H11..x
20	386	7.1	637	9	AL782121	AL782121 AL782121
21	335	6.1	404	17	AO889169	AO889169 HS-2161.B
22	307	5.6	553	17	AQ320928	AQ320928 RPTC11-93
23	263	4.8	630	17	AQ112439	AQ112439 CIT-HP-2
24	260	4.8	219	17	AQ283886	AQ283886 RPTC11-78
25	253	4.6	251	12	BF903662	BF903662 IL2-M7018
26	231	4.2	509	10	AW418826	AW418826 haz2E11..x
27	224	4.0	840	12	BF207840	BF207840 601862546
28	221	4.0	714	9	AL657756	AL657756 AL657756
29	208	3.8	577	13	BJ037401	BJ037401 BJO37401
30	200	3.7	1058	13	BM477340	BM477340 AGENCOURT
31	189	3.5	728	17	A2720059	A2720059 RPTC-24-8
32	179	3.3	412	14	H25984	H25984 J156907..r1
33	177	3.2	625	17	A2614134	A2614134 IM0442N17
34	167	3.1	675	10	BH108531	BH108531 BH108531
35	164	3.0	499	9	A1023795	A1023795 ox08603..x
36	131	2.4	515	14	BQ656804	BQ656804 MR2-GN003
37	123	2.3	668	17	A2762115	A2762115 IM0556N15
38	122	2.2	429	17	A2484615	A2484615 IM0311P08
39	120	2.2	345	13	BG994836	BG994836 PMO-H7116
40	117	2.1	342	17	A2805292	A2805292 2M0066B12
41	116	2.1	586	13	BG994334	BG994334 PMO-H7116
42	113	2.1	434	10	BF705086	BF705086 BF705086
43	111	2.0	571	12	BF080490	BF080490 231404.MA
44	108	2.0	546	12	A2362463	A2362463 IM0107N03
45	106	1.9	384	17	BE833335	BE833335 QV3-OT006

ALIGNMENTS

RESULT	1
LOCUS	BH293386
DEFINITION	BH293386 697 bp DNA linear GSS 30-NOV-2001 CH230-0-44G15.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
ACCESSION	CH230-44G15, DNA sequence.
VERSION	BH293386
KEYWORDS	BH293386.1 GI:17205794
SOURCE	GSS.
ORGANISM	Norway rat. Rattus norvegicus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
AUTHORS	1 (bases 1 to 697) Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn

,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de
Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)
Other_GSSS: CH230-44G15.TU
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhaoc@tigr.org

Clones are derived from the rat BAC library CHORI-230
(<http://www.chori.org/bacpac/rat230.htm>). For BAC library
availability, please contact Pieter de Jong (pdejong@mai.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/orering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 44 row: G column: 15
Seq primer: T7
Class: BAC ends.

FEATURES

Location/Qualifiers

1..697
/organism="Rattus norvegicus"
/strain="BN/SSNhd/MCW"
/db_xref="taxon:10116"
/clone="CH230-44G15"
/clone_1ib="CHORI-230 Segment 1"
/sex="Female"
/cell_type="Brain"
/note="Vector: pPARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SSNhd/MCW) BAC library produced by
Pieter de Jong"

BASE COUNT 182 a 165 c 190 g 160 t
ORIGIN

Alignment Scores:

Pred. No.: 5.66e-136 Length: 697
Score: 996.00 Matches: 185
Percent Similarity: 91.27% Conservative: 24
Best Local Similarity: 80.79% Mismatches: 20
Query Match: 18.25% Indels: 1
DB: 17 Gaps: 0

US-09-697-089-2 (1-1024) x BH293386 (1-697)

QY 266 Lysglusnhsarphelyasametyalilevalthrtrhrthrglucysleuarg 285
|||||
Db 11 AAGGAAAACCATCG-TTTAAGAACATGGTCTATTGTACACACCGACGAGTGCCTGAGG 69
QY 286 Histlearglnphaglyalaleuthralagluvalglyaspmetthrgluaserala 305
|||||
Db 70 CACATGACGACGTTGGGCCCTGACTGTGAGAGTGGAGATATGACCGAAGACAGCGCC 129
QY 306 Glnalaleuileargluvalleuileylsgluleuagluylleuileuglnle 325
::: |||||||
Db 130 CGAGTTCTCATCCGGAAGTGTGATAAATGACGTGTAAGGCTGTGTCCAGATG 189
QY 326 Glnlyserargcysleuargasnleumetylthrprouleuphevalilethrcys 345
|||
Db 190 CAGAGAGCCAGAGTCTGAGAAATCTGATGAGAGCCCTCTCTCTGTGTGATTAACCTGT 249
QY 346 AlalleglnmetgluylusergluPheHisSerHisThrGlnThrThrleuPheHisThr 365
|||||
Db 250 GCCATTCAGATGGGCACTGAGGAATTCACAGCTCAACCAAGCTTCCAAACCC 309
QY 366 PheTyrAspleuileuileglnlyasnllyshislyshislygllyvalalalaaserasp 385
|||||
Db 310 TTTCACACACCTCCGATGACAGAAAAACAGGCGACAGACACATGAGAGAACTTCAGGTAT 369
QY 386 PheilearTserleuasprhscysgllyaspleuialaleuglulgllyvalPheSerHislys 405
|||||
Db 370 TTTCAGAGGAGCCATGACTCTGTGAGAGACCTGCGCCCTGGAAGGTGTGTCTCCACAAAG 429

QY 406 Pheasphegluileuglnaspvalsersevalasnluaspvalleuileuthrthrgly 425
|||||
Db 430 TTTATTTCCAGACTTGGAGAGTGTGACAGCATGAATGAGACCTCTGCGTACAGACGGG 489
QY 426 LeuleucyslytyrthrtrhalaglnarphelysProlystyrlysphepHeHisLysSer 445
|||||
Db 490 CTCTCTGTAGTACAGCGGCTCAGAGGCTGAGCCCGACAGTAAATCTTTCAATAATCC 549
QY 446 PheGlnlytyrThrAlaArgleuSerSerleuileuthrSerHisGluProglu 465
|||||
Db 550 TTTCAGAGATACACAGAGGTCGAGACTCAGACTGTGTGAAGTCCAGAGCCAGAG 609
QY 466 GluAlaThrlysglyasnlytyrleuGlnlysmetyalserIleaseraspIleThrSer 485
|||||
Db 610 GAGGTGACCAAGGAGATAGCTACTTGAGAAATGTTTCCATCTCCGACATCATCC 669
QY 486 ThrTyrSerSerleuLeuArgTyrThr 494
|||||
Db 670 CTGTATGTATCTGCTCTGACACT 696

RESULT 2

AO309404/c 552 bp DNA linear GSS 22-DEC-1998
LOCUS
DEFINITION
CITBI-E1-2528J13.TF CITBI-E1 Homo sapiens genomic clone 2528J13,
DNA sequence.
ACCESSION
AO309404
KEYWORDS
AO309404.1 GI:4041438
GSS.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 552)
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Sun,E., Wible,C., Shizuya,H., Simon,M. and
Venter,J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
Unpublished (1998)
Other_GSSS: CITBI-E1-2528J13.TF
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

TITLE
JOURNAL
COMMENT

FEATURES

Location/Qualifiers

1..552
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2528J13"
/clone_1ib="CITBI-E1"
/sex="male"
/cell_type="sperm"
/note="Vector: pBelobAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"

BASE COUNT 144 a 121 c 130 g 157 t
ORIGIN

Alignment Scores:

Pred. No.: 7.52e-133 Length: 552
Score: 974.00 Matches: 183
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 17.84% Indels: 0
DB: 17 Gaps: 0

US-09-697-089-2 (1-1024) x A0309404 (1-552)

Qy 477 MetValSerIleSerAspIlePheSerThrTyrosSerSerLeuLeuArgTyThrCysGly 496
|||||
Db 550 ATGGTTCACATTTCCGACATTCATCCACTTATACACAGCTCTCCGGTACACCTGTGGG 491
Qy 497 SerSerValGluAlaThrArgAlaValMetLysHisLeuAlaAlaValTyrcInHisGly 516
|||||
Db 490 TCATCTGTGGAAGCCACCGAGGCTGTATGAAAGCCCTCGCAGCAGTATCAACACGCGC 431
Qy 517 CysLeuLeuGlyLeuSerIleAlaLysArgProLeuTrpArgGlnGlnSerLeuGlnSer 536
|||||
Db 430 TGCCTCTCGGACCTTTCATCGCCACAGAGGCTCTCTCGAGACAGGAATCTTTGCAAGT 371
Qy 537 ValLysAsnThrThrGlnGlnGlnLuuLeuLysAlaIleAsnIleAsnSerPheValGlu 556
|||||
Db 370 GTGAAAAACACCACTGACAGCAAAATTCGAAAGCCATTAACATCAATTCCTTTGTAGAG 311
Qy 557 CysGlyIleHisLeuTyrcInGlnGlnSerThrSerLysSerAlaLeuSerGlnGlnPheGlu 576
|||||
Db 310 TGTGGCATCCATTATATCAAGAGATCATCAATCAAGCCCTGAGCCAGAAATTTGAA 251
Qy 577 AlaPhePheGlnGlyLysSerLeuTyrcInLeuAsnSerGlyAsnIleProAspTyrcLeuPhe 596
|||||
Db 250 GCTTCTTTCAGAGTAAAGCTTATATCATCACTCAGGAAACATCCCGATTACTATT 191
Qy 597 AspPhePheGlnHisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPhe 616
|||||
Db 190 GACTCTTGTGAACATTTCCCAATGTGTCAAGTGTCTGTGACTTCATTAACCTGACACTTT 131
Qy 617 TyrcGlyGlyAlaMetAlaSerTrpGluLysAlaAlaGluAspThrGlyIleHisMet 636
|||||
Db 130 TATGGGGAGCATGCTTCATGAGAAAGCTCGCAGAGACACAGGTGAATCCACATG 71
Qy 637 GluGluAlaProGluThrTyrcInLeuProSerArgAlaValSerLeuPheAsnTrpLys 656
|||||
Db 70 GAAGAGGCCCCAGAAACTACATTCGCCAGAGGCTGTATCTTCTTCACTGGAAG 11
Qy 657 GlnGluPhe 659
|||||
Db 10 CAGGAATTC 2

RESULT 3
BB627584 650 bp mRNA linear EST 26-OCT-2001
LOCUS BB627584 RIKEN full-length enriched, adult male urinary bladder Mus
DEFINITION BB627584 musculus cDNA clone 9530011p19 5', mRNA sequence.
ACCESSION BB627584
VERSION BB627584.1 GI:16465218
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 650)

REFERENCE
AUTHORS AraiKawa,T., Carinici,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
'Hizemoto,K.', Horii,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
'M.', Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
'D.', Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (AraiKawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenho-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,

URL: <http://genome.gsc.riken.go.jp/>
Carinici,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
'M.', Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwara,S., Inoue,K., Togawa,K., Izawa,M., Ohara,E.,
Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura
'S.', Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carinici,P., Sugahara
'Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Kondo,S., Shingawa,A., Saito,T., Kiyosawa,H., Yamanka,I., Alzawa
'K.', Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.
e mouse tissues.

FEATURES
source location/Qualifiers
1. 650
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="9530011p19"
/clone_lib="RIKEN full-length enriched, adult male urinary
bladder"
/sex="male"
/tissue_type="urinary bladder"
/dev_stage="adult"
/lab_host="DH10B"
/note="Site_1: Sali; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTNN 3'], cDNA was
GAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTNN 3'], cDNA was
transcribed by using trihalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 370.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGATTCGACTTATTAATTAATTAATCCCCCCCCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from
Lambda FLC I."

BASE COUNT 164 a 174 c 173 g 139 t
ORIGIN

Alignment Scores:
Pred. No.: 1.2e-117 Length: 650
Score: 872.00 Matches: 163
Percent Similarity: 84.26% Conservative: 19
Best Local Similarity: 75.46% Mismatches: 34
Query Match: 15.97% Indels: 0
Gaps: 0
Db: 10

US-09-697-089-2 (1-1024) x BB627584 (1-650)

Qy 129 AsnLeuLysSerThrPheThrGluProValLeuTrpArgLysAspGlnHisHisArg 148
|||||
Db 2 AATCTGGAGAAAACCTTCACGAACCTTATCATGTGGAAGAGACCATGTCATACCGT 61
Qy 149 ValGlnGlnLeuThrLeuAsnGlyLeuLeuGlnSerProCysIleIleGlu 168
|||||

```

Db 62 GTGAGCAGCTGACTTTGGGACGCTCTCGAGGCTCTGAAGAGCCCTGCTGATTGAA 121
QY 169 GYGLUserGLysGLysSerThrLeuLeuInArgIleAlaMetLeuPGLysEr 188
    |||||
Db 122 GGGGAGCTGGCAAGGAGAGTCCACCCCTGCTGAGAGAAATCGTATGCTCTGGGCTCT 181
QY 189 GYLYScysGLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSerArgAla 208
    |||||
Db 182 GGGGGCTGCAGAGGCTCTGAGAGGCTTCACTTCTTCATCCACCTGAGAACGCC 241
QY 209 GYGLUleuPheGluThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 228
    |||||
Db 242 ATGGGGGAGCTATTCGAAACACTGTACAGTACGCTCTGAACTACCCGAGCTTCATCAGC 301
QY 229 LysGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArgValLeuPheLeuLeuAsp 248
    |||||
Db 302 AAGCCGACCTTCAGAGCTGCTGCTGCTGAGTACACAGAGAGTCCCTCTTCTCTGAT 361
QY 249 GYLYTrsGlnLysPheLysPheLysPheLysPheLysPheLysPheLysPheLysPheLys 268
    |||||
Db 362 GGTTCACATGATTCATCCACCCAGAACCTGCCAGAAATTGAAAGCCCTGATTAAGAAAAC 421
QY 269 HisArgPheLysAsnMetValIleValIleThrThrThrThrGluCysLeuArgHisIleArg 288
    |||||
Db 422 CATGCTTCAGAGACATGCTCATTTGTCCACACAGAGTGCCTGAGGCAATATCAGA 481
QY 289 GlnPheGlyAlaLeuThrAlaGluValAlaGlyAspMetThrGlnAspSerAlaGlnAlaLeu 308
    |||||
Db 482 CATGTTGGCGCCCTGATGCGGAGGTGGAGATATGACCGAAGACAGTCCAAAGATCTC 541
QY 309 IleArgGluValLeuIleLysGlnLeuAlaGluGlyLeuLeuLeuGlnIleGlnLysSer 328
    |||||
Db 542 ATCGAGCAGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 601
QY 329 ArgCysLeuArgAsnLeuMetLysThrProLeuPheValIleThr 344
Db 602 AGGTGCTGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 649

```

```

RESULT 4
LOCUS B1824482 741 bp mRNA linear EST 04-OCT-2001
DEFINITION 603038854F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5179909 5',
            mRNA sequence.
ACCESSION B1824482
VERSION B1824482.1 GI:15936032
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 741)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
            Email: cgaabs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.lnl.gov
            Plate: ILAM11448 row: k column: 14
            High quality sequence start: 3
            High quality sequence stop: 705.
            Location/Qualifiers
                1..741

```

FEATURES

```

source
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="IMAGE:5179909"
    /clone_lib="NIH_MGC_115"
    /lab_host="DH10B"

```

```

/note="Organ: pooled brain, lung, testis; Vector:
PCMV-SPOrt6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH MGC Library."

```

```

BASE COUNT      233 a      147 c      164 g      197 t
ORIGIN
Alignment Scores:
Pred. No.:      9,29e-115      Length:      741
Score:          853.00      Matches:      168
Percent Similarity: 96.55%      Conservative: 0
Best Local Similarity: 96.55%      Mismatches: 1
Query Match:    15.63%      Indels:      6
DB:             13      Gaps:      0

```

US-09-697-089-2 (1-1024) x B1824482 (1-741)

```

QY 1 MetAsnPheIleLysAspAsnSerArg--AlaLeuIleGlnArgMetGlyMetThrValI 20
    |||||
Db 228 ATGAAATTCATTAAGACAAATAGCCGAGCCCTTATTCAAAGATGGAATGACTGTTA 287
QY 20 IeLysGlnIleThrAspAsnLeuPheValIleTrpAsnValLeuAsnArgGlnGluValAsnI 40
    |||||
Db 288 TAAAGCAATATCAGATGACTTATTTGTATGAAATGTTTGAAATCGCGAAGAAATTAACA 347
QY 40 IeIeCysCysGluLysValAlaGluGlnAspAlaAlaArgIleIleHisMetIleLeuI 60
    |||||
Db 348 TCATTGCTGCGAAGAGTGGAGCAGATGCTGTAGAGGATCATTCACATGATTTTGA 407
QY 60 YsLysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTrpProI 80
    |||||
Db 408 AAAAGGCTTCAGAGTCCCTGTACCTCTTCTTAATCCCTTAAGAGTGCAGAACTATCCTC 467
QY 80 eupheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspA 100
    |||||
Db 468 TATTTCAGGACTTAAATGAGACAAAGTCTTTTTCATCAGACATCAGAAAGAGACTTGGACG 527
QY 100 spleuAlaGlnAspLeu--LysAspLeuTrpHisThrProSerPheLeuAsnPheTrpPro 119
    |||||
Db 528 ATTGGCTCAGAGATTTACAAGACTTGTACCATACCCCATTTTTCGAACCTTTATCCC 587
QY 120 LeuGlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheTrpGluProVal--Le 139
    |||||
Db 588 CTTGTGAGAGATATTGACATTAATTTTAACTTGAAGAACCTTCACAGAACCTGTCTCT 647
QY 139 uTrpArgLysAspGlnHisHisArgValAlaGluGlnLeuThrLeuAsn--GlyLeuLeuG 159
    |||||
Db 648 GTGAGAGAGAGACCAACACCATCACCGGTGAGACAGCTGACCTGAAATGGGTCTCTGC 707
QY 159 InAlaLeuGlnSerProCysIleIleGluGly 169
    |||||
Db 708 AAGCTTCACAGAG--CCCTGCATCATTTGAAGG 738

```

```

RESULT 5
LOCUS AV719179/c 480 bp mRNA linear EST 16-OCT-2000
DEFINITION AV719179 GLC Homo sapiens cDNA clone GICED010 5', mRNA sequence.
ACCESSION AV719179
VERSION AV719179.1 GI:10816331
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 480)
AUTHORS Qian,B., Wu,T., Huang,Q., Kang,B., Gao,X., Xu,Z., Xiao,H.,
        , Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z., Zeng,L.,

```

Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Yang, Y., Gu, Y., Chen, Z. and Han, Z.
Homo sapiens CDNA GLC clones
Unpublished (2000)
Contact: Zeguang Han

FEATURES	Location/Qualifiers
source	1. .480

```

/ote="Vector: pbluescript sk(-); Site_1: EcoRI; Site_2
XhoI"
BASE COUNT      138 a      120 c      85 g      137 t
ORIGIN

```

US-09-697-089-2 (1-1024) x AV719179 (1-480)

Cy 869 HSGI^LIleuIIeaSPargMetAsnValLeuGI^LIleuThrAlaLeuMetLeuProTrp 888
|||||
|||
Dβ 480 CATGAACGATCGACAGARGAACGTCTAGAACAAGCTCAACGCACACTGATCTGCCCCGG 421

Dy 889 GlycysaspValGlnIlySerLeuSerSerLeuleuYshIsleugluGlvalProIn 9088
Dz 420 GgCTGTGAAGTGCACGGCAGCGTTGAACAATTGGAGAGGTCGCCAAC 361

Dy 909 LeValLysLeuGlyLeuLysAsnTParGleThrAspThrgluIleArgIleLeuGly 928
Dd 360 CTCGTCAAGCTTGGCTTGAAACCTGAGACTCACAGATACAGAGATTAGCATTTTAGGT 30DD

Dy 929 AlaPhePheGlyLysAsnProLeuYsaSnpPheGlnGlnLeuAsnLeuAlaGlyAsnArg 948
|||||
Db 300 GCATTTTGGAAAGAACCTCTGA AAAAC TTCACAGACTTGAA TTTGGCGGGAATCGT 2411

QY 949 ValSerSerAspGlyTyrPheLeuAlaPheMetGlyValPheGluAsnLeuGlySgInLeuVal 968
 |||
 Db 240 GTGAGCACTGATGGATGGCTTGCCTTCATGGGTGTATTGAGAACTTAAACCAATTAGTG 1811

Dy 969 PhePheaspPheSerThrLysGluPheLeuProAspProAlaLeuValArgLysLeuSer 988
Db 180 TTTTGTACTTAGCTAAAGAATTCTACCTGATCCAGCATTAAGTCAGAAAACTTACG 1211

Dy 989 GlnValLeuSerIysLeuThrPheLeuGlnGluAlaArgLeuValGlyTrpGlnPheasp 100
Dd 120 CAAGTGTAATCCAAGTTAACTTTTCGCCAAGAAGCTAGCGTTGTGGGTGCCAATTGAT 61

qy 1009 AspaspaspseuserValIlethrGlyAlaPheNylsleuValThrAla 1024
 |||||
 Db 60 GATGATGATCTCAGTGTATTACAGAGAGCTTTTAACTAGTAACGTCT 13

RESULT 6					
BI908869					
LOCUS	BI908869	748 bp	mRNA	linear	EST 16-OCT-2001
DEFINITION	603065455F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5215669 5', mRNA sequence.				

ACCESSION	BI908869
VERSION	BI908869.1
KEYWORDS	GI:16171950
SOURCE	EST.
	human.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
Mammalia; Euthalia; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 748)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished. (1999)
Contact: Robert Strausberg, Ph.D.

```

FEATURES
source
    Plate: L1AM1541 row: m column: 14
    High quality sequence start: 7
    High quality sequence stop: 744.
    location/Qualifiers
    1.. 748

```

and directionally clon

1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note:

BASE COUNT	236 a	148 c	166 g	198 t
ORIGIN				

Pred. No.:	9.38e-111	Length:	748
Score:	826.00	Matches:	160
Percent Similarity:	96.41%	Conservative:	1

Query Match:	15.13%	Indels:	4
DB:	13	Gaps:	0

QY 1 MetAsnPhelIelLysAspAsnSerArgAlaLeuIleGlnArgMetClyMetThrValIle 20

Oy	101	LeuA1ag1na5pleu-	-lysasp1eutyrih5thPr0se5Phe1eusa5nPheryrPol	120
Db	552	TTGGCTCAGGATTTACAAAGAGACTTGTCACATACCCACTCTTTTGTGAACCTTATATCCC		611
Oy	120	eug1glua5plleasplle1lepheas5nleu1y5serTh1pherTh1uap1ovalleut		140
Db	612	TTTGGTGAAGATATWGCATTTATTTTAACTCTGAAAGACACCTTCACAGACCTGCTCCGT		671
Oy	140	rPar1y5a5p1e1nh1sh1sh1a5gva1giug1nleutTh1leua5ncl1y1eug1na		160
Db	672	GGAGGAAGACCAAC-CATCACCCGCTGAGACACCTGCAGCTGATAGG-CTCCTGACAG		729
Oy	160	1a1eug1n5erProcys	165	
Db	730	CTCTCAGAGCCCTGCG	746	
RESULT 7				
LOCUS	AZ360053	602 bp	DNA	linear
DEFINITION	1M0103H11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic			
ACCESSION	AZ360053			
VERSION	AZ360053.1	GI:10473753		
KEYWORDS	GSS.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Ham1,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D., Weiss,R.			
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0103 row: H column: 11 Seq primer: CGTGTGAAGACGACGGCCAGT Class: plasmid ends High quality sequence stop: 602. Location/Qualifiers 1. 602 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGC1M0103H11" /clone_lib="Mouse 10kb plasmid UUGC1M library" /sex="Male" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114[gb]IA129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and			

TITLE	JOURNAL	COMMENT
Jong, P. and Fraser, C.M. Rat BAC End Sequences from Library CHORI-230 EcoRI segment Unpublished (1999)		Other_GSSs: CH230-42F7.TJ

Clones are derived from the rat BAC library CHO1-230 (<http://www.cho1.org/bacpac/rat230.htm>). For BAC library availability, please contact Pater de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.cho1.org/bacpac/or_eirlng_information.htm). BAC end plates: http://www.fligr.org/ltb/bac_ends/rat/bac_end_intro.html Plate: 42 row: F column: 7

Seq primer: T7

Class: BAC ends.

FEATURES	Location/Qualifiers
source	1. .518

BASE COUNT	133 a	124 c	146 g	115 t
ORIGIN				

Alignment Scores:	
Pred. No.:	4,47e-98
Score:	739.00
Percent Similarity:	51.72%
Best Local Similarity:	79.68%
Query Match:	13.54%
DB:	17
Gaps:	0
Length:	5
Matches:	1
Conservative:	1
Mismatches:	2
Indels:	1
Gaps:	0

US-09-697-089-2 (1-1024) x BH348412 (1-518)

QY	261	lIleuAlaIleuIleuylsGluAsnHisArgPheIysAsnMetValIleValThrThr	280
Db	2	ATCGAGGCGCCGTGGTAAAGGAAACCAACGCTTTCAAGAACATGGTCATTTGCACCACCACC	61
QY	281	ThrGluCysLeuArgHisIleArgGlnPheGluValAlaLeuThrAlaGluValAspMet	300
Db	62	ACGGAGTGCCTGAGGCGCATCGACACAGCTTGGCGCCCTTGACTGTGGAGGTGGGAGATATG	121
QY	301	ThrGluAspSerAlaGlnAlaIleuArgGluValLeuIleuylsGluAlaGluGly	320
Db	122	ACGGAAACAGCGCCCGAGTCTTCATCGCGGAAGTGTGTAATATGAACGTGGCGTGAAGGC	181
QY	321	LeuLeuLeuGlnIleGlnIlySerArgCysLeuArgAsnIleuIlyThrProLeuPhe	340
Db	182	TTGTGTTCTTCAGATGCGGAGGATCCAGGTGCTTGAGAAATGTGATGAGAGCCCTCTCTTC	241
QY	341	ValValIleThrCys-AlaIleGlnMetGluIleSerGlnPheHisSerHisThrGlnTh	360
Db	242	GTTGGTGAACCTGTGACCATCCAGATGGCGAGTGGAAATGTCMACTCACTCAAC	301
QY	360	TrpIleuPheHisThrPheTyrAspLeuLeuIleGlnIlyAsnIlyHisIlyHisIlyGly	380
Db	302	CATGCTCTGCCAAACCTTACGACGCTCGATATACGAAAAACAGGCGGACACACATGG	361
QY	380	yValAlaIleSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGlnGlu	400
Db	362	AGCAATCTTCAGTGCATTTTGTACAGGACCTCAAGACTACTGTGGAGACCTGGCCGTGAAG	421

Qy	400	YVALPHESEKRTSLKSPHEAPPHGILNLEUCLNAPYLAISERSEVALNSGLNAPPA	420
	422	TEGTGTCCTCCACAAAGTTGATTTGCACTTGAGGATGTGTGCACANTGAATGAGACGT	481
Qy	420	ILLEULFTHRTHRGYLEULCYS	428
Db	482	CCTGTGTGAGGACGGGGCTCTCTGT	506

RESULT	9	
BH267158/c		
LOCUS	BH267158	619 bp
DEFINITION	CH230-19B32.TJ CHORI-230 Segment 1	DNA linear GSS 30-NOV-2001
	CH230-19B32, DNA sequence.	Rattus norvegicus genomic clone
ACCESSION	BH267158	
VERSION	BH267158.1	GI:17179098
KEYWORDS	GSS.	
SOURCE	Norway rat.	
ORGANISM	Rattus norvegicus	

REFERENCE 1 (bases 1 to 619)
AUTHORS Zhao S., Shetty J., Shatsman, S., Tsagaye, G., Geor, K., Shvartsbeyn
TITLE 'A', Gebzegeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de
JOURNAL Rat BAC End Sequences from Library CHORI-230 EcoRI segment
COMMENT Unpublished (1999)
OTHER_GSSS: CH230-19B22.TV

(clones are derived from the rat BAC library CHORI-230
<http://www.chori.org/dacpac/rat330.htm>). For BAC library
 availability, please contact Pieter de Jong (pdejong@emil.chi.org)
 Clones may be purchased from BACpac Resources
<http://www.chori.org/dacpac/orling-information.htm>. BAC end
 page: http://www.tlgr.org/t2db/bac_ends/rat/bac_end_intro.html
 Plate: 19 row: B column: 22
 Seq primer: SP6
 class: BAC ends.

FEATURES	Location/Qualifiers
source	1. .619

BASE COUNT	163	a	141	c	158	g	157	t
ORIGIN								
Alignment Scores:								
Pred. No.:	6,59e-84	Length: 619						
Score:	644.00	Matches: 115						
Percent Similarity:	84.38%	Conservative: 25						
Best Local Similarity:	71.88%	Mismatches: 20						
Query Match:	11.80%	Indels: 0						
GB:	17	Gaps: 0						

US-09-697-089-2 (1-1024) x BH267158 (1-619)

QY 88 SerLeuPheHisGlnThrSerCugIAspLeuAspAspLeuAclnAspLeuTysAsp 107
:::|||||
482 GGCCTTTTTCATCAGAACTTGAAAGAAGACTTGATGTTCTGGCCACAGACTTAAAGAC 423

QY	108	LeuYrYrIshTrProSerPheunusapheryrProleuNglyLVAAspIleaspllele	127
Db	422	TTATRACACAGCCCGTGTTTTAAGACATCTTCTCTCGGTGGAGATATGCACATCA	363
QY	128	PheasneLeuYsSerThrPheThrGluProValLeuTrParGlyAspGlnHisHis	147
Db	362	TTTCATCTGCGAGATCACTTCACAGAACCTGCTGTGTGGAGGAAGCACATCGTATCAC	303
QY	148	ArgValGluGluInleuThrLeuAsnGlyLeuAsnGlnAlaLeuGlnSerProCysIlele	167
Db	302	CGAGTAGAGCGAGATACCTGTGGCGAGCTGTGGAGGCTGTGAGACAGTCCCTGCTCA	243
QY	168	GluGlyGlnSerGlyLySgLySgLySerThrLeuLeuGlnArgIleAlaMetLeuTrpely	187
Db	242	GAAGGGAGTCTGGCAAGGGAAGTCCACCCCTGCTGCAAAAATATGCCATGCTGTGGCC	183
QY	188	SerGlyLyScysLySAlaLeuThrLySLeuLySLeuValPhePheLeuArgLeuSerArg	207
Db	182	TATGGAAATGTGCCCGCTGACACCACTGAATATGTCTTCATTCCTCGCTGAGCAGT	123
QY	208	AlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeuLeuAspIleProGlyThrIle	227
Db	122	GCTAGGGGTGGCGCTGTGTGAACAATGTATGATTCAGCTCGTGAACATACCTGATCCATC	63
QY	228	ArgLySglnThrPheMetAlaMetLeuLeuLySLeuArgGlnArgValLeuPheLeuLeu	247
Db	62	AGCAAAACCAACCTTCAGGCGTCTGCTGTGGAAGTACACAAGAAGTCTCTTCTCTCTC	3
RESULT 10			
LOCUS	B1854236	775 bp	mRNA linear EST 10-OCT-2001
DEFINITION	603381263p1 NC1_CGNP_Mam4 Mus musculus cDNA clone IMAGE:5389239 5',		
ACCESSION	B1854236		
VERSION	B1854236.1	GI:15994983	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-rt@mail.nih.gov		
	Tissue Procurement: lothar Hemmighausen Ph.D., Priscilla Furch		
	Ph.D.		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		
	Plate: L1MAM1191 row: m column: 16		
	High quality sequence stop: 764.		

	ORIGIN
Alignment Scores:	
Pred. No.:	2.08e-81
Score:	628.00
Percent Similarity:	82.32%
Best Local Similarity:	71.95%
Query Match:	11.50%
DB:	13
US-03-697-089-2 (1-1024) x B1854236 (1-775)	
	Length: 775
	Matches: 118
	Conservative: 17
	Mismatches: 29
	Indels: 0
	Gaps: 0

Fax: 301 838 0208
Email: szhoo@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Plietier de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or_oring_information.htm). BAC end
page: http://www.tigr.org/db/bac_ends/rat/bac_end_intro.html
Plate: 18 row: E column: 7
Seq primer: SP6
Class: BAC ends.

FEATURES

source

Location/Qualifiers
1..817
/organism="Rattus norvegicus"
/strain="BN/SSNHsd/MCW"
/db_xref="taxon:10116"
/clone_1id="CH230-18E7"
/clone_1lb="CHORI-230 Segment 1"
/sex="Female"
/cell_type="Brain"
/note="Vector: pTRBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by
Plietier de Jong"

BASE COUNT 211 a 182 c 199 g 225 t

ORIGIN

Alignment Scores:
Pred. No.: 3,72e-79 Length: 817
Score: 613.00 Matches: 115
Percent Similarity: 84.91% Conservative: 20
Best Local Similarity: 72.33% Mismatches: 24
Query Match: 11.23% Indels: 2
DB: 17 Gaps: 0

US-09-697-089-2 (1-1024) x BH358172 (1-817)

OY 88 SerLeuPheHISGlnThrSerGluGlyAspLeuAspLeuAlaGlnAspLeuLysAsp 107
DB 475 GGTCTTTTTCATCAGAACTGGAGAGAGCTTGATGTTCTGGCCAGAGCTTAAGAGC 416
OY 108 LeuTYrHISThrProSerPheLeuAsnPheryrProLeuGlyGluAspIleAspIle 127
DB 415 TTATACACAGCCGCTTTTAAGAACTCTTCTCGGCGAGAGATATGACATCATC 356
OY 128 PheAsnLeuLysSerThrPheThrGluProValLeuTrpArgLysAspGlnHisHis 147
DB 355 TTCAATCTGCAGATCCTTCACAGACCTCTCTGTGGAGAGAGACCATGTCATCAC 296
OY 148 ArgValGluGlnLeuThrLeuAsnGlyLeuGlnAlaLeuGlnSerProCysIleIle 167
DB 295 CGAGTAGAGCAGATACCTGGGAGCCTGCTGAGGCTGTGAAGATCCTGCTCAT 236
OY 168 GlnGlyGluSerGlyLysSerThrLeuLeuGlnArgIleAlaMetLeuTrpGly 187
DB 235 GAAGGGAGTGTGGCAAGGAGATCCACCCGCTGCAAAAATATGCCATGCTGGGCC 176
OY 188 SerGlyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSerArg 207
DB 175 TCTGGAGATGCTGCCAGCTGTGAACCAATGATGCTCTCTCATCGGCTGAGAGT 116
OY 208 AlaGlnGlyGluLeuPheGlnThrLeuGlyCysAspGlnLeuLeuAsnIleProGlyThrIle 227
DB 115 GCTAAGGGTGGCTCTTTGAACATTTGA-TGATCAGCTGCTGAACATTCCTGATCCATC 57
OY 228 ArgLysGlnThrPheMetAlaMetLeuLeuLysArgGlnArgValLeuPheLeu 246
DB 56 AGCAACACCAACCTTCAGGGCTCTGCTGCT-AGATTACACAAAGAGTCTCTTTCTC 1

RESULT 12
A1263294/c A1263294 364 bp mRNA linear EST 03-FEB-1999
LOCUS qx57b01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2005417 3',
DEFINITION mRNA sequence.

ACCESSION A1263294
VERSION A1263294.1 GI:3871497
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TUMOR Gene Index
Tumor Cancer Institute, Cancer Genome Anatomy Project (CGAP),
unpublished (1997)

JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 2146 Std Error: 0.00
Seq primer: -400P from Glbco
High quality sequence stop: 364.
Location/Qualifiers

FEATURES

source

1..364
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1id="IMAGE:2005417"
/clone_1lb="NCI_CGAP_Pan1"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/note="Organ: pancreas; Vector: pCMV-Sport6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"

BASE COUNT 117 a 84 c 55 g 108 t

ORIGIN

Alignment Scores:
Pred. No.: 4.97e-79 Length: 364
Score: 609.00 Matches: 114
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 11.16% Indels: 0
DB: 9 Gaps: 0

US-09-697-089-2 (1-1024) x A1263294 (1-364)

OY 911 LysLeuGlyLeuLysAsnTrpArgLeuThrAspThrGluIleArgIleLeuGlyAlaPhe 930
DB 364 AAGCTTGGGTTGAAAACCTGGAGACTCACAGTACAGAGATTAGATTAGTGCATTT 305
OY 931 PheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsnArgValSer 950
DB 304 TTGGAAAGAACCTCTGAAAACCTTCACAGCAGTTGATTTGGCGGAAATGCTGAGC 245
OY 951 SerAspGlyTrpLeuAlaPheMetGlyValPheGluAsnLeuLysGlnLeuValPhePhe 970
DB 244 AGTATGATGATGCTGCTTCATGCGGTGATTTGAGAACTTAAACCAATTAAGTCTTTT 185
OY 971 AspPheSerThrLysGlnPheLeuProAspProAlaLeuValArgLysLeuSerGlnVal 990
DB 184 GACTTAGTACTAAGAAATTTCTACCTGATCCAGCATTAAGTCAGAAACTTAGCCAGTG 125
OY 991 LeuSerLysLeuThrPheLeuGlnGlnAlaArgLeuValGlyTrpGlnPheAspAsp 1010
DB 124 TTATCCAGTAGTAATCTTCTGCAAGAGCTAGGCTTGTTGGGTGCATTTGATGATGAT 65
OY 1011 AspLeuSerValIleThrGlyAlaPheLysLeuValIleThrAla 1024
DB 64 GATCTCAGTGTATTATACAGGTGCTTTTAACTAGTAAGTCTGCT 23

RESULT 13
AV656315

LOCUS AV656315 371 bp mRNA linear EST 16-JAN-2002
 DEFINITION AV656315 GLC Homo sapiens cDNA clone GICEQA10 3', mRNA sequence.
 ACCESSION AV656315
 VERSION AV656315.1 GI:9877329
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 371)
 Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W., Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z., and Han, Z.
 Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
 Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
 JOURNAL 21625106
 MEDLINE
 COMMENT Contact: Zeguang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China
 Tel: 86-21-50801922 (ex.45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.
 FEATURES
 source
 1..371
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="GICEQA10"
 /clone_1lb="GIC"
 /tissue_type="corresponding non cancerous liver tissue"
 /dev_stage="Adult"
 /lab_host="SOLR"
 /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"
 BASE COUNT 112 a 85 c 91 g 82 t 1 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.3e-75 Length: 371
 Score: 586.00 Matches: 114
 Percent Similarity: 98.31% Conservative: 2
 Best Local Similarity: 96.61% Mismatches: 2
 Query Match: 10.73% Indels: 0
 DB: 10 Gaps: 0
 US-09-697-089-2 (1-1024) x AV656315 (1-371)
 QY 625 GUAUYSALAAAGUAUASPThrGlyGlyLeuIleHisMetGluGluAlaProGluThrTyrIle 644
 |||||||
 Db 1 GAANAAGCTGCAGAAACACAGAGTGGAATCCACATGGAAGAGCCGCCGAACCTACTT 60
 QY 645 ProSerAlaValSerLeuPheAsnTrpLysGlnGluPheArgThrLeuGluVal 664
 |||||||
 Db 61 CCCAGCAGGCGTATCTTGTCTTCACTGGAAGCAGAAATTCAGACTCTGGAGGTC 120
 QY 665 ThrLeuArgPheSerLysLeuAsnLysGlnAspIleThrTyrLeuGlyLysIlePhe 684
 |||||||
 Db 121 ACACTCGGGGATTTCAGCAAGTGAATTAAGCAATATCAATATCTGGGAAATAATTC 180
 QY 685 SerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyValAlaGlySerLeu 704
 |||||||
 Db 181 AGCTCTGCCACAGAGCTCAGCTCAATTAAGAGATGCTGGGTGGCTGGAAGCCTC 240
 QY 705 SerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGluAlaSerProLeu 724
 |||||||
 Db 241 AGTTTGGCTCCACACACTGTAAAGACATTTATCTCTCAATGCGGGAAGCCAGTCCCTC 300
 QY 725 ThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThrLeuSer 742

Db 301 ACCATAGAGATGAGGACGACATCATCTGTAAACAACCTGGACAGCTTGGGT 354
 RESULT 14
 BQ204082/c 719 bp mRNA linear EST 02-MAY-2002
 LOCUS BQ204082
 DEFINITION UI-R-DN1-cmv-e-08-0-UI-s1 UI-R-DN1 Rattus norvegicus cDNA clone
 UI-R-DN1-cmv-e-08-0-UI 3', mRNA sequence.
 ACCESSION BQ204082
 VERSION BQ204082.1 GI:20420547
 KEYWORDS EST.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 719)
 Bonaldo, M.F., Lennon, G., and Soares, M.B.
 Normalization and subtraction: two approaches to facilitate gene discovery
 Genome Res. 6 (9), 791-806 (1996)
 JOURNAL 97044477
 MEDLINE
 COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@blue.weeg.uiowa.edu
 The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized distal colon library cDNA library preparation: M.B. Soares lab clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 12-210, >L1B3#LINE/L1
 Seq primer: M13 forward
 POLYA=yes.
 FEATURES
 source
 Location/Qualifiers
 1..719
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-DN1-cmv-e-08-0-UI"
 /clone_1lb="UI-R-DN1"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: p773D-Pac (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; The UI-R-DN1 library is a normalized Rat Distal Colon library (nRDC) constructed in p737 PAC vector according to the procedure described by Bonaldo, Lennon & Soares (Normalization and subtraction: Two approaches to facilitate Gene Discovery. Genome Research 6: 791-806, 1996). The oligonucleotide used to prime first strand synthesis contained the sequence tag GAAGTCCTCC between the Not I cloning site and DRI8 stretch. The Rat Distal Colon tissue was provided by Tom Freeman of the Sanger Center.
 TAG_LIB=UI-R-DN1
 TAG_TISSUE=distal colon
 TAG_SEQ=GAAGTCCTCC"
 BASE COUNT 184 a 185 c 146 g 203 t 1 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.87e-69 Length: 719
 Score: 547.00 Matches: 104
 Percent Similarity: 82.64% Conservative: 15
 Best Local Similarity: 72.22% Mismatches: 25
 Query Match: 10.02% Indels: 0
 DB: 14 Gaps: 0

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 31, 2003, 08:40:36 : Search time 85 seconds
(without alignments) 3694.553 Million cell updates/sec

Title: US-09-697-089-2

Perfect score: 5459

Sequence: 1 MNFKDSRALIQRMGMTVL.....MQPDDDLSTVITGAFKLVTA 1024

Scoring table:

PAM120	4.0	Xgapex	12.0
Xgapop	4.0	Ygapex	12.0
Ygapop	6.0	Xgapex	7.0
Delop	6.0	Delxex	7.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-O=/cgn2.1/USPTO.spool/US09697089/runat_29012003_092505_19177/app_query.fasta.1.1223
-DB=Issued_Patents.NA -QEMT=fastac -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=pam120 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15
-MODE=LOCAL -OUTPMF=ptco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09697089 -RCGN.1.1.46 -rcnat_29012003_092505_19177 -NCPU=6 -ICPU=3
-NO_XLPMX -NO_MMAB -LARGEQUERY -NEG.SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=4 -XGAPEXT=12 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=4 -YGAPEXT=12 -DELOP=6 -DELEXT=7

Database : Issued_Patents.NA.*

- 1: /cgn2.6/ptodata/2/1na/5A.COMB.seq.*
- 2: /cgn2.6/ptodata/2/1na/5B.COMB.seq.*
- 3: /cgn2.6/ptodata/2/1na/6A.COMB.seq.*
- 4: /cgn2.6/ptodata/2/1na/6B.COMB.seq.*
- 5: /cgn2.6/ptodata/2/1na/PCUTS.COMB.seq.*
- 6: /cgn2.6/ptodata/2/1na/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	279	5.1	5502	3	US-08-836-134-1
2	279	5.1	5502	4	US-09-493-784-1
3	95	1.7	3573	4	US-09-353-585-4
4	95	1.7	6471	4	US-09-353-585-1
5	94	1.7	1386	2	US-08-910-731-5
6	82	1.5	250	2	US-08-824-701A-8
7	82	1.5	2568	4	US-09-228-986-2
8	81	1.5	1470	4	US-09-099-041A-27
9	81	1.5	1470	4	US-09-245-281-27
10	81	1.5	1470	4	US-09-207-359B-27
11	81	1.5	2859	4	US-09-099-041A-9
12	81	1.5	2859	4	US-09-245-281-9

13	81	1.5	2859	4	US-09-207-359B-9	Sequence 9, Appli
14	81	1.5	3080	4	US-09-099-041A-25	Sequence 25, Appl
15	81	1.5	3080	4	US-09-245-281-25	Sequence 25, Appl
16	81	1.5	3080	4	US-09-207-359B-25	Sequence 25, Appl
17	81	1.5	3382	4	US-09-099-041A-7	Sequence 7, Appli
18	81	1.5	3382	4	US-09-245-281-7	Sequence 7, Appli
19	81	1.5	3382	4	US-09-207-359B-7	Sequence 7, Appli
20	81	1.5	3979	4	US-09-180-439-1	Sequence 2, Appli
21	81	1.5	3979	4	US-09-180-439-2	Sequence 2, Appli
22	81	1.5	32042	4	US-09-245-281-44	Sequence 44, Appl
23	80	1.5	4141	4	US-09-245-281-42	Sequence 42, Appl
24	80	1.5	4141	4	US-09-207-359B-42	Sequence 42, Appl
25	79	1.4	4123	4	US-09-180-439-7	Sequence 7, Appli
26	77	1.4	3541	4	US-09-180-439-5	Sequence 5, Appli
27	76	1.4	1435	5	PCT-US95-05322A-1	Sequence 1, Appli
28	76	1.4	2589	4	US-08-569-749-1	Sequence 1, Appli
29	76	1.4	2589	5	PCT-US96-12860-1	Sequence 1, Appli
30	76	1.4	3532	2	US-09-205-204-1	Sequence 1, Appli
31	76	1.4	3732	3	US-09-212-971-7	Sequence 7, Appli
32	76	1.4	3732	3	US-08-800-929A-7	Sequence 7, Appli
33	76	1.4	3732	4	US-09-617-053A-7	Sequence 7, Appli
34	75	1.4	1058	1	US-08-238-163-1	Sequence 13, Appl
35	75	1.4	2862	4	US-08-569-749-13	Sequence 13, Appl
36	75	1.4	2862	5	PCT-US96-12860-13	Sequence 13, Appl
37	75	1.4	3151	3	US-09-212-971-13	Sequence 13, Appl
38	75	1.4	3151	3	US-08-800-929A-13	Sequence 13, Appl
39	75	1.4	3151	4	US-09-617-053A-13	Sequence 13, Appl
40	74	1.4	626	3	US-09-019-942-4	Sequence 4, Appli
41	74	1.4	626	4	US-09-470-271-4	Sequence 4, Appli
42	74	1.4	1185	2	US-08-391-916A-3	Sequence 3, Appli
43	74	1.4	1215	1	US-08-242-663A-1	Sequence 1, Appli
44	74	1.4	1215	3	US-08-954-536-17	Sequence 17, Appl
45	74	1.4	1215	4	US-08-748-547-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-836-134-1
: Sequence 1, Application US/08836134A
: Patent No. 6020127
: GENERAL INFORMATION:
: APPLICANT: Mackenzie, Alex E.
: APPLICANT: Korneluk, Robert G.
: APPLICANT: Mahadevan, Mani S.
: APPLICANT: McLean, Michael
: APPLICANT: Roy, Natalie
: APPLICANT: Ikeda, John
: TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and
: Patent No. 6020127
: TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy
: FILE REFERENCE: 3477-112, 033477/139914
: CURRENT APPLICATION NUMBER: US/08/836,134A
: CURRENT FILING DATE: 1997-06-20
: NUMBER OF SEQ ID NOS: 23
: SOFTWARE: Patentia Ver. 2.0
: SEQ ID NO 1
: LENGTH: 5502
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-08-836-134-1
Alignment Scores:
Pred. No.: 2.39e-31
Score: 279.00
Percent Similarity: 53.80%
Best Local Similarity: 32.61%
Query Match: 5.11%
DB: 3
Gaps: 6
US-09-697-089-2 (1-1024) x US-08-836-134-1 (1-5502)
OY 150 GUGInLeuThrLeuAsnGlyLeuLeuGInaLeuGInserProCyrtIleIleGluGly 169


```

Db 2223 ATATACGGAAGCTTTTACATAATATAGACTGCTGCGAAAGTTATGTTACTTT 2282
Qy 326 GlnlySerArgCysLeuArgAsnLeuMetLysThrProLeuPheValIleThrCys 345
Db 2283 GGAAGAACCAAGTTTGGAGAGATACGAAACCTCTCTTGTGGCGGAGATCTGT 2342
Qy 346 Ala-IleGlnMetGlyGluSerGluPheHisSerHisThrGlnThrThrLeuPheHis 365
Db 2343 GCTCATGTGTTTCAGATGATCTTTTGACCCATCTTT-GATGATGTCGCTGTTTCAAGTC 2401
Qy 365 rPheTyArgAspLeuLeuIleGlnLysAsnLysHisLysHisGlyValAlaAlaSerAs 385
Db 2402 CTATATGGAACCTTCTCTTAAGCAACAA-----GCGACAGCTGAAT 2446
Qy 385 pPheIleArgSerLeuAspHisCysGlyAspSerLeuAlaLeuGluGlyValPheSerHisLys 405
Db 2447 TCTCAAGCAAGCTGTCCTCTCTGCTGAGCTGCTGAAAGGGCTTTTTCATGTTG 2506
Qy 405 sPheAspPheGlnLeuGlnAspVal-----SerSerValAsnGluAspValLeuLeu 423
Db 2507 CTTTGAGTTTATGATGATGATCTCGCAGAACAGGCGTTGATGAGATGAAGATCTAAC 2566
Qy 423 rThrGlyLeuLeuCysLysTyThrAlaGlnArgPheLysProLysTyThrLysPhePhe 443
Db 2567 CATGTCCTGATGACCAATTTATACACCCAGACTAAGACCATTCCTACCGGTTTTTAAG 2626
Qy 443 sLysSerPheGlnGlnLysTyThrAlaGlyArgArgLeuSerSerLeuLeuThrSerHisG 463
Db 2627 TCTGCTGCTTCAAGAAATTTCTTCCGGGATGAGCTGATGAACCTCTGATTCACATAG 2686
Qy 463 uProGluGluValThrLysGlyAsnGlyLysMetLysMetValSerIleSerAspI 483
Db 2687 GCAGAGAACATCAAGATTTGGAGCTGATCATTTGAAACAATCAACTCACCATGATGAC 2746
Qy 483 eThrSerThrTySerSerLeuLeuArgTyThrCysGly---SerSerValGlnAla 502
Db 2747 TCTAAGCGCTTCAACAAATTTTGAACATATGTCTCCAGCTCCCTTCAACAAAGCAGG 2806
Qy 502 rArgAlaValMetLysHisLeu 509
Db 2807 GCCCAAAATTTGCTCATTTG 2828

RESULT 3
US-09-353-585-4
; Sequence 4, Application US/09353585
; Patent No. 6287865
; GENERAL INFORMATION:
; APPLICANT: Dixon, Mark S
; Jones, David A
; Jones, Jonathan DG
; TITLE OF INVENTION: Plant pathogen resistance genes and uses
; thereof
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye PC
; STREET: 8th Floor, 1100 No. 6287865th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/353,585
; FILING DATE: 15-Jul-1999
; CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C12O
; 1/68
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/930,277
; FILING DATE: 27-OCT-1997

```

```

; APPLICATION NUMBER: PCT/GB96/00785
; FILING DATE: 01-APR-1996
; APPLICATION NUMBER: GB 9506558.5
; FILING DATE: 31-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ms Mary J Wilson
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 620-69
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3573 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Tomato
; STRAIN: Cf2
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-353-585-4

Alignment Scores:
Pred. No.: 0.00176 Length: 3573
Score: 95.00 Matches: 24
Percent Similarity: 66.15% Conservative: 19
Best Local Similarity: 36.92% Mismatches: 21
Query Match: 1.74% Indels: 1
Gaps: 1

US-09-697-089-2 (1-1024) x US-09-353-585-4 (1-3573)
Qy 733 ThrSerValThrAsnLeuLysThrLeuSerIleHisAspLeuGlnAsnGlnArgLeuPro 752
Db 977 GCTTCAATTTGGGAATCTGAAAAACTTGTCTAGCTGAATCTGTATATATACGCTTCT 1036
Qy 753 GlyGlyLeuThrAspSerLeuGlnLysAsnLeuLysAsnLeuThrLysLeuIleMetAsp 772
Db 1037 GGCTCATATCTGCTTCATTTGGGAATCGAACACTGCTATGTTATCTTACAAAT 1096
Qy 773 IleLysMetAsnGlnLysAspAlaIleLysLeuAlaGluGlyLeuLysAsnLeuLys 792
Db 1097 AACCACTTCTGGCTCATATCTGCTTCTGCTTCTGCGGAAT--CTGAACAACCTGTCTATG 1153
Qy 793 MetCysLeuPheHis 797
Db 1154 TTGTATCTTTACAAAT 1168

RESULT 4
US-09-353-585-1
; Sequence 1, Application US/09353585
; Patent No. 6287865
; GENERAL INFORMATION:
; APPLICANT: Dixon, Mark S
; Jones, David A
; Jones, Jonathan DG
; TITLE OF INVENTION: Plant pathogen resistance genes and uses
; thereof
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye PC
; STREET: 8th Floor, 1100 No. 6287865th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible

```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/353,585
FILING DATE: 15-Jul-1999
CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C12O 1/68
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/930,277
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: PCT/GB96/00785
FILING DATE: 01-APR-1996
APPLICATION NUMBER: GB 9506658.5
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ms Mary J Wilson
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-69
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6471 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Tomato
STRAIN: Cf2
FEATURE:
NAME/KEY: mat-peptide
LOCATION: 1754..5012
FEATURE:
NAME/KEY: sig-peptide
LOCATION: 1677..1753
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-353-585-1
Alignment Scores:
Pred. No.: 0.00403 Length: 6471
Score: 95.00 Matches: 24
Percent Similarity: 66.15% Conservative: 19
Best Local Similarity: 36.92% Mismatches: 21
Query Match: 1.74% Indels: 1
DB: 4 Gaps: 1
US-09-697-089-2 (1-1024) x US-09-353-585-1 (1-6471)
QY 733 ThrSerValThrAsnLeuLysThrLeuSerIleHisAspLeuGlnAsnGlnArgLeuPro 752
Db 2661 GCTTCATTCGGGAATCTGAAAACCTGCTCTAGCTGATCTTGTAAATATACACGCTTCT 2720
QY 753 GlyGlyLeuThrAspSerLeuGlnAsnLeuLysAsnLeuThrLysLeuIleMetaspasn 772
Db 2721 GGCCTCATTCCTGCTCTATTCGGGAATCTGAACAACCTGTCTATGTTGATCTTACAT 2780
QY 773 IleLysMetAsnGlnGlnAspAlaIleLysLeuAlaGlnGlyLeuLysAsnLeuLysLys 792
Db 2781 AACCAAGCTTCCTGGCTCATTCCTGCTCATTTGGGGAAAT--CTGAACAACCTTGCTATG 2837
QY 793 MetCysLeuPheHis 797
Db 2838 TTGATCTTTACAT 2852
RESULT 5
US-08-910-731-5
Sequence 5, Application US/08910731
Patent NO. 5932440
GENERAL INFORMATION:
APPLICANT: CHATTERJEE, DEB K.

APPLICANT: SHANDILYA, HARINI
TITLE OF INVENTION: Mammalian Ribonuclease Inhibitors and Use Thereof
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., N.W., SUITE 600
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,731
FILING DATE: (Herewith)
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/795,395
FILING DATE: 04-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/794,546
FILING DATE: 03-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/024,057
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0942.3440003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1386 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
US-08-910-731-5
Alignment Scores:
Pred. No.: 0.000672 Length: 1386
Score: 94.00 Matches: 27
Percent Similarity: 59.78% Conservative: 28
Best Local Similarity: 29.35% Mismatches: 34
Query Match: 1.72% Indels: 3
DB: 2 Gaps: 1
US-09-697-089-2 (1-1024) x US-08-910-731-5 (1-1386)
QY 807 GlyMetAspTyrIleValLysSerLeuSerGlnProCysAspLeuGlnIleGln 826
Db 214 GCGCGCATTCGCGCTCCAGGCGCTGCAGACCCCTCTCAGATCCAGAACCTGAGC 273
QY 827 LeuValSerCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHisn 846
Db 274 CTCAGAACTGCTGCTCAGCGGGCGCGCTGCGGCTCTGTCAGACACTAGGCC 333
QY 847 LeuValLysLeuSerIleLeuAspLeuSerGlnAsnTyrLeuGlnLysAspGlyAsnGln 866
Db 334 CTGCCACCTCGCAGAGACTGCACTGACCTGACGACAACTCTGGGGGATGCGGCGTGCAG 393
QY 867 AlaLeuHisGlu--LeuIleAspArgMetAsnValLeuGlnGlnLeu--ThrAlaLeu 885
Db 394 CTGCTCTCGAAGACCTCTGACCCCAAGTGCAGGAAAGCTGCACTGAGAT 453
QY 885 etLeuProTyrGlyCysAspValGlnGlySer 895
Db 454 TGCAGCTCTGCGCTGCCAGCTGCCAGCCCT 485

RESULT 6
US-08-824-701A-8
; Sequence 8, Application US/08824701A
; Patent No. 5882868
; GENERAL INFORMATION:
; APPLICANT: Funanage, Vicki L.
; APPLICANT: Scavina, Mena
; TITLE OF INVENTION: Method of Diagnosing Spinal Muscular Atrophy
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jeffrey C. Lew
; STREET: 501 Silverside Road Suite 124
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19809
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: Windows for Workgroups 3.11
; SOFTWARE: Ami Pro 3.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,701A
; FILING DATE: 14-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lew, Jeffrey C.
; REGISTRATION NUMBER: 35935
; REFERENCE/DOCKET NUMBER: 47066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 798-0700
; TELEFAX: (302) 798-5970
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: no
; US-08-824-701A-8

Alignment Scores:
Pred. No.: 0.00423 Length: 250
Score: 82.00 Matches: 23
Percent Similarity: 54.79% Conservative: 17
Best Local Similarity: 31.51% Mismatches: 32
Query Match: 1.50% Indels: 1
DB: 2 Gaps: 1

US-09-697-089-2 (1-1024) x US-08-824-701A-8 (1-250)

Qy 218 AspglnleuLeuAspIleProglyThrIleArgLysGlnThrPhenMetAlaMetLeuLeu 237
|||||
Db 2 GACCAGCTCCCTAGAGAAAGAGATCTGTACTGAAATGTCATGAGACATTCACAG 61
|||||
Qy 238 LysLeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGlnPheLeuProGlnAsn 257
|||||
Db 62 CAGTTAAAGAAATCAGGCTCTTATCTTATGATGACTACAAAGAAATATGTTCAATCCCT 121
|||||
Qy 258 CysProGluIleGluAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleVal 277
|||||
Db 122 ---CAAGCATATGAGAAACCTGATTCATAAAAAAACCTATATCCCGGAGCTGCGCTATTTGATT 178
|||||
Qy 278 ThrThrThrThrGluGluCysLeuArgHisIleLeuArgGlnPhe 290
|||||
Db 179 GCTGTCGTACAAACAGGCGCAGGACATCCGCGATATC 217
|||||

RESULT 7
US-09-228-986-2
; Sequence 2, Application US/09228986
; Patent No. 6359198

; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwehuizen, Niels
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 2568
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-228-986-2

Alignment Scores:
Pred. No.: 0.108 Length: 2568
Score: 82.00 Matches: 18
Percent Similarity: 64.15% Conservative: 16
Best Local Similarity: 33.96% Mismatches: 19
Query Match: 1.50% Indels: 0
DB: 4 Gaps: 0

US-09-697-089-2 (1-1024) x US-09-228-986-2 (1-2568)

Qy 733 ThrservalThrAsnLeuLysThrIleuSerIleHisAspLeuGlnAsnGlnArgLeuPro 752
|||||
Db 508 ACMAAGCTGGGATCTCTAGAGAGCTCAGTCTTGTCTGCATCTAACACAGCTCACT 567
|||||
Qy 753 GlyGlyLeuThrAspSerLeuGlnLysAsnLeuLysAsnLeuThrLysLeuIleMetAspAsn 772
|||||
Db 568 GGGCAATACCGGCAAGTTTAGGTACCTGGGAGCTTGACAGAGTTATATTGAGTTTC 627
|||||
Qy 773 IleLysMetAsnGluGluAspAlaIleLysLeuAlaGlu 785
|||||
Db 628 AATCGCTCTTGTGCTGCATTCCTCAATGAAAGATAGCCGAT 666
|||||

RESULT 8
US-09-099-041A-27
; Sequence 27, Application US/09099041A
; Patent No. 6340576
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/09/099,041A
; CURRENT FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 1470
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-099-041A-27

Alignment Scores:
Pred. No.: 0.0708 Length: 1470
Score: 81.00 Matches: 20
Percent Similarity: 58.70% Conservative: 7
Best Local Similarity: 43.48% Mismatches: 19
Query Match: 1.48% Indels: 0
DB: 4 Gaps: 0

US-09-697-089-2 (1-1024) x US-09-099-041A-27 (1-1470)

Qy 156 GlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGluGlnSerGlyLysGlyLys 175
|||||
Db 448 GGCAATCTCATATGAGCAAGGTGAGACCATCTTCAATCTGCTGATGTGGGGTGGCAAG 507
|||||


```

? Patent No. 6369196
? GENERAL INFORMATION:
? APPLICANT: Bertin, John
? TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
? TITLE OF INVENTION: AND USES THEREOF
? FILE REFERENCE: 07334/118001
? CURRENT APPLICATION NUMBER: US/09/245, 281
? CURRENT FILING DATE: 1999-02-05
? EARLIER APPLICATION NUMBER: US 09/207, 359
? EARLIER FILING DATE: 1998-12-08
? EARLIER APPLICATION NUMBER: US 09/099, 041
? EARLIER FILING DATE: 1998-06-17
? EARLIER APPLICATION NUMBER: US 09/019, 942
? EARLIER FILING DATE: 1998-02-06
? NUMBER OF SEQ ID NOS: 44
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 9
? LENGTH: 2859
? TYPE: DNA
? ORGANISM: Homo sapiens
? US-09-245-281-9

```

Alignment Scores:		
Pred. No.:	0.179	Length: 2859
Score:	81.00	Matches: 20
Percent Similarity:	58.70%	Conservative: 7
Best Local Similarity:	43.48%	Mismatches: 19
Query Match:	1.48%	Indels: 0
DB:	4	Gaps: 0

Oy	156	Glycineutgnalaleuglnsepprocysllelllelueglusnerglylsyllys	175
Dd	565	GGCATCCGCATGAGCAGCGGAGACCATCTTCATCCTGGGTATCCTGGGGTGGGCCAAC	624
Oy	176	Serthrleuenglnangllleallamelleuntpolyseryllysylscylsalaleuthr	195
Dd	625	TCCATGCGCTACACGGCGCTACAGACGCTCTGGGGCACGGGCCGGCTAGACGCAAGGGGTC	684

Qy	196	LysPheLysPheValPhe	201
Db	685	AAATCTCTCTCCACTTT	702

RESULT 13
US-09-207-359B-9
; Sequence 9, Application US/09207359B

```

? Patent NO.: 0469140
? GENERAL INFORMATION:
? APPLICANT: Bellin, John
? TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
? FILE REFERENCE: 07334-112001
? CURRENT APPLICATION NUMBER: US/09/207,359B
? PRIOR FILING DATE: 1998-12-08
? PRIOR APPLICATION NUMBER: US 09/099,041
? PRIOR FILING DATE: 1998-06-17
? PRIOR APPLICATION NUMBER: US 09/019,942
? NUMBER OF SEQ ID NOS: 47
? SOFTWARE: FASTEDSO FOR Windows Version 4.0
? SEQ ID NO 9
? LENGTH: 2859
? TYPE: DNA
? ORGANISM: Homo sapiens
? OS-09-207-359B-9

```

Alignment Scores:	
Pred. No.:	0.179
Score:	81.00
Percent Similarity:	58.70%
Best Local Similarity:	43.48%
Query Match:	1.48%
Length:	2859
Matches:	20
Conservative:	7
Mismatches:	19
Indels:	0

DB:	4	Gaps:	0
US-09-697-089-2 (1-1024) x US-09-207-359B-9 (1-2859)			
QY	156 GlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGluGlyGlnSerGlyGlyLys 175		
	:		
Db	565 GGCAATCCGCATGAGCAGGCGTGAACCATCTCTAATCCTGGGTATGCTGGGGTGGGCAAG 624		
QY	176 SerThrLeuGlnAlaArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThr 195		
Db	625 TCCATGCTGCCTACGCGGCTGTGCAGAGCCTCTGGGCGCACGGCGCTAGACGAGGGGCTC 684		
QY	196 LysPheLysPheValPhe 201		
Db	685 AAATCTCTCTCCACTTT 702		

```

RESULT 14
US-09-099-041A-25
: Sequence 25, Application US/09099041A
: Patent No. 6340576
: GENERAL INFORMATION:
: APPLICANT: Bertin, John
: TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
: TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
: FILE REFERENCE: 07334-076001
: CURRENT APPLICATION NUMBER: US/09/099,041A
: CURRENT FILING DATE: 1998-06-17
: PRIOR APPLICATION NUMBER: 09/019,942
: PRIOR FILING DATE: 1998-02-06
: NUMBER OF SEQ. ID NOS: 37
: SOFTWARE: FastSeq for Windows Version 4.0

```

```

? LENGTH:3080
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)..(1470)
? OS-09-099-041A-25

```

Alignment Scores:
Pred. No.: 0.198
Score: 81.00

Best Local Similarity:	43.48%	Mismatches:	19
Query Match:	1.48%	Indels:	0
DB:	4	Gaps:	0

[illegible]

```

RESULT 15
US-09-245-281-25
: Sequence 25, Application US/09245281
: Patent No. 6369196
:
GENERAL INFORMATION:
:
APPLICANT: Berlin, John
:
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
:
TITLE OF INVENTION: AND USES THEREOF
:
FILE REFERENCE: 07334/118001
:
CURRENT APPLICATION NUMBER: US/09/245,281
:
CURRENT FILING DATE: 1999-02-05

```

EARLIER APPLICATION NUMBER: US 09/207,359
EARLIER FILING DATE: 1998-12-08
EARLIER APPLICATION NUMBER: US 09/099,041
EARLIER FILING DATE: 1998-06-17
EARLIER APPLICATION NUMBER: US 09/019,942
EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 3080
TYPE: DNA
ORGANISM: Homo sapiens
US-09-245-281-25

Alignment Scores:

Pred. No.:	0.198	Length:	3080
Score:	81.00	Matches:	20
Percent Similarity:	58.70%	Conservative:	7
Best Local Similarity:	43.48%	Mismatches:	19
Query Match:	1.48%	Indels:	0
DB:	4	Gaps:	0

US-09-697-089-2 (1-1024) x US-09-245-281-25 (1-3080)

QY 156 GlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGlnGlyGlnSerGlyLysGlyLys 175
||||:|||||
Db 448 GGCAATCCCTCAATGAGCAGGCGTGCAGACCAATCTCATCTGCGGTGATGGGTGGGCAAG 507
QY 176 SerThrLeuLeuGlnArgIleAlaMetLeuThrProGlySerGlyLysCysLysAlaLeuThr 195
||| |||||||||||:|||||:|||||:|||||:|||||
Db 508 TCATGCTGCTACAGCGGCTGCAGAGCCTCTGGGCCACGGCCGGCTAGACGCAGGGGTC 567
QY 196 LysPheLysPheValPhe 201
||||| ||| |||
Db 568 AATTCCTCTCCACTT 585

Search completed: January 31, 2003, 10:46:23
Job time : 106 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 31, 2003, 08:47:16 ; Search time 111 Seconds
(without alignments)

4144.569 Million cell updates/sec

Title: US-09-697-089-2

Sequence: 1 MNFKDNRALIQRMGMVTI.....WQFDDDLSTVITGAFKLYTA 1024

Scoring table:

PAM120	4.0	Xgapex	12.0
Xgapop	4.0	Ygapex	12.0
Fgapop	6.0	Fgapex	7.0
Delop	6.0	Delext	7.0

Searched: 396772 segs, 224632407 residues

Total number of hits satisfying chosen parameters: 793544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+g2n.model -DEV=xlh
-O=/cgn2_1/USPTO/US09697089/runat_29012003_092506_19222/app-query.fasta.1.1223
-DB=Published_Applications_NA -QFM=fastcap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -SPART=1 -END=1 -MATRIX=pam120
-TRAN=humand40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09697089.ecgn1.1.60_rumat.29012003_092506_19222
-NCP=6 -ICPU=3 -NO_ALPXY -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEROUT=120 -WARN_TIMEROUT=30 -THREADS=1 -XGAPOP=4 -XGAPEXT=12 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=4 -YGAPEXT=12 -DELOP=6 -DELEXT=7

Database : Published Applications_NA:*

1:	/cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2:	/cgn2_6/ptodata/1/pubpna/PCt_NEW_PUB.seq:*
3:	/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4:	/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5:	/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6:	/cgn2_6/ptodata/1/pubpna/PCtUS_PUBCOMB.seq:*
7:	/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8:	/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9:	/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
10:	/cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11:	/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12:	/cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13:	/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14:	/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	5459	100.0	3072	10	US-09-841-739-3
2	5459	100.0	3133	10	US-09-841-739-1
3	5438	99.6	3396	9	US-09-864-921-96
4	5188	95.0	3612	10	US-09-841-739-6

5	5188	95.0	3615	10	US-09-841-739-4	Sequence 4, Appli
6	5188	95.0	3615	10	US-09-841-739-12	Sequence 12, Appl
7	1598	29.3	891	9	US-09-864-921-179	Sequence 179, App
8	1424	26.1	1395	9	US-09-864-921-98	Sequence 98, Appl
9	1084	19.9	618	9	US-09-864-921-181	Sequence 181, App
10	1005	18.4	608	10	US-09-864-921-339	Sequence 339, App
11	853	15.6	768	9	US-09-864-921-102	Sequence 102, App
12	725	13.3	522	10	US-09-864-921-754	Sequence 754, App
13	493	9.0	578	9	US-09-864-921-100	Sequence 100, App
14	485	8.9	261	9	US-09-864-921-177	Sequence 177, App
15	435	8.0	421	10	US-09-864-761-4236	Sequence 4236, App
16	391	7.2	220	10	US-09-864-761-20988	Sequence 20988, A
17	369	6.8	483	10	US-09-728-445-337	Sequence 337, App
18	287	5.3	165	9	US-09-864-921-183	Sequence 183, App
19	279	5.1	5504	8	US-08-913-322-1	Sequence 1, Appli
20	279	5.1	6124	8	US-08-913-322-21	Sequence 21, Appl
21	279	5.1	6124	10	US-09-967-768A-184	Sequence 184, App
22	279	5.1	6133	8	US-08-913-322-2	Sequence 2, Appli
23	279	5.1	6228	8	US-08-913-322-23	Sequence 23, Appl
24	117	2.1	1233	10	US-09-917-265-14	Sequence 14, Appl
25	117	2.1	1233	10	US-09-917-265-16	Sequence 16, Appl
26	114	2.1	526	10	US-09-917-265-17	Sequence 17, Appl
27	114	2.1	526	10	US-09-917-265-19	Sequence 19, Appl
28	114	2.1	1230	10	US-09-917-265-23	Sequence 23, Appl
29	114	2.1	1230	10	US-09-917-265-25	Sequence 25, Appl
30	89	1.6	321	9	US-09-864-921-89	Sequence 89, Appl
31	81	1.5	1470	9	US-10-118-984-27	Sequence 27, Appl
32	81	1.5	1470	10	US-09-728-721-27	Sequence 27, Appl
33	81	1.5	1470	12	US-10-105-931-27	Sequence 27, Appl
34	81	1.5	2859	9	US-10-118-984-9	Sequence 9, Appli
35	81	1.5	2859	10	US-09-728-721-9	Sequence 9, Appli
36	81	1.5	2859	12	US-10-105-931-9	Sequence 9, Appli
37	81	1.5	3080	9	US-10-118-984-25	Sequence 25, Appl
38	81	1.5	3080	9	US-09-728-721-25	Sequence 25, Appl
39	81	1.5	3080	12	US-10-105-931-25	Sequence 25, Appl
40	81	1.5	3382	9	US-10-118-984-7	Sequence 7, Appli
41	81	1.5	3382	10	US-09-728-721-7	Sequence 7, Appli
42	81	1.5	3382	12	US-10-105-931-7	Sequence 7, Appli
43	81	1.5	32042	9	US-10-118-984-44	Sequence 44, Appl
44	81	1.5	32042	10	US-09-728-721-63	Sequence 63, Appl
45	80	1.5	888	9	US-09-864-921-173	Sequence 173, App

ALIGNMENTS

RESULT 1
US-09-841-739-3
; Sequence 3, Application US/09841739
; Patent No. US20020034784A1
GENERAL INFORMATION:
APPLICANT: Berlin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH
FILE REFERENCE: 07334-329001
CURRENT APPLICATION NUMBER: US/09/841,739
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 09/697,089
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 3072
TYPE: DNA
ORGANISM: Homo sapiens
US-09-841-739-3

Alignment Scores:

Pred. No.:	0	Length:	3072
Score:	5459.00	Matches:	1024
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0

DB: 10 Gaps: 0
US-09-697-089-2 (-1-1024) x US-09-841-739-3 (-1-3072)
Oy 1 MetanphelellelyaspasnserrgAlaleuIleGlnargmetGlymethrValIle 20
Db 1 ATGAATTTTCATTAAGACAAATAGCCGAGCCCTTATTCAAAGAAATGCGAATGACTGTATA 60
Oy 21 LysGlnIleThrAspAspleuPheValTrpAsnValIleAsnArgGluPalasniIle 40
Db 61 AAGCAAAATCACAGATGACCTATTGTATGAAATGTTCTGAATGCGGAGAAATAAACATC 120
Oy 41 IleCyCyGluLysValGluGlnAspAlaAargGlyIleIleHisMetIleLeuLys 60
Db 121 ATTTCTGCGAGAGAGTGGAGCAGATGCTCTAGAGGATCATTCATGATTTTGAA 180
Oy 61 LysGlySerGluSerCyAsnLeuPheLeuLysSerIleuLysGluTrpAsnTrpProLeu 80
Db 181 AAGGATTGAGATCTCTGAAACCTCTTTAAATCCCTTAAAGAGTGGAACTATCCTCTA 240
Oy 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGluLysAspAsp 100
Db 241 TTTCAGGACTTCATAGCAAAAGTCTTTTTCATCAGACATCAGAAAGAGACTTGGACAT 300
Oy 101 LeuAlaGlnAspLeuLysAspLeuTrpHisThrProSerPheLeuAsnPheTrpProLeu 120
Db 301 TTGGCTCAGAGATTAAAGACTTGTACCATACCCCATCTTTCTGAACCTTTATCCCTT 360
Oy 121 GlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTrp 140
Db 361 GGTGAAGATATTGACATTAATTTTAACTGAAAGACACCTTCACAGAAACCTCTCTGTGG 420
Oy 141 ArgLysAspGlnHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla 160
Db 421 AGGAAGACAAACACACATCACCGCGCTGGAGCAGCTGACCTTAATGGCTCTCTGCAAGCT 480
Oy 161 LeuGlnSerProCyAlleIleGluGlyGlnSerGlyLysGlyLysSerThrLeuLeuGln 180
Db 481 CTTTCAGAGCCCTGCATCATTTGAAGGGGATCTGGCAAAAGGCAAGCCATCTGCTGCAG 540
Oy 181 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 200
Db 541 CGCATTTGCCATGCTGTGGGGCTCGCGAAAGTCAAGGCTCTGACCAAGTTCAAAATTCGTC 600
Oy 201 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCyAspGlnLeu 220
Db 601 TTCTTCCTCCGCTCAGCAGAGGCCAGGGTGGACTTTTGAACCCCTCTGTATCAACCTC 660
Oy 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 240
Db 661 CTGGATATACCTGGCAATCAGAAAGCAGACATTCATGGCCATGCTGCTGAAGCTGGCG 720
Oy 241 GlnArgValLeuPheLeuLeuAspGlyTrpAsnGluPheLysProGlnAsnCyProGlu 260
Db 721 CAGAGGGTCTTCTTCCTTGTATGCTTACAAATGAATTAACCCCGAGAACGCCAGAA 780
Oy 261 IleGlnAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr 280
Db 781 ATCGAAGCCCTGATTAAGAAACCAACCGCTTCAAGAACATGTGCTATGCTCAACCTACC 840
Oy 281 ThrGluCyLysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValLysPheMet 300
Db 841 ACTGAGTCCCTGAGCACAATACGCGAGTTTGGTCCCTGACACGCTGAGAGTGGGGATATG 900
Oy 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAsnIleGluGly 320
Db 901 ACAGAGACAGGCGCCAGGCTCTCATCCGAGAGAGTGTGATTAAGAGAGTCTCTGAAGCC 960
Oy 321 LeuLeuLeuGlnIleGlnLysSerArgCyLysLeuArgAsnLeuMetLysThrProLeuPhe 340
Db 961 TTGTGTGCTCAAAATTCAGAAATCCAGGTGCTGAGAGAAATCTATGAAGACCCCTCTCTTT 1020
Oy 341 ValValIleThrCyAlaIleGlnMetGlyGlnSerGluPheHisSerHisThrGlnThr 360

Db 1021 GTGGTCATCAGCTTGTGCATCCAGATGGGTGMAAGTGAGTTCCACTCCACACAAACA 1080
Oy 361 ThrLeuPheHisThrPheTrpAspleuLeuIleGlnLysAsnLysHisLysGly 380
Db 1081 ACGTGTTCATACCTTCTATGATCTGTTGATACAGAAAACAAACAAACATATAAGGT 1140
Oy 381 ValAlaAlaSerAspPheIleArgSerLeuAspHisCyGlyAspLeuAlaLeuGluGly 400
Db 1141 GTGGCTGCAAGAGACTTTCATTCGGAGCCTGGAGCCACTGTGGAGACTTGTGGAGGGT 1200
Oy 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420
Db 1201 GTGTTCCCAACAAATTTGATTTCAACTGCGAGATGTGTCCAGCGTGAATGAGGATGTC 1260
Oy 421 LeuLeuThrThrGlyLeuLeuLysCysLysTrpThrAlaGlnArgArgLeuSerLeuThr 440
Db 1261 CTGCTGACAACTGGGCTCTGTAAATATACAGCTCAAAAGGTTTAAAGCCAAAGTATAA 1320
Oy 441 PhePheHisLysSerPheGlnGluTrpThrAlaGlyArgArgLeuSerSerLeuThr 460
Db 1321 TTCTTTCACAGTCAATTCAGAGATGACACAGCAGACGAAAGCTACGAGTTTATGACG 1380
Oy 461 SerHisGluProGluGluValThrLysGlyAsnGlyTrpLeuGlnLysMetValSerIle 480
Db 1381 TCTCATGAGCCAGAGAGAGGTGACCAAGGGGAATGGTTACTTGCAGAAATGGTTCCATT 1440
Oy 481 SerAspIleThrSerThrTrpTrpSerSerLeuLeuArgTrpThrCyGlyLysSerValGlu 500
Db 1441 TCGGACATTTACATCCATTAAGACGCTGTCCGGTACCTGTGGGTCACTGTGGAA 1500
Oy 501 AlaThrArgAlaValaMetLysHisLeuAlaValaTrpGlnHisGlyCysLeuLeuGly 520
Db 1501 GCCACAGAGCGCTTATATGAGACACCTCCGACAGAGTATCAACACAGCGCTTCCGA 1560
Oy 521 LeuSerIleAlaLysArgProLeuTrpArgGlnSerLeuGlnSerValLysAsnThr 540
Db 1561 CTTTCCATCGCCCAAGAGCCTCTCTGAGACAGGAATCTTGGCAAAAGTGTGAAAAACAC 1620
Oy 541 ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560
Db 1621 ACTGAGCAAGAAATTCGAAACCATTAACATCAATTCCTTGTGAGAGTGGCAATCAT 1680
Oy 561 LeuTrpGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln 580
Db 1681 TTATATCAAGAGATACATCCAAATCAGCCCTGAGCCCAAGATTTGAAGCTTCTTCAA 1740
Oy 581 GlyLysSerLeuTrpIleAsnSerGlyAsnIleProAspTrpLeuPheAspPhePheGlu 600
Db 1741 GGTAAAGCTTATATATCAACTCAGGAGAAACATCCCGATTACTGTATTGACTTCTTGA 1800
Oy 601 HisLeuProAsnCyAlaSerAlaLeuAspPheIleLysLeuAspPheTrpGlyLysAla 620
Db 1801 CATTTGCCCAATGTGCAGAGTCTGTGACTTCAATTAACGTGACTTTTATAGGGGAGCT 1860
Oy 621 MetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaPro 640
Db 1861 AMGGCTTCATGGGAAAGGCTGCAGAACACAGGTGGAGATCCACATGGAAGAGGCCCA 1920
Oy 641 GluThrTrpIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArg 660
Db 1921 GAACCTCATATCCAGCAGAGGCTGTATCTTGTCTTCAATGGAAACAGAAATTCAGG 1980
Oy 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTrpLeu 680
Db 1981 ACTCTGGAGGTACACTCCGGGATTTTCAGCAAGTTGAATTAACCAAGATATCAATATCTG 2040
Oy 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCyAlaGlyAla 700
Db 2041 GGGAAAAATTTAGCTGTGCCCAAGGCTCAGCGTCAAAATTAAGAGATGTCTGTGGTG 2100
Oy 701 AlaGlySerLeuSerLeuValLeuSerThrCyLysAsnIleTrpSerLeuMetValGlu 720

Db 2101 GCTGGAGGCTCAGTTGGTCCCTCAGACACCTGTAAGAACATTTATCTCATGGTGA 2160
Qy 721 AIsaSerProLeuThrIleGluaspGluArgHisIleThSerValThrAsnLeuysPthr 740
Db 2161 GCCAGTCCCTCACCATTGAGAGATGAGAGGACATCATCTGTGTAACAAACCTGAAAAAC 2220
Qy 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 760
Db 2221 TTGAGTATTTCAGACCTACAGAAATCAAGCGCGCGGGGTGCTGCTACGTACAGCTTGGGT 2280
Qy 761 AsnLeuLysAsnLeuThrLysLeuIleMetLaspAsnIleLysMetAsnGluLusPala 780
Db 2281 AACTTGAAGAACCCTTACAAAGCTCATATGATTAACATAAAGATGAAGAAGATGCT 2340
Qy 781 IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800
Db 2341 ATAAAGTAGCTGAAGGCTGAAAAAAGCTGAAGAAGATGTGTTATTTTCATTGACCCAC 2400
Qy 801 LeuSerAspIleGlyGlyGlyMetAspTyrIleValLysSerLeuSerSerGluProCys 820
Db 2401 TTGTCTGACATTGGAGAGGAGATGATTAACATGCAAGTCTCTGTCAAGTGAACCTCT 2460
Qy 821 AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840
Db 2461 GACCTTGAAGAATTCATTAATGCTCTGCTGCTGCTGCTGCAAAATGACAGTGAATCCCTA 2520
Qy 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860
Db 2521 GCTCGAAATCTTCACAAATTTGGTCAAACTGACACTTCTGATTATCAAGAAATTAACCTG 2580
Qy 861 GluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGln 880
Db 2581 GAAAAAGATGGAATGAAAGCTCTTCATGACATGATCGAAGATGAACGTGCTAAGACAG 2640
Qy 881 LeuThrAlaLeuMetLeuProTropGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900
Db 2641 CTCACCGCAGTATGCTCCCTGGGGCTGTGACGTGAAGGACGCTGACGCTGCTGTG 2700
Qy 901 LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThr 920
Db 2701 AAACCTTTGGAGAGAGTCCCAACTCGTCAAGCTTTGGGTTAAAACTGGAGACTCACA 2760
Qy 921 AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940
Db 2761 GATACAGAGATTAGAAATTTAGGTGCATTTTGGAAAGAACCCCTGAAAAAATCTCCAG 2820
Qy 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPheAlaPheMetGlyVal 960
Db 2821 CAGTTGAATTTGGCGGGAATCGTGTGACAGTGAATGATGCTTGCCTTCATGGGTGA 2880
Qy 961 PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980
Db 2881 TTTGGAATCTTAAACAAATGTGTTTTTTTGTAGCTTAAAGAAATTTCTTACCTGAT 2940
Qy 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla 1000
Db 2941 CCAGCATTAAGCAGAAAACTTAAGCAAGTATTATCCAAAGTTACTTTCTGCAAGAGCT 3000
Qy 1001 ArgLeuValGlyTyrPheGlnPheAspAspAspLeuSerValIleThrGlyAlaPheLys 1020
Db 3001 AGGCTTTGTGGGTGGCAATTTGATGATGATGATCTCAGTGTATTAACAGTCTTTTAAA 3060
Qy 1021 LeuValThrAla 1024
Db 3061 CTAGTACTGCT 3072

RESULT 2
US-09-841-739-1

; Sequence 1, Application US/09841739
; Patent No. US20020034784A1
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE

; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/09/841,739
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1
; LENGTH: 3133
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)..(3107)
US-09-841-739-1

Alignment Scores:

Pred. No.:	0	Length:	3133
Score:	5459.00	Matches:	1024
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-697-089-2 (1-1024) x US-09-841-739-1 (1-3133)

Qy 1 MetaAspPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
Db 36 ATGATTTTCATTAAGACACATAGCCGAGCCCTTATTCAAAGATGGAATGACTGTATA 95
Qy 21 LysGlnIleThrAspAspLeuPheValTyrAsnValIleAsnArgGluGluValAsnIle 40
Db 96 AAGCAATACAGATGACCTTATTTGATGAATGTCTGAATCGGAGAAATTAACATC 155
Qy 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
Db 156 ATTGCTCGAAGAAAGGTGAGCAGAGTGTCTAGAGGATCATTCACATGATTTTGA 215
Qy 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTyrAsnTyrProLeu 80
Db 216 AAGGTTTCAAGTCTCTGTAACCTCTTCTTAATCCCTTAAGAGTGAACATATCTCTGA 275
Qy 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluLysAsnAspAsp 100
Db 276 TTTCAAGACTTGAATGACAAAGCTTTTCTTCATCAAGACATCAAGAGACTTGGACGAT 335
Qy 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu 120
Db 336 TTGGCTCAGGATTTAAAGACTTGTACCATACCATCTTTTCTGAACTTTTATCCCTT 395
Qy 121 GlyLysAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTyr 140
Db 396 GGTGAAGATTAATGACATTAATTTTAACCTGAAACACACTTCACAGAACTTCTCTGG 455
Qy 141 ArgLysAspArgHisHisHisArgValGlnGlnLeuThrIleAsnGlyLeuLeuGlnAla 160
Db 456 AAGGAAGACCAACACCATCACCGCTGAGCGCTGACCTGAAAGGCTCTCTGAGGCT 515
Qy 161 LeuGlnSerProCysIleIleGluGlyLysSerGlyLysGlyLysSerThrLeuGln 180
Db 516 CTTCAAGACCCCTGCATCATTTGAAGGGAATGTGCAAAAGCAATCCACTGTGCTGAG 575
Qy 181 ArgIleAlaMetLeuTyrPheGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 200
Db 576 CGCATTCGCATGCTCTGGGGCTCCGGAAGTCAAGGCTGTGACCAAGTCAAAATTCGTC 635
Qy 201 PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGlnThrLeuCysAspGlnLeu 220
Db 636 TTCTTCCTCCGCTCAGCAGGCGCCAGGGTGGACTTTTGAAGCCCTGTGATCAACTGC 695
Qy 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 240

|||||
Db 696 CTGATATACCTGGCACAAATCAGAGACAGACATTCATGGCCATGCTGTAACCTCGG 755
Qy 241 GlnArgValIleuPheIleuLeuAspGlyTyrAsnGluPheLysProGlnAsnGlyProGlu 260
Db 756 CAGAGGGTCTCTTCTCTTCTGATGGCTACAAATTAATCAAGCCCGAAGACTGCCAGAA 815
Qy 261 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr 280
Db 816 ATGCAACCCCGATTAAGAAAGAAACACCGCTTCAAGAAACATGATCGTACACATACC 875
Qy 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300
Db 876 ACTAGAGCCTGAGGACATACGGCAGATTGGTCCCTGACTGCTGAGGTGGGAGATAG 935
Qy 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValIleuIleLysGluLeuAlaGluGly 320
Db 936 ACAGAAACAGACGCCAGGCTCTATCCGAGAAAGTGGATCAAGAGACTTGTGAAGGC 995
Qy 321 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340
Db 996 TTGTGGTCCAAATTCAGAAATCCAGGAGCTTGAGGAATCTCATGAAGACCCCTCTCTT 1055
Qy 341 ValValIleThrCysAlaIleGlnMetGlyLysSerGluPheHisSerHisThrGlnThr 360
Db 1056 GTGCTCATCACTTGTCATTCAGATGAGTGAAGTGAAGTCACTCCACACACAAACA 1115
Qy 361 ThrIleuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGly 380
Db 1116 ACCGTCTTCCATACCTTCTATGATCTGTGATACAGAAACAAACACAAACATTAAGT 1175
Qy 381 ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly 400
Db 1176 GTGCTCAAGTCACTTCATTCATTCGAGAGCTGAGACCACTGTGAGACCTGAGAGAGT 1235
Qy 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420
Db 1236 GTGTCTCCCAACAATTGATTTGCAACTGCAAGATGTCACCGTAAAGAGAGATGTC 1295
Qy 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440
Db 1296 CTGCTGACAACTGGGCTCCCTGTGAATATATACACTCAAAAGTTCAGCCAAAGTATAA 1355
Qy 441 PhePheHisLysSerPheGlnGluTyrThrAlaGluArgGluSerSerLeuLeuThr 460
Db 1356 TTCTTTTACAAAGTATTCACAGAGTACACACAGACAGAACATCAGAGTTTATTCAGC 1415
Qy 461 SerHisGluProGlnGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480
Db 1416 TCTCATGAGCCAGAGAGAGTACCAAGGGGAATGGTTACTTGCAAGAAATGGTTCCATT 1475
Qy 481 SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500
Db 1476 TCGACATTAATCACTTAATAGCAGCGCTGCTCCGGTACACTGAGGGTCACTGTGTGAA 1535
Qy 501 AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly 520
Db 1536 GCCACACAGGGCTGTATTAGAACACCTCCACAGAGTATCAACAACAGCGCTGCTTCGGA 1595
Qy 521 LeuSerIleAlaLysArgProLeuThrParGlnGlnLysSerLeuGlnSerValLysAsnThr 540
Db 1596 CTTTTCATCGCCAGAGAGCGCTCTGAGACAGAGAAATCTTGCAAAAGTAAAAAACCC 1655
Qy 541 ThrGlnGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560
Db 1656 ACTAGACAGAAATTCGAAAGCCATTAACATCAATTCCTTTGTAGAGTGTGGCATTCAT 1715
Qy 561 LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln 580
Db 1716 TTATATCAAGAGATACATTCAAATCAAGCCCTGAGCCAAAGATTTGAAGCTTTCTTCAA 1775
Qy 581 GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPheLeu 600
|||||
Db 1776 GGTAAAGCTTATATATCAACTCAGGAGACATCCCGATTACTTATTTGACTCTTTGAA 1835
Qy 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyAla 620
Db 1836 CATTTGCCCAATTTGCAAGTGGCTGTGACTTCAATTAACTGACCTTTATGGGGAGCT 1895
Qy 621 MetaIleSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaPro 640
Db 1896 ATGCTTCATGGGAAAGGCTGAGAGACACAGAGTGAATCCACATGAGAAAGAGGCCCA 1955
Qy 641 GluThrTyrIleProSerArgAlaValSerLeuPheAsnTrpLysGlnGluPheArg 660
Db 1956 GAAACCTACATTCCTCCACAGGGCTGTATCTTTGTCTTCAACTGGAACAGGAATTCAGG 2015
Qy 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu 680
Db 2016 ACTCTGAGAGTACACCTCCGGGATTTACAGCAAGTTGAATTAAGCAAGATACACATATCTG 2075
Qy 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700
Db 2076 GCGAAATATTCACCTCTGCGCACACAGCTCAGCGTCAAAATTAAGAGATGTGCTGTGTG 2135
Qy 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu 720
Db 2136 GCTGGAAGCCCTCAGATTTGGTCTCAGACCTGTAAAGACATTTATCTCATGGTGGA 2195
Qy 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740
Db 2196 GCCAGTCCCTCCACCATTAAGAGATGAGAGGACATCACTGTATACAAACCTGAAACCC 2255
Qy 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyLeuThrAspSerLeuGly 760
Db 2256 TTGAGTATTCATGACCTACAGAAATCAACGGCTCGGGGTGTCTGACTGCACGTTGGGT 2315
Qy 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluAspAla 780
Db 2316 AACTTGAAAGACCTTACAAACCTCATTAATGATACATTAAGATCAATGAAGAAAGATCT 2375
Qy 781 IleLysLeuAlaGluGlyLeuLysAsnLeuLysAlaLysMetCysLeuPheHisLeuThrHis 800
Db 2376 ATAAACATAGCTGAAGGCTGAAAAACCTGAAAGAAAGTGTATTATTCATTGATGCCACC 2435
Qy 801 LeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCys 820
Db 2436 TTGTCTGACATTTGAGAGGGAATGATTACATTAATCAAGTCTGTCAAGGAAGCCCTGT 2495
Qy 821 AspLeuGlnGluIleGlnLeuValSerCysLysSerLeuSerAlaAsnAlaValLysIleLeu 840
Db 2496 GACCTTGAAAGAAATTCATTTAGTCTCCTGCTGCTGTGCTGCAAAATGCAAGTCAAAATCTTA 2555
Qy 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860
Db 2556 GCTCAGAAATCTTCACAATTTGGTCAAACTGAGACTGTCTTGATTTATGAGAAATTAACCTG 2615
Qy 861 GluLysAspGlyAsnGluAlaLeuHisGlnLeuIleAspArgMetAsnValLeuGlnGln 880
Db 2616 GAAAAAGATGGAATGAAGCTTTCATGAACTGATCAACAGAGTGAACGTCGTAGAACAG 2675
Qy 881 LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900
Db 2676 CTCACCCGACTGATGCTGCCCTGGGGCTGTGACGTGCAAGGACACCTGACAGACGCTGTG 2735
Qy 901 LysHisLeuGlnGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThr 920
Db 2736 AAACCTTTGGAGGAGGCTCCCAACCTGCTCAAGCTTGAGTTGGAAGAACTGGAGACTACA 2795
Qy 921 AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940
Db 2796 GATACAGAGATTAAGAAATTTTGGTGCAATTTTGGAAAGAACCTCGAAAAACCTTCCAG 2855
Qy 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyVal 960
Db 2856 CAGTTGAATTTGGCGGGAATGCTGTGACAGTGTGATGGCTTGCCCTCATGGGTGTA 2915
|||||

QY	421	Leu	Thr	Thr	Thr	Gly	Leu	Leu	Cys	Lys	Tyr	Thr	Ala	Gln	Arg	Phe	Leu	Pro	Lys	Tyr	Lys	440	
Db	1337	CTGCTGCAAACTGGGCTCTCTGTAATATATACAGCTCAAAAGTTTAAAGCCAAAGATATAA																				1596	
QY	441	Phe	Phe	His	Lys	Ser	Phe	Gln	Gln	Iu	Tyr	Thr	Ala	Gly	Arg	Arg	Leu	Ser	Ser	Leu	Leu	Thr	460
Db	1597	TTCTTTTCCAAAGTCATCTCCAGAGATACAGAGCAGAGCAAGACTCAGCAGTTTATTAGCG																				1656	
QY	461	Ser	His	Glu	Pro	Gln	Glu	Val	Thr	Tyr	Gly	Asn	Gly	Tyr	Leu	Gln	Lys	Met	Val	Ser	Le	480	
Db	1657	TCTCATGTGCGCAGAGGGAGGGAGCCAAAGGGAAGTGTACTTCCAAAAATGGTTTCCATT																				1716	
QY	481	Ser	Asp	Leu	Thr	Ser	Thr	Tyr	Ser	Ser	Leu	Leu	Arg	Tyr	Thr	Cys	Gly	Ser	Ser	Val	Leu	500	
Db	1717	TCCGACATATACCTACTTATACAGGCTGCTCCGGTACACCTGGGGGATCATGTGGAA																				1776	
QY	501	Ala	Thr	Arg	Ala	Val	Met	Lys	His	Leu	Ala	Val	Tyr	Gln	His	Gly	Cys	Leu	Leu	Gly	520		
Db	1777	GCCACACAGGCGGTGTATGAAGCACCTCCGACGCTGTATCAACACGCGCTTCCGGA																				1836	
QY	521	Leu	Ser	Leu	Ala	Val	Arg	Pro	Leu	Tyr	Arg	Gln	Ser	Leu	Gln	Ser	Val	Lys	Asn	Thr	540		
Db	1837	CTTTCCATCCGCAAGAGCGCTCTCTGGAGACAGAGATCTTTCCAAAGTGTGAAAACACC																				1896	
QY	541	Thr	Gln	Gln	Iu	Leu	Lys	Ala	Leu	Asn	Leu	Ser	Phe	Val	Glu	Cys	Gly	Leu	His	560			
Db	1897	ACTGACGCAAAATTCGAAAGCCATAAACATCAATCTTTGTATGAGTGTGGCATCAT																				1956	
QY	561	Leu	Tyr	Gln	Gln	Ser	Thr	Ser	Lys	Ser	Ala	Leu	Ser	Gln	Iu	Phe	Gln	Val	Phe	Phe	Leu	580	
Db	1957	TTATATTCAGAGAGTACATCCAAATCAGCCCTGAGCCAAAGATTTGAAGCTTCTTTGAA																				2016	
QY	581	Gly	Lys	Ser	Leu	Tyr	Leu	Asn	Ser	Gly	Asn	Leu	Pro	Asp	Tyr	Leu	Phe	Asp	Phe	Phe	Glu	600	
Db	2017	GGTAAAGCTTATATATACACTCAGGGAACATCCCGGATCTTATTTGACTTCTTGAA																				2076	
QY	601	His	Leu	Pro	Asn	Cys	Ala	Ser	Ala	Leu	Asp	Phe	Leu	Lys	Asp	Phe	Tyr	Gly	Gly	Val	620		
Db	2077	CATTGGCCAAATGTGGAAAGTCCCTGGAGCTTCATTAACTGAGCTTTATATGGGGAGCT																				2136	
QY	621	Met	Ala	Ser	Tyr	Glu	Lys	Ala	Gln	Asp	Thr	Gly	Gly	Leu	His	Met	Glu	Glu	Val	Leu	Pro	640	
Db	2137	ATGGCTCATGGAAGAGCGTCGCAAGAACACAGCGTGAATCCACATGGGAAGAGGCCCA																				2196	
QY	641	Glu	Thr	Tyr	Leu	Pro	Ser	Arg	Ala	Val	Ser	Leu	Phe	Asn	Tyr	Ply	Gln	Iu	Phe	Arg	660		
Db	2197	GAACCTACATATCCACACAGGCGGTGATCTTCTTCACTGAGACAGGAATTCAGG																				2256	
QY	661	Thr	Leu	Gln	Val	Thr	Leu	Arg	Asp	Phe	Ser	Lys	Leu	Asn	Lys	Gln	Asp	Leu	Thr	Tyr	Leu	680	
Db	2257	ACTCTGAGAGTCAACACTCCGGGATTTTCAGCAAGTTTAATACCAAGATATCAGATATCTG																				2316	
QY	681	Gly	Lys	Leu	Phe	Ser	Ser	Ala	Thr	Ser	Leu	Arg	Leu	Gln	Leu	Lys	Arg	Cys	Ala	Gly	Val	700	
Db	2317	GGGAAATATTCACACTCTGCCACAAAGCTCAGGCTCAATTAAGATGAAGATGCTCGTGTG																				2376	
QY	701	Ala	Gly	Ser	Leu	Ser	Leu	Val	Leu	Ser	Thr	Cys	Lys	Asn	Leu	Tyr	Ser	Leu	Met	Val	Leu	720	
Db	2377	GCTGGAAAGCTCACTTTTGTCCTCAGACCTGTAAACAACTTATATCTCTCACTGGTGAA																				2436	
QY	721	Ala	Ser	Pro	Leu	Thr	Leu	Gln	Asp	Gly	Arg	His	Leu	Thr	Ser	Val	Thr	Asn	Leu	Lys	Thr	740	
Db	2437	GCCAGTCCCTCCACACATAGAAGATGAGAGGCACATCACTGTGAACAACTGAAAACC																				2496	
QY	741	Leu	Ser	Leu	His	Asp	Leu	Gln	Asn	Gln	Arg	Leu	Pro	Gly	Gly	Leu	Thr	Asp	Ser	Leu	Gly	760	
Db	2497	TTTGAGTATTCATGACTACACAGAAATCAACGCGTCCCGGCTGCTCACTACAGACTTGCGT																				2556	
QY	761	Asn	Leu	Lys	Asn	Leu	Thr	Lys	Leu	Leu	Met	Asp	Asn	Leu	Lys	Met	Asn	Gln	Glu	Asp	Val	780	
Db	2557	AACCTTGAAGACCTTACAAAGCTCATATATGATGAACATTAAGATGAAGAAGATGCT																				2616	

QY	761	ILE	YS	LEU	VAL	AG	UGL	LEU	LYS	ASN	LEU	LYS	LYS	MET	CYS	LEU	PH	EN	ILE	THR	HIS	800	
Db	2617	ATAAA	ACTAG	CTGA	AGG	CGCTG	AAAAA	CCCTGA	AGA	GATG	TTT	TAT	TTT	CAT	TTT	GAC	CC	CAC				26176	
QY	801	LEU	SER	ASP	ILE	GL	UGL	LYM	ET	ASP	TYR	ILE	VAL	LYS	SER	LEU	SER	SER	GLU	PRO	CYS	820	
Db	2677	TTGTCT	GCAC	ATTGG	AGAG	GAATGG	ATTAC	ATTAG	TCA	AGTCTCT	GTCTCA	AGTGA	ACCTCTGT									2736	
QY	821	ASP	LEU	GLUGL	ILE	GL	LEU	VAL	SER	CYS	CYS	LEU	SER	ALA	ASN	ALA	VAL	LYS	ILE	LEU		840	
Db	2737	GACCTT	GAAG	AAATTC	ATTAG	CTCTCTCTG	CTGCTGTG	CTGCAAA	TGTGCA	AAATGAC	AGTGA	AAATCCTA										2796	
QY	841	ALA	GLN	ASN	LEU	ASN	ILE	ASN	LEU	VAL	LYS	SER	SER	ILE	LEU	ASN	SPLE	SER	GLU	ASN	TYR	LEU	860
Db	2797	GCTCGA	ATCTTC	ACAA	TTTGG	TGCAAA	CTGAG	CATCTTG	TAT	TAT	CAGAAA	ATTTAC	CTG										2856
QY	861	GLU	LYS	ASP	GL	LYS	ASN	GLA	LEU	ASN	ILE	GLU	LEU	ILE	ASP	ARG	ME	TASN	VAL	LEU	GLUGL	880	
Db	2857	GAAAA	AGATG	GAATGA	AGCTCT	TCATG	AAC	TGATGC	ACAG	CAGAG	ATGA	AGAC	GTGCTGA	ACAG									2916
QY	881	LEU	THR	ALA	LEU	MET	LEU	PRO	TRP	GL	LYS	ASP	VAL	GLN	GLY	SER	LEU	SER	SER	LEU		900	
Db	2917	CTCAC	CGCAG	CATG	CTCTCC	CTGGGG	CTGTG	ACGTGC	AGGCA	AGCAG	CCTGAG	CAGCCTGTG											2976
QY	901	LYS	HN	ILE	UGL	UGL	VAL	PRO	GL	LEU	VAL	LYS	LEU	GLY	LEU	LYS	ASN	TRP	ARG	LEU	THR	920	
Db	2977	AAAC	ATTTGG	AGAG	AGTCC	ACCA	ACTGCTCA	AGCTGG	GTGGA	ATAAA	AACTGG	AGACTCA											3036
QY	921	ASP	THR	GLU	ILE	ARG	ILE	LEU	GLY	ALA	PH	EPH	EPH	GLY	LYS	ASN	PRO	LEU	LYS	ASP	PH	GLN	940
Db	3037	GATAC	AGAG	ATTAG	CAATTT	TAGTGT	CTCAT	TTTGTG	GAAGA	ACCCTCTG	AAAAA	ATTTCAG											3096
QY	941	GLN	LEU	ASN	LEU	VAL	GLY	ASN	ARG	VAL	SER	SER	ASP	GLY	TRP	LEU	ALA	PH	ME	GLY	VAL	960	
Db	3097	CAGTT	GAA	TTTGG	CGCGG	AAATCG	TGTG	AGCG	ATGATG	CGCTTC	ATGAGGTGA												3156
QY	961	PH	EPH	ASN	LEU	LYS	GLN	LEU	VAL	PH	EPH	EPH	SPH	SER	THR	LYS	GLU	PH	EPH	LEU	PRO	ASP	980
Db	3157	TTTGG	AATCTTA	AGCA	ATTA	AGTGT	TTTGTACT	TTGTAG	TACTAA	AGAA	ATTTCTAC	CTGAT											3216
QY	981	PRO	ALA	LEU	VAL	ARG	LYS	LEU	SER	GLN	VAL	LEU	SER	LYS	LEU	THR	PH	EPH	GLN	GLA	1000		
Db	3217	CCAG	CATTTAG	TCAG	AAAAC	CTTAG	CCAA	CTGTAT	CCAA	AGTAA	CTTTCTG	CAGAA	AGCT										3276
QY	1001	ARG	LEU	VAL	GLY	TRP	GLN	PH	EPH	SPH	ASP	ASP	SPLE	SER	VAL	ILE	THR	GLY	ALA	PH	ELYS	1020	
Db	3277	AGG	CTTGT	GGGTGG	CAATTT	GATG	ATGATG	ATCAT	CATG	TATTA	TATAC	AGAG	CTTTTAAA										3336
QY	1021	LEU	VAL	THR	ALA	1024																	
Db	3337	CTAG	TAACTG	CT	3348																		

RESULT 4

US-09-841-739-6

; Sequence 6, Application US/09841739

; Patent No. US20020034784A1

; GENERAL INFORMATION:

; APPLICANT: Berlin, John

; FILE REFERENCE: 07334-329801

; CURRENT APPLICATION NUMBER: US/09/841.739

; PRIOR APPLICATION NUMBER: US 09/697,089

; PRIOR FILING DATE: 2000-10-26

; PRIOR APPLICATION NUMBER: US 60/161,822

; PRIOR FILING DATE: 1999-10-27

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO 6

; LENGTH: 3612

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-841-739-6

Alignment Scores:

Pred. No.:	0	Length:	3612
Score:	5188.00	Matches:	1014
Percent Similarity:	98.16%	Conservative:	1
Best Local Similarity:	98.07%	Mismatches:	1
Query Match:	95.04%	Indels:	18
	10	Gaps:	1

US-09-697-089-2 (1-1024) x US-09-841-739-6 (1-3612)

Oy 1 Metasphenielysaspasnserrarglaleuileginargmetglymerthvalile 20
Db 418 GTGAATTTCAATAAGCAATAGCCGAGCCCTTATTCAAGAATGGAACTGTATA 477
Oy 21 Lysglnilethraspaspheleuphevaltrpaspnvalileasarglvalasnlle 40
Db 478 AAGCAATCCACAGATGACCTATTGTATGGAATGTCGAATCGGAAGAACTAAACATC 537
Oy 41 Ilecyscysglulysvaliglulnaspalaalaargglylleilehismetileleuys 60
Db 538 ATTTCCTCGAGAGAGTGGAGCAGATGCTGCTAGAGGATCATTCACATGATTTTGANA 597
Oy 61 Lysglyserglusercysasnleupheleuysserleuysglutrpasntrprouen 80
Db 598 AAGGCTCAGAGTCTCTGTAACCTTTCTTAAATCCCTTAAAGAGTGAATCATCTCTGA 657
Oy 81 Pheglnaspheasnnglyglinser----- 88
Db 658 TTTTCAGAGCTTGAATGGAAGAAATTTTGAAGACAGACAGAAATGGGCTCTTTAAACATC 717
Oy 89 -----Leuphehisglntrserglulnaspheasnspheula 102
Db 718 ACCTTCTCTAATAGGCTTTTTCATCAGACATCAGAAAGGAGATTTGGCATTTGGCT 777
Oy 103 Glnaspheleuysaspheutyrhisrtrprouenprouenprouenprouenprouen 122
Db 778 CAGGATTTAAAGAGACTTGTACATACCATCTTTTGAACCTTTTAAATCCCTTGTGTA 837
Oy 123 Aspileaspheileleupheasnleuyssertrprouenprouenprouenprouen 142
Db 838 GATATTTGACATTTATTTTAACTTGAAGCAACCTTCAAGAACTCTCTGTGGAGGAG 897
Oy 143 Aspglnhisshisargvaliglulnleupheasnnglyleuenglnaleuengln 162
Db 898 GACCAACACATCACCGGCTGGAGAGCTGACCTGAAATGGCTCTCTGACGAGCTTTCAG 957
Oy 163 Serprocyileileleuglygluserglulysglulyssertrprouenprouenprouen 182
Db 958 AGCCCTGCATCATGAGGGAATCTGCAAGCAAGTCACATCTCTGTCGACGGAAT 1017
Oy 183 Alametleuptrpserglulyscysstysalaleutntrprouenprouenprouen 202
Db 1018 GCCATGCTCTGGGCTCGGAAAGTGAAGGCTGTGACCAAGTTCAAATTCCTCTTCTTC 1077
Oy 203 Leuargleuserarglalniglyleupheglntrprouenprouenprouenprouen 222
Db 1078 CTCGCTCAGACAGGCGCCAGGCTGACTTTTGAACCCCTCTGTGATCACTCTGAT 1137
Oy 223 Ileproglythrilearglulysglntrprouenprouenprouenprouenprouen 242
Db 1138 ATACTGCGACAAATCAGAGACAGACATTCATGCGCATGCTCTGACACTGCGGAGAG 1197
Oy 243 Valileupheleuileuaspgllytrrasnglulphelulysproginasnrcysproglulile 262
Db 1198 GTTCTTTCTCTTGTGAGGCTGACATGATTAAGCCCGAAGTTCGCCAGAAATTCGAA 1257
Oy 263 Alaleuileuysgluasnhisargprouenprouenprouenprouenprouenprouen 282
Db 1258 GCCCTGATTAAGGAAACACCGGCTTCAAGAAATGATGCTGACACACTACACTGAG 1317
Oy 283 Cysleuarghisilearglulphelulysalaleutntrprouenprouenprouenprouen 302
Db 1317 TTTTCTTTCTCTTGTGAGGCTGACATGATTAAGCCCGAAGTTCGCCAGAAATTCGAA 1257

Db 1318 TGCCAGAGCACATACGGCAGTTTGTGCTGCTGAGAGTGGGATATGACAGAA 1377
Oy 303 Aspseralaglnaleuilearglulvalileuileuysglulaleuaglnleu 322
Db 1378 GACAGGCGCCAGGCTCTCTCCGAGAAAGTGTGATCAAGAGACTTGTGAGGCTTGTG 1437
Oy 323 Leuglnileglnlyserargcysleuargasnleuylttrprouenprouenprouen 342
Db 1438 CTCCAATTCACAAATCCAGTGTGAGATTCATGACAAACCCCTCTCTTGTGCTG 1497
Oy 343 IlethrCysAlaileglnmetglulserglulphelulysserhisrtrprouenprouen 362
Db 1498 ATCACTTGTGCAATCCAGATGCGGTGAAGTGTGCTTCACTCTCACACAAACACGCTG 1557
Oy 363 Phehisrtrprouenprouenprouenprouenprouenprouenprouenprouen 382
Db 1558 TTCCATACCTCTTATGATCTGTGATACAGAAACAAACAAACATTAAGTGTGCT 1617
Oy 383 Alaseraspheileargserleuaspheleuyscysglulaleuaglnleu 402
Db 1618 GCAAGTACTTATTCGAGGCTGAGACACTGTGAGACACTGTGAGAGGCTGTTC 1677
Oy 403 Serhisrtrprouenprouenprouenprouenprouenprouenprouenprouen 422
Db 1678 TCCCAAGTGTGATTTGCAATCTGAGATGCTGAGAGTGAATGAGATGCTGCTG 1737
Oy 423 Thrtrprouenprouenprouenprouenprouenprouenprouenprouenprouen 442
Db 1738 ACAAGTGGCTCTCTGTAATATACAGTCAAGTTCACAAAGTTCACAAAGTTCCTT 1797
Oy 443 Hisrtrprouenprouenprouenprouenprouenprouenprouenprouenprouen 462
Db 1798 CACAAGTACTTACAGAGTACACAGAGACAGACAGACAGACAGAGTATGAGCTGCTCAT 1857
Oy 463 Gluprouenprouenprouenprouenprouenprouenprouenprouenprouen 482
Db 1858 GAGCCAGAGAGTACCAAGGGAATGCTTCTGCAAGAAATGCTTCCATTTCCGAGC 1917
Oy 483 Ilethrsertrprouenprouenprouenprouenprouenprouenprouenprouen 502
Db 1918 ATTACATCCACTTATGAGAGCTGCTGAGATACCTGCTGAGTCAATGCTGAGACCCACC 1977
Oy 503 Argalaalmetleuileuileuileuileuileuileuileuileuileuileuileu 522
Db 1978 AGGCTGTATATACACACTGCGACAGATGATCAACAGGCTGCTCTGAGACTTTC 2037
Oy 523 Ilealalyargprouenprouenprouenprouenprouenprouenprouenprouen 542
Db 2038 ATGCCAAGAGGCTCTCTGAGACAGAAATCTTGAAGTGTGAAGAAACACACACTGAG 2097
Oy 543 Glnlulileuileuileuileuileuileuileuileuileuileuileuileuileu 562
Db 2098 CAAGAAATTCGAAAGCAATTAACATCAATCTTGTGAGATGCTGAGATTCATTAAT 2157
Oy 563 Glnlusertrprouenprouenprouenprouenprouenprouenprouenprouen 582
Db 2158 CAAGAGATACATCAAAATTCAGCCCTGAGCCAGAAATTTGAAGCTTCTTCAAGTAA 2217
Oy 583 Serleuyltrleasnserglulysasnleuprouenprouenprouenprouenprouen 602
Db 2218 AGCTTATATCACTCACTGAGGAAACATCCCGATCTTATTAATGATCTTGTGAACATTTG 2277
Oy 603 Proasnrcysalaseraleuaspheileuysalaleuaspheileuysalaleuaspheileu 622
Db 2278 CCCAATTTGCAAGTCCCTGAGCTTCAATTAACATGAGCTTATAGGAGGAGCTATGCT 2337
Oy 623 Sertrprouenprouenprouenprouenprouenprouenprouenprouenprouen 642
Db 2338 TCATGGAAGAAAGGCTGAGAAAGACAGAGTGAATCCACATGGAAGAGCCCGCAAGAAC 2397
Oy 643 Tyrleuprouenprouenprouenprouenprouenprouenprouenprouenprouen 662
Db 2398 TACATTTCCAGAGGCTGTATCTTGTCTTCACTGGAAGCAAGAAATTCAGGACTCTG 2457

QY 663 GluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeuGlyLys 682
 DB 2458 GAGGTACACACTCCGGAGTTTCAGCAAGTGTGAATAGCAAGATATACAGATATCTGGGAAA 2517
 QY 683 IlePheSerSerIleThrSerLeuArgLeuGlnIleLysArgCysAlaGlyValAlaGly 702
 DB 2518 ATATTTCAGCTTCGCCACAAAGCCTCAGCTGCMAATTAAGAATATGTGGTGGTGGTGA 2577
 QY 703 SerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGluAlaSer 722
 DB 2578 AGCTTCAGTTGGTCCCTCAGACACTGTAGAACATTTATTTCTCAGTGTGAAGCCAGT 2637
 QY 723 ProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysTyrLeuSer 742
 DB 2638 CCCCTCACATAGAAAGATGAGAGGCACATCATCTGTAAACAACCTGAAACCTTGAGT 2697
 QY 743 IleHisAspLeuGlnAsnGlnArgLeuProGlyLysLeuThrAspSerLeuGlyAsnLeu 762
 DB 2698 ATTATGACCTACAGAAATCAACGGCTCGCGGTCTGACTGCACAGCTTGGTAAACTTG 2757
 QY 763 LysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluAlaAspAlaIleLys 782
 DB 2758 AAGAACTTACAAAGCTCATATATGATACATTAAGATGATGAAGAAGATGCTATATAA 2817
 QY 783 LeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeuSer 802
 DB 2818 CTACCTGAGAGGCTCGAAAAACCTGAGAAAGATGTTTATTTATTTGATTTGACCACTTGTCT 2877
 QY 803 AspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAspLeu 822
 DB 2878 GACATTGAGAGGAAATGAGATTAATGATGATCAAGTCTGTCAAGTGAAGAACTTGTGACCTT 2937
 QY 823 GluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGln 842
 DB 2938 GAAATAATTTCAATAGTCTCTGCTGCTGTCTGCAAAATGCAAGTGAATAATCTTACCTAG 2997
 QY 843 AsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGluLys 862
 DB 2998 AATCTTCACAATTTGGTCAAACTGAGCATCTTGTATATGAGAAATATACCTGGAATAA 3057
 QY 863 AspLysAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThr 882
 DB 3058 GATGAAATGAAAGCTTTTCAGAACTGATGCACAGAGAAAGCTGTGAACACCTCCACC 3117
 QY 883 AlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLeuLysHis 902
 DB 3118 GCATCTGATGCTGCCCTGGGGCTGTGACCTGCAGAGCAGCCTGAGCAGCTTTGAAACAT 3177
 QY 903 LeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrPargLeuThrAspThr 922
 DB 3178 TTGGAGAGGCTCCCAACCTGCTCAAGCTTGGTTGAAATACTGGAAGCTCACAGATACA 3237
 QY 923 GluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnIleu 942
 DB 3238 GAGATTGAAATTTAGTGCAATTTTGTGAAAGAACCTTCGAAATACTTCACACAGTTG 3297
 QY 943 AsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPheValaPheMetGlyValPheGlu 962
 DB 3298 AATTTCGGGGAAATCTGTGTAGCAGATGATGATGCTTGCCTTCATGGGGTGTATTTAG 3357
 QY 963 AsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAspProAla 982
 DB 3358 AATCTTAAGCAATAGTGTGTTTGTGACTTGTACTAAAGAAATTTCTACCTGCATCCAGCA 3417
 QY 983 LeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAlaArgLeu 1002
 DB 3418 TTACTTCAGAAATCTTACCAAGTGTATCCAAAGTTAACTTTTCGCAAGAAAGTAGGCTT 3477
 QY 1003 ValGlyTyrPargIlePheAspAspAspLeuSerValIleThr 1016
 DB 3478 GTTGGGTGGCAATTGATGATGATGATCTCAGTGTATTACA 3519

RESULT 5
 US-09-841-739-4
 : Sequence 4, Application US/09841739
 : Patent No. US20020034784A1
 : GENERAL INFORMATION:
 : APPLICANT: Bertin, John
 : TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH
 : FILE REFERENCE: 0734-329001
 : CURRENT APPLICATION NUMBER: US/09/841,739
 : PRIOR FILING DATE: 2001-08-29
 : PRIOR APPLICATION NUMBER: US 09/697,089
 : PRIOR FILING DATE: 2000-10-26
 : PRIOR APPLICATION NUMBER: US 60/161,822
 : NUMBER OF SEQ ID NOS: 16
 : SOFTWARE: FastSeq for Windows Version 4.0
 : SEQ ID NO 4
 : LENGTH: 3615
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: (1)...(3612)
 : US-09-841-739-4
 Alignment Scores:
 Pred. No.: 0 Length: 3615
 Score: 5188.00 Matches: 1014
 Percent Similarity: 98.16% Conservative: 1
 Best Local Similarity: 98.07% Mismatches: 18
 Query Match: 95.04% Indels: 1
 DB: Gaps: 1
 US-09-697-089-2 (1-1024) x US-09-841-739-4 (1-3615)
 QY 1 MetAsnPhelIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
 DB 418 GTGAATTTCAATAAAGGACAAATAGCCGAGCCCTTTTCAAAGAAAGGAAATGACGTATA 477
 QY 21 LysGlnIleThrAspAspLeuPheValThrAsnValLeuAsnArgGluValAsnIle 40
 DB 478 AAGCAATACACAGATGACCTTTTGTATGCAATTTCTGCAATCCCGAAGAAAGTAAACATC 537
 QY 41 IleCysGlyLysValGluGlnAspAlaAlaArgIleIleHisMetIleLeuLys 60
 DB 538 ATTTCGCGGAGAAAGTGGAGACAGATGCTGTAGAGGATTCATCATGATTTTGAA 597
 QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTyrPargLeu 80
 DB 598 AAGGTTTCAGAGTCTGTAACTCTTTCTTAATCCCTTAAGAGTGAACATATCTCTA 657
 QY 81 PheGlnAspLeuAsnGlyGlnSer----- 88
 DB 658 TTTTCAAGACTTGAATGACAAAGTTTGGAGAGACACAGAAATTTGGCTTTTAAACATC 717
 QY 89 -----LeuPheHisGlnThrSerGluLysAspLeuAspAspLeuAla 102
 DB 718 ACCTCTTCTAATAGGCTTTTTCATCAGACATCAAGAGAGCTTGGAGATTTGGCT 777
 QY 103 GlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPhetYrProLeuGlyGlu 122
 DB 778 CAGGATTTAAAGACTTGTACATACCACCATCTTTTGTGAACCTTTTATCCCTTGTGTGAA 837
 QY 123 AspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuThrPargLys 142
 DB 838 GATATTGACATTAATTTTAACTTGAAGAAAGCACTTCACAGAACTGTCTGTGAGAGAG 897
 QY 143 AspGlnHisHisIleAspValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuGln 162
 DB 898 GACCAACACATCACCGCGGTGGAGACACTGACCTGAAATGGCTTCGCGAGGCTTTCAG 957
 QY 163 SerProCysIleIleGlyGlyGluSerGlyLysGlyLysSerThrLeuLeuGlnArgIle 182

Dh 958 AGCCCTGCATCATTTGAAGGGGAATCTGGCAAGCAAGTCCACTCTGCTGACGCAATT 1017
Qy 183 AlAmeLeuThrGlySerGlyCysLysAlaLeuThrLysPheLysPheValPhePhe 202
Dh 1018 GCCATGCTTGGGGCTCCCGAAAGTGCAGAGCTGTGCACCAAGTTCAAATTCCTCTTCTTC 1077
Qy 203 LeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeuAsp 222
Dh 1078 CTCGGCTACGACAGGCGCCAGGGGTGACTTTTGAACCCTGTGTGATCAACTCTCGGAT 1137
Qy 223 IleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArg 242
Dh 1138 ATACCTGGCACAATCAGGAAGCAGACATTCATGGCCATGCTGTAAGCTGGCGCAGAG 1197
Qy 243 ValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnGlyProGluIleGlu 262
Dh 1198 GTTCTTTTCTCTTGATGGCTACAAATGAAATTCAGCCCAAGACCTGCCAATAATTCGAA 1257
Qy 263 AlAleuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThrThrGlu 282
Dh 1258 GCCCTGATTAAGGMAAACCCAGCGCTTCAAGAACATGTCATGTCACCTACCTACCTGAG 1317
Qy 283 CysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMetThrGlu 302
Dh 1318 TGCTTGAGGCACATACGCGAGTTGGTGGCTGACTGCTGAGGTGGGGGATATGACAGAA 1377
Qy 303 AspSerAlaGlnAlaLeuIleArgGluValIleuIleLysGluLeuAlaGluLeuLeu 322
Dh 1378 GACAGGCGCCAGGCTCTCTCCGAAAGTGTGATCAAGAGACCTGTGCAAGGCTTGTG 1437
Qy 322 LeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPheValVal 342
Dh 1438 CTCCAATTCACAATAATCCAGAGGCTTGAGAGATCTCATGAACACCCCTCTCTTGTGGTC 1497
Qy 343 IleThrCysAlaIleGlnMetGlyLysGluPheHisSerHisThrGlnThrThrLeu 362
Dh 1498 ATCACTTGTCGAATCCAGATGGGTGAAGTGAATGCACTCTCAACACAAACCAAGCGCT 1557
Qy 363 PheHisThrPheThrAspLeuLeuIleGlnLysAsnLysHisLysGlyValAla 382
Dh 1558 TTCCTACCTTTATGATCTGTGATACGAAACAAACAAACAAATTAAGGTGGGT 1617
Qy 383 AlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluLysValPhe 402
Dh 1618 GCAAGTGAATTCATTCGGAGCGCTGGACACACTGTGAGACCTAGCTGTGAGGGTGTGTTTC 1677
Qy 403 SerHisLysPheAspPheGlnLeuGlnAspValSerSerValAsnGluAspValLeuLeu 422
Dh 1678 TCCCAAGATTGATTTGCAACTGCAGAGATGTCTCAGCGGTGAATGAGGATGCTCTGCTG 1737
Qy 423 ThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLysPhePhe 442
Dh 1738 ACAATGGGCTCTCTGTAATATACAGCTCAAAAGTTCAACCCAAAGATTAATTCCTT 1797
Qy 443 HisLysSerPheGlnGlnLysThrAlaGlyArgArgLeuSerSerLeuLeuThrSerHis 462
Dh 1798 CACAAGTCATTCACAGAGTACACACAGCAGACAGACACTCAGAGTTTATGACGTCTCAT 1857
Qy 463 GluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerLieserAsp 482
Dh 1858 GAGCCAGAGGAGTGCACCAAGGGGAATGTACTTGCAGAAATAATGTTCCATTTCCGGAC 1917
Qy 483 IleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGluIleThr 502
Dh 1918 ATTATATTCACATTATACAGACCTGCTCCGGTACACCTGTGGGTCAATCTGTGGAACCCACC 1977
Qy 503 ArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGlyLeuSer 522
Dh 1978 AGGCGTGTATATGACACACCTCCACAGATATCAACAGCGGTGCTCTCTGGAATTTCC 2037
Qy 523 IleAlaLysArgProLeuThrArgGlnGlnLysLeuGlnSerValLysAsnThrThrGlu 542
Dh 2038 ATCCCAAGAGGCTCTCTGTGAGACAGAAATCTTTGCAAAAGTGTGAAAAACACCACTGAG 2097

Qy 543 GlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHisLeuTyr 562
Dh 2098 CAAAGAAATTTCTGAAGCCATAAATCAATTCCTTTGTAAGATGTGGCATCATTTATAT 2157
Qy 563 GlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGlnGlyLys 582
Dh 2158 CAAGAGAGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTTCTTCAAGGTAAA 2217
Qy 583 SerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPheGlnHisLeu 602
Dh 2218 ACCTATATATCACTACAGGAACAATCCCGATTAATCTTATTTGACTTTTGAACATTTG 2277
Qy 603 ProAsnGlyAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyLysAlaMetAla 622
Dh 2278 CCCAATGTGCAAGTGCCTGTGACTTCAATTAACGTGACTTTTATGGGGGACTATGGGT 2337
Qy 623 SerTPGluLysAlaGluAspThrGlyIleHisMetGluGluAlaProGluThr 642
Dh 2338 TCATGGMAAAGCTGCAGAACACACAGGTGGAATCCACATGGAAGAGGCCCAAGAAC 2397
Qy 643 TyrIleProSerArgAlaValSerLeuPhePheAsnTPrLysGlnGluPheArgThrLeu 662
Dh 2398 TACATTCACAGCAGGCTGTATCTTTGTTCTTCACTGGAACAGGAATTCAGACTGTG 2457
Qy 663 GluValIThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeuGlyLys 682
Dh 2458 GAGGTACACTCCGGGGAATTCAGCAAGTTGAATGAAGCAAGATATCATCTGGGGGAA 2517
Qy 683 IlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyValAlaGly 702
Dh 2518 AATTCACGCTGCCACAAGCTCAGCGTGCCAATTAAGATGTGTGTGTGCTGGA 2577
Qy 703 SerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGluAlaSer 722
Dh 2578 AGCCTCAGTTGGTGTCTCAGCAGCTGTAAAGCAATTTATCTCATGTGTGGAACCCAGT 2637
Qy 723 ProLeuThrIleGluAspGluArgHisIleThrSerValIleAsnLysThrLeuSer 742
Dh 2638 CCCCTCACCATGAAAGATGAGAGGCACATCACTGTGTAACAACTGAACCTGAAACCTTGAGT 2697
Qy 743 IleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGlyLysLeu 762
Dh 2698 ATTCAATGACCTACAGAAATCAACAGCGCTGCCGGGTGTCTGACTGACAGCTGGTAACTTG 2757
Qy 763 LysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaLys 782
Dh 2758 AAGAACCTTACAAACCTCATATATGATTAACATTAAGATGAAGAAGATGCTATAAA 2817
Qy 783 LeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeuSer 802
Dh 2818 CTAGCTGAAGGCTGTAAANAACCTGAAGAGATGTGTTATTTCAATTTAACCACACTGTGCT 2877
Qy 803 AspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAspLeu 822
Dh 2878 GACATTTGAGAGGGAATGATTAATACATGCAAGTCTGTCAAGTGAACCCGTGACCTT 2937
Qy 823 GluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGln 842
Dh 2938 GAAGAAATTCATATGATCTCCGTGCTGTGCTGCAAAATGCAAGTGAATAATCTAGCTCAG 2997
Qy 843 AsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGluLys 862
Dh 2998 AATCTTCAATTTGGTCAAACTGACATTTCTTGATTTATCAAGAAATTTACCTGGAATA 3057
Qy 863 AspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThr 882
Dh 3058 GATGGAATTAAGGCTTTCATGAATCACTGATGCAAGATGAAGCTGTGAACAGCTCAAC 3117
Qy 883 AlaLeuMetLeuProTPRGlyCysAspValGlnGlySerLeuSerSerLeuLeuLysHis 902
Dh 3118 GCACGTGATGTGCGCTGTGGGCTGTGACGTGCAAGGCAACGCTGAGACGCTGTGGAACAT 3177

QY 903 LeuGlulValAlProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAspThr 922
Db 3178 TTTGAGGAGGCTCCACACCTGTCAGCTTGTTGAAAACTGAGACTCAGATACCA 3237
QY 923 GluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGlnLeu 942
Db 3238 GAGATTAGAAATTTTAGGTGCAATTTTGGANAGAACCTCTGANAACCTTCAGAGCTTG 3297
QY 943 AsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyValPheGlu 962
Db 3298 AATTGGCGGGAATCGTGAGCAGCATGTGATGGCTTGCTCATGGGTATTTGAG 3357
QY 963 AsnLeuLysGlnLeuValPhePheAspPheSerThrLysGlnPheLeuProAspProAla 982
Db 3358 AATCTTAAGCAATTAGCTTTTTCACCTTACTTAAGAATTTCTACTGATCCAGCA 3417
QY 983 LeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnAlaArgLeu 1002
Db 3418 TTAGTCAGAAATCTTACGCCAAGTGTATCCAAAGTTAACTTTTCGCAAGAGTAAGCTT 3477
QY 1003 ValGlyTrpGlnPheAspAspAspAspSerValIleThr 1016
Db 3478 GTTGGGTGCAATTTGATGATGATGATGATCTCAGTGTATTACA 3519
RESULT 6
US-09-841-739-12/c
; Sequence 12, Application US/09841739
; Patent NO. US20020034784A1
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/09/841,739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26 US 60/161,822
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 3615
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-841-739-12
Alignment Scores:
Pred. No.: 0 Length: 3615
Score: 5188.00 Matches: 1014
Percent Similarity: 98.16% Conservative: 1
Best Local Similarity: 98.07% Mismatches: 1
Query Match: 95.04% Indels: 18
DB: 10 Gaps: 1
US-09-697-089-2 (1-1024) x US-09-841-739-12 (1-3615)
QY 1 MethAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
Db 3198 GTGAATTCATTAAGACAAATAGCCGAGCCCTTATTCAAAGATGGGAATGACTGTATA 3139
QY 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGlnGluValAsnIle 40
Db 3138 AAGCAAAATCACAGATGACCTATTTGTATGAAATGTTCTGATCCGGAAGTAACATTC 3079
QY 41 IleCysCysGlnLysValGlnGlnAspAlaIleArgGlyIleIleHisMetIleLeuLys 60
Db 3078 ATTGCTGTCGAGAGAGGTGAGCAGAGATGCTCTGAGAGGAGATTCACATATTTTGAA 3019
QY 61 LysLysSerGlnSerCysAsnLeuPheLeuLysSerLeuLysGlnTrpAsnTrpProLeu 80
Db 3018 AAGGGTTCAGAGTCTCTGTAACCTCTTCTTAATCCCTTAAGAGTGAAGTATACCTCTTA 2959
QY 81 PheGlnAspLeuAsnGlyGlnSer----- 88

Db 2958 TTTGAGGACTTGAATGAGCAAAAGTTTGAGGAGACACAGAAATTTGGTCTTTAAACATC 2899
QY 89 -----LeuPheHisGlnThrSerGlnGlyAspLeuAspLeuAla 102
Db 2898 ACCCTTCTCTAATAGGCTTTTTCATCAGACATCAGAGAGACTTGAGAGATTTGGCT 2839
QY 103 GlnAspLeuLysAspLeuThrHisThrProSerPheLeuAsnPheTrpProLeuGlyGlu 122
Db 2838 CAGATTTAAAGACTGTGTACATACCACCTTTCTGAACTTTATACCCCTTGCGAA 2779
QY 123 AspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTrpArgLys 142
Db 2778 GATATTGACATTAATTTTAACTTGAAGAAAGCACTTCACAGAACTGTCCTGTGAGGAAG 2719
QY 143 AspGlnHisHisArgValGlnGlnLeuThrLeuAsnGlyLeuGlnAlaLeuGln 162
Db 2718 GACCAACACATCACCCGGTGAGCAGCTGACCTGTAAATGGCTCTGACAGGCTCTTCAG 2639
QY 163 SerProCysIleIleGlnGlyGlnSerGlyLysGlyLysSerThrLeuLeuGlnArgIle 182
Db 2658 AGCCCTGTCATCATTTGAAGGGGAATCTGGCAAGCAAGTCCACTCTGTCGACAGCAAT 2599
QY 183 AlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheValPhePhe 202
Db 2598 GCCATGCTCTGGGCTCCGGAAAGTGCAGAGCTGTACCAAGTCAAAATTCGTCTTCTC 2539
QY 203 LeuArgLeuSerArgAlaGlnGlnGlyLeuPheGlnThrLeuCysAspGlnLeuLeuAsp 222
Db 2538 CTCGGTCTCAGCAGAGGCCAGGGTGAGCTTTTAAACCTCTGTATCAACTCTTGAT 2479
QY 223 IleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArg 242
Db 2478 ATACTGGCACAATCAGGAAGCAGACATTCATGGCCATGCTGAGAGCTCGGACAGAG 2419
QY 243 ValLeuPheLeuLeuAspGlyTrpAsnGlnPheLysProGlnAsnGlyProGlnIleGln 262
Db 2418 GTTCTTTTCTCTTGTGAAGGCTTACAAATTAAGCCCAAGCTGCCGGAATTCGAA 2359
QY 263 AlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValIleThrThrThrGlu 282
Db 2358 GCCCTGATTAAGGAAACACCCGCTTCAGAAACATGGTCATGTCACACATCAACACTGAG 2239
QY 283 CysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMetThrGlu 302
Db 2298 TGCCCTGAGCAGCATATGAGCAGTGTGGTCCCTGACTGCTGAGTGGGAGATATACAGAA 2239
QY 303 AspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGlnLeuAlaGlnGlyLeuLeu 322
Db 2238 GACAGCGCCAGGCTCTCATCCGAGAGTGTGATCAAGAGCTGTGAGAGGCTTGTG 2179
QY 323 LeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPheValIle 342
Db 2178 CTCCAATTCAGAAATCCAGATGCTGTGAGATCTCATGAAGACCCCTCTCTTGTGTGTC 2119
QY 343 IleThrCysAlaIleGlnMetGlyLysSerGlnPheHisSerHisThrGlnThrLeu 362
Db 2118 ATCACTGTGCAATCCAGATGAGTGAAGATGATCCACTCTCACACAAACAAACCGCTG 2059
QY 363 PheHisThrPheTrpAspLeuLeuIleGlnLysAsnLysHisLysHisGlyValAla 382
Db 2058 TTCCATACCTTCTATGATCTGTGATACAGAAAAACAAACAAACATTAAGGCTGTGCT 1999
QY 383 AlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGlnGlyValPhe 402
Db 1998 GCAAGTACTTCATTCGGAGCTGTGACACACTGTGAGAACCTGTGAGAGGTGTGTC 1939
QY 403 SerHisLysPheAspPheGlnLeuGlnAspValSerSerValAsnGluAspValLeuLeu 422
Db 1938 TCCCACAAGTTGATTCGAACTGACAGATGTGCCAGCGTGAATGAGATGTCTGCTGCT 1879
QY 423 ThrThrGlyLeuLeuCysLysTrpThrAlaGlnArgPheLysProLysTyLysPhePhe 442
|||||

Db 1878 ACAAGTGGCTCTCTGTAATATATACAGCTCAAGAGTTTCAAGCCAAAGTAAATCTTT 1819
QY 443 HisLysSerPheGlnGluYrThrAlaGlyArgArgLysSerSerLeuLeuThrSerHis 462
Db 1818 CACAAGCATCTCCAGGAGTACACAGCAGCAAGACTCAGACTTTATTTAGACTCTCAT 1759
QY 463 GluProGlnGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerLieserAsp 482
Db 1758 GAGCAGAGAGAGGTGACCAAGGGGAATGTTACTCTGCAAAAATGTTTCCATTTCGGAC 1699
QY 483 IleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGluAlaThr 502
Db 1698 ATTACATCCACTATAGCACCCTGCTCCGCTACACCTGTGGTGCATCTGTGGAAGCCACC 1639
QY 503 ArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGlyLeuSer 522
Db 1638 AGGGCTTTATGAAACCTCCGACAGCTATACACACGGCTGCTTCTTCGGACTTTCC 1579
QY 523 IleAlaLysArgProLeuTyrArgGlnGlnLysLeuGlnSerValLysAsnThrThrGlu 542
Db 1578 ATCGCCAAAGAGGCTCTCTGGAGACAGAAATCTTTCGAAAGTGGAAAAACACACTGAG 1519
QY 543 GlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGlyCysGlyIleHisLeuTyr 562
Db 1518 CAGAAATTCGTGAAGCCATAAACATCAATCTTGTGTAGAGTGGCATCCATTTATAT 1459
QY 563 GlnGluSerThrSerLysSerAlaLeuSerGlnGlnLupheGlnAlaPhePheGlnGlyLys 582
Db 1458 CAGAGAGTCAATCCAAATACAGCCCTGAGCAAGAAATTTGAAGTTTCTTTCAGAGTAA 1399
QY 583 SerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhePheGlnHisLeu 602
Db 1398 AGCTTATATATCAACTCAGGGAACATCCCGATTAATTGACTTTTGAACATTTG 1339
QY 603 ProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyIleAlaMetAla 622
Db 1338 CCCAATTTGTCAAGTGCCTGGACTTCATTAACCTGGACTTTTATGGGGAGCTATGCT 1279
QY 623 SerTrpGlnLysAlaAlaGlnAspThrGlyIleHisMetGlnGlnAlaProGlnThr 642
Db 1278 TCATGGAAAAAGCTGCAGAAAGACACAGGTGGAAATCCACATGGAAAGGCCCGAAGAAC 1219
QY 643 TyrIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnLupheArgThrLeu 662
Db 1218 TACATTCGCCAGAGGCTGTATCTTGTCTTCACTGAGAGCAGAAATTCAGACTCTG 1159
QY 663 GluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeuGlyLys 682
Db 1158 GAGGTCACTCCGGGATTTTCACCAAGTTGAATTAAGCAAGATATCAAGATATCTGGGGAAA 1099
QY 683 IlePheSerSerAlaThrSerLeuArgLysGlnIleLysArgCysAlaGlyValAlaGly 702
Db 1098 ATATTCAAGTCTGCTGCACACACCTCAGCTCCAAATTAAGATGTGCTGTGGCTGGA 1039
QY 703 SerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGluAlaSer 722
Db 1038 AGCTGAGTTGGTCCCTCAGACACTGTAAACAATATTCTCTCAAGTGGGAAGCCAGT 979
QY 723 ProLeuThrIleGlnAspGlnArgHisIleThrSerValThrAsnLeuLysThrLeuSer 742
Db 978 CCCCTCACCATAGATGAGAGGACACATCATCTGTAAACAAACCTGAAACCTTGAGT 919
QY 743 IleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGlyAsnLeu 762
Db 918 ATTCAATACCTACAGATCAACGGCTGCCGGGTGGTCTGTGACTACACCTTGGGTAACCTTG 859
QY 763 LysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGlnGluAlaIleLys 782
Db 858 AAGAACCTTCAAAAGCTCAATATGATTAACATTAAGATGATGATGATGATGATGATGATGAT 799
QY 783 LeuAlaGlnGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeuSer 802
Db 798 CTAGCTGAAGGCTGAAAAAAGCTGAGAGATGTGTTTATTTATTTGACCCACTTGTCT 759

QY 803 AspIleGlnGlnGlyMetAspTyrIleValLysSerLeuSerSerGlnProCysAspLeu 822
Db 738 GACTTGGAGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 679
QY 823 GlnGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGln 842
Db 678 GAAGAAATTCATATAGTCTCTGCTGCTGTCTGCAAAATCAGTGAAGAAATCTAGCTCAG 619
QY 843 AsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGlnAsnTyrLeuGlnLys 862
Db 618 AATCTTCACAAATTTGGTCAACACGACATCTTGTGATTTATCAGAAATTTACCTGGAAAAA 559
QY 863 AspGlyAsnGlnAlaLeuHisGlnLeuIleAspArgMetAsnValLeuGlnGlnLeuThr 882
Db 558 GATGGAATGAACTCTTCATGAACATATGACAGATGAAAGTGCATGACAGCTCACC 499
QY 883 AlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLysHis 902
Db 498 GCACTGATGCTGCCCTGGGCTGTGACGTGCAAGGACAGCTGAGACACTGTGAAACAT 439
QY 903 LeuGlnGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAspThr 922
Db 438 TTGGAGAGGTCCACACATCTGTCACAGCTTGGGTGAAAAACTGGACACTCAGATACA 379
QY 923 GluIleArgIleLeuGlnAlaPhePheGlyLysAsnProLeuLysAsnPheGlnLeu 942
Db 378 GACTTATGAATTTTATAGTGCATTTTGGAAAGAACCTCTGAAAACTTCCAGCACTTG 319
QY 943 AsnLeuAlaGlnLysArgValSerSerAspGlyTrpLeuAlaPheMetGlyValPheGln 962
Db 318 AATTTGGCGGAAATCTGTGAGACAGATGATGATGATGATGATGATGATGATGATGATGAT 259
QY 963 AsnLeuLysGlnLeuValPhePheAspPheSerThrLysGlnPheLeuProAspProAla 982
Db 258 AATCTTAAGCAATTAAGTGTGTTTGTGACTTATGACTTAAGCAAAATTTCTACCTGATCCAGCA 199
QY 983 LeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGlnAlaArgLeu 1002
Db 198 TTATGTCGAAAACTTACCAAGTGTATCCAGTAACTTTTTCGCAAGAGCTAGGCTT 139
QY 1003 ValGlyTrpGlnPheAspAspAspLeuSerValIleThr 1016
Db 138 GTTGGGTGGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 97

RESULT 7
US-09-864-921-179
; Sequence 179, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sung-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
; TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use
; FILE REFERENCE: P-17 4752
; CURRENT APPLICATION NUMBER: US/09/864, 921
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579, 240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686, 347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275, 980
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 179

```

; LENGTH: 891
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(891)
US-09-864-921-179

```

```

Alignment Scores:
Pred. No.: 4.62e-229 Length: 891
Score: 1598.00 Matches: 296
Percent Similarity: 99.66% Conservative: 0
Best Local Similarity: 99.66% Mismatches: 1
Query Match: 29.27% Indels: 0
DB: Gaps: 0

```

US-09-697-089-2 (1-1024) x US-09-864-921-179 (1-891)

```

QY 161 LeuGlnSerProCysIleIleGlnGlyGluSerGlyLysGlyLysSerThrLeuGln 180
      |||
      1 CTTCAAGAGCCCTGCATCATTTGAAGGGGAATCTGCAGCAAGCTCACTGCTGCAG
      |||
QY 181 ArgIleAlaMetLeuThrProGlySerGlyLysCysLysAlaLeuThrLysPheVal 200
      |||
      61 CCGATTGCCATGCTCTGGGGCTCCGAAAGTGAAGGCTCTGACCAAGTTCAATTGCTC
      |||
QY 201 PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu 220
      |||
      121 TTCTTCCTCCGCTCAGACAGGGCCAGGGGTGGACTTTTGAACCCCTGCTGATCAACTC
      |||
QY 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 240
      |||
      181 CTGGATATACCTGGCAATCAGAGAGACATTCATGTGCCATGTCTGCGAAGCTGCGG
      |||
QY 241 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGln 260
      |||
      241 CAGAGGGTCTTTCTCTTCTGATGCTACATGAATTCAGCCCAAGACTGCCAGAA
      |||
Db 241 CAGAGGGTCTTTCTCTTCTGATGCTACATGAATTCAGCCCAAGACTGCCAGAA 300
      |||
QY 261 IleGluAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThr 280
      |||
      301 ATCGAAGCCCTGATAAGGAAAAACCCCTTCAGAACATGTGTCATCGCACCTACAC
      |||
Db 301 ATCGAAGCCCTGATAAGGAAAAACCCCTTCAGAACATGTGTCATCGCACCTACAC 360
      |||
QY 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300
      |||
      361 ACGAGATGCTGAGGACATACGCGAGTTGTGCTGACCTGAGGTTGAGGGGGAATAG
      |||
Db 361 ACGAGATGCTGAGGACATACGCGAGTTGTGCTGACCTGAGGTTGAGGGGGAATAG 420
      |||
QY 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 320
      |||
      421 ACGAAGACAGCGCCAGGCTCTCATCCGAGAAAGTCTGTATCAAGAGCTGTGTAAGGC
      |||
Db 421 ACGAAGACAGCGCCAGGCTCTCATCCGAGAAAGTCTGTATCAAGAGCTGTGTAAGGC 480
      |||
QY 321 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340
      |||
      481 TTGTTCTCTCAAAATTCAGAAATTCAGAGTCTTGAGAAATCTCATGAAGACCCCTCTTT
      |||
Db 481 TTGTTCTCTCAAAATTCAGAAATTCAGAGTCTTGAGAAATCTCATGAAGACCCCTCTTT 540
      |||
QY 341 ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr 360
      |||
      541 GTGGTATATCATCTTGCAATCCAGATGGGTAAGTGAAGTCCACCTCAGACACAAACA
      |||
Db 541 GTGGTATATCATCTTGCAATCCAGATGGGTAAGTGAAGTCCACCTCAGACACAAACA 600
      |||
QY 361 ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGly 380
      |||
      601 ACGCTGTTCCATACCTTCTATGATCTGTGATACAGAAAAACAACAACAATAAAGGT
      |||
Db 601 ACGCTGTTCCATACCTTCTATGATCTGTGATACAGAAAAACAACAACAATAAAGGT 660
      |||
QY 381 ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGlnGly 400
      |||
      661 GTGGCTGCAAGTGAATCTTGAGACCTTGAGACCACTGAGAGACTTACCTGAGAGGT
      |||
Db 661 GTGGCTGCAAGTGAATCTTGAGACCTTGAGACCACTGAGAGACTTACCTGAGAGGT 720
      |||
QY 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420
      |||
      721 GTGTTCTCCCAACAAGTTTATTTGAACTGCAAGGATGTCTCCAGCCTGATGAGGATGTC
      |||
Db 721 GTGTTCTCCCAACAAGTTTATTTGAACTGCAAGGATGTCTCCAGCCTGATGAGGATGTC 780
      |||
QY 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440
      |||
      781 CTGCTGACAACTGGGCTCTCTGTAAATATATACAGCTCAAAAGTTCAAGCCAAAGTATATA
      |||
Db 781 CTGCTGACAACTGGGCTCTCTGTAAATATATACAGCTCAAAAGTTCAAGCCAAAGTATATA 840

```

```

QY 441 PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSer 457
      |||
      841 TTCTTTCACAGATCATTCACAGAGATACACAGCAGAGCAAGACTCAGACAGT 891

```

RESULT 8

US-09-864-921-98

; Sequence 98, Application US/09864921

; Patent No. US20020176853A1

; GENERAL INFORMATION:

; APPLICANT: Reed, John C.

; APPLICANT: Plo, Frederick F.

; APPLICANT: Godzik, Adam

; APPLICANT: Stehlik, Christian

; APPLICANT: Damiano, Jason S.

; APPLICANT: Lee, Sug-Hyung

; APPLICANT: Oliveira, Vasco A.

; APPLICANT: Hayashi, Hideki

; APPLICANT: Pawlowski, Krzysztof

; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing

; TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use

; FILE REFERENCE: P-1J 4752

; CURRENT APPLICATION NUMBER: US/09/864,921

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 09/579,240

; PRIOR FILING DATE: 2000-05-24

; PRIOR APPLICATION NUMBER: US 09/686,347

; PRIOR FILING DATE: 2000-10-10

; PRIOR APPLICATION NUMBER: US 60/275,980

; PRIOR FILING DATE: 2001-03-14

; NUMBER OF SEQ ID NOS: 195

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 98

; LENGTH: 1395

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (277)...(1353)

US-09-864-921-98

US-09-697-089-2 (1-1024) x US-09-864-921-98 (1-1395)

```

Alignment Scores:
Pred. No.: 9.58e-203 Length: 1395
Score: 1424.00 Matches: 271
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.63% Mismatches: 0
Query Match: 26.09% Indels: 0
DB: Gaps: 0

```

```

QY 753 GlyGlyLeuThrAspSerLeuGlyAsnLeuLysAsnLeuThrLysLeuIleMetAspAsn 772
      |||
      538 AGTGGCTCTACAGTACAGCTTGGGTAACTTGAAGAACCTTACAAAGCTCAATATGATAC
      |||
Db 538 AGTGGCTCTACAGTACAGCTTGGGTAACTTGAAGAACCTTACAAAGCTCAATATGATAC 597
      |||
QY 773 IleLysMetAsnGluGluAspAlaIleLysLeuAlaGluGlyLeuLysAsnLeuLysLys 792
      |||
      598 ATAAAGATGAATGAAGAAGATGCTATTAATAAGCTGAAGGGCTGAAAAAACCCTGAAGAAG
      |||
Db 598 ATAAAGATGAATGAAGAAGATGCTATTAATAAGCTGAAGGGCTGAAAAAACCCTGAAGAAG 657
      |||
QY 793 MetCysLeuPheHisLeuThrHisLeuSerAspIleGlyGluGlyMetAspIyrIleVal 812
      |||
      658 ATGTGTTATTTTCATTGACCCACCTTGTGACATTTGAGAGGAGGATGATTAATATGATC
      |||
Db 658 ATGTGTTATTTTCATTGACCCACCTTGTGACATTTGAGAGGAGGATGATTAATATGATC 717
      |||
QY 813 LysSerLeuSerSerGluProCysAspLeuGluGluIleGlnLeuValSerCysLeu 832
      |||
      718 AAGTCTCTCTCAAGTAAACCTCTGTACCTTGAAGAAATTCATTAAGTCTCTGCTGCTTG
      |||
Db 718 AAGTCTCTCTCAAGTAAACCTCTGTACCTTGAAGAAATTCATTAAGTCTCTGCTGCTTG 777
      |||
QY 833 SerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuValLysLeuSerIle 852
      |||
      778 TCTGCAAAATGACGATGAATAATCTAGCTCAGAAATCTTCACAAAATTTGGTCAAACTGAGCAAT
      |||
Db 778 TCTGCAAAATGACGATGAATAATCTAGCTCAGAAATCTTCACAAAATTTGGTCAAACTGAGCAAT 837
      |||
QY 853 LeuAspLeuSerGluAsnTyrLeuGluLysAspGlyAsnGluAlaLeuHisGluLeuIle 872
      |||
      853 |||

```

Db 838 CTTGATTATACAGAAAATTAACCTGAGAAAAGATGAAATGAACTCTTATGAACTGATC 897
Qy 873 ASPARGMETHASVALLEUGLUGLNULEUTHRALALEUWETLEUPROTTPGLCYASAPVAL 892
Db 898 GACAGGATGAACTGCTAGAACAGCTCACCGCACTGATGCTGCCGTGGGCTGTGAGCTG 957
Qy 893 GLNGLYSERLEUSERSERLEULEULYSHISLEUGLUGLNUVALPROGLNULEUVALLYSLEU 912
Db 958 CAAGGACGCTGAGACGCGCTGTGAACAATTGGAGAGAGTCCACAGACCTGCACACTT 1017
Qy 913 GLYLEULYSASNTTPRARGLEUTHRASPRTHGLUILEARGLLEUGLALAPHEPEGLY 932
Db 1018 GGGTTGAAAAAATCGAGACTCACAGATACAGAGATTAGAAATTTAGTGATTTTGGGA 1077
Qy 933 LYSASNPROLEULYSASNPEHGLNULEULYSALAGLYASNARGVALYSERSEASP 952
Db 1078 AAAAAACCTTGAAAAAATCTTCAGCACTGTAATTTGGCGGAAATCTGTGACAGAGAT 1137
Qy 953 GLYTPLEUALAPHEMETGLYVALPHEGLUASNLEULYSGLNULEUVALPHEPEASPPHE 972
Db 1138 GGATGGCTTCCTTCAGGCTGTATTTGAGAACTTAAAGCAATTAGCTTTTGGACTTT 1197
Qy 973 SETTHRYSGLUPHELEUPROASPPROALALEUVALARGLYLEUSERGLNUVALLEUSER 992
Db 1198 AGTACTTAAGAAATTTCTACCTGATCCAGCATAGTCAAGAAACTTAGCCAAAGTTATCC 1257
Qy 993 LYSLEUTHRHELEUGLNUVALAARGLEUVALGLYTPRGLNPEASPPASPPASPLEU 1012
Db 1258 AACTTTAACTTTTCTGCAGAGAGCTAGGCTTGGTGCGCAATTTGATGATGATCTC 1317
Qy 1013 SEVALIETHRGLYALAPHELYSLEUVALTHRALA 1024
Db 1318 AGTGTTATTACAGCTGCTTTTAAACTAGTACTGCT 1353

RESULT 9
US-09-864-921-181
; Sequence 181, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sung-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
; TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use
; FILE REFERENCE: P-1J 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 181
; LENGTH: 618
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(618)
US-09-864-921-181

Alignment Scores: 2.42e-152 Length: 618
Pred. No.: 1084.00 Matches: 206
Score:

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 19.86% Indels: 0
DB: 9 Gaps: 0

US-09-697-089-2 (1-1024) x US-09-864-921-181 (1-618)

Qy 760 GLYASNLEULYSASNLEUTHRILYSLEULIEMETASPSNLIYSMETASNGLUGLUASP 779
Db 1 GGTAACTTGAAGAACCTTACAAAGCTCATATATGATTAATGAATGAATGAAGAGAT 60
Qy 780 ALAILEULYSLEUALAGLUGLYLEULYSASNLEULYSMETCYSEUPHENISLEUTHR 799
Db 61 GCTATAAATACTAGCTGAAAGCCTGAAAAAACCCTGAAGAAGATGTTATTATTCATTGACC 120
Qy 800 HISLEUSERSPIEGLYUGLYMETASPTYLILEVALYSSERLEUSERSERGLUPRO 819
Db 121 CACTTGCTGACATTGGAGAGGAAATGGATTACATAGTCAAGTCTGTCAAGTGAACCC 180
Qy 820 CYASAPLEUGLUGLNULEULYSERCYSCYSEUSERALASNALAVALYSILE 839
Db 181 TGTGACCTTGAAGAAATTCATTAATAGTCTCCTGCTGTCTGCAAAATGCAAGAAATC 240
Qy 840 LEUALAGLNASNLEULISASNLEUVALLYSLEUSERILEUASPLEUSERGLUASNTYR 859
Db 241 CTAGCTCAGAACTTTCACAAATTTGGTCAAACTGACGATTTGATTTATCAGAAAAATTAC 300
Qy 860 LEUGLULYSASPLYSANGLUALALEUHNISGLNULEULIEMASPRYMETASVALLEUGLU 879
Db 301 CTGAAAAAATGGAATGAAGACCTTCATGATGATGATGATGATGATGATGATGATGATGAT 360
Qy 880 GLNLEUTHRALALEUWETLEUPROTTPGLCYASAPVALGLNLYSERLEUSERSERLEU 899
Db 361 CAGCTCAGCCGACGTGAGTGCCTCGGGCTGTGAGCTGCAAGCGACGCTGACGACCTG 420
Qy 900 LEULYHISLEUGLUGLNUVALPROGLNULEUVALLYSLEUGLYLEULYSASNTPRARGLEU 919
Db 421 TTGAACATTTGAGAGAGGCTCCACAACTGCTGACAGCTTGCTGAAAAAATGCAAGCTC 480
Qy 920 THRASPTHGLIUEARGLLEUGLYALAPHEPEGLYLYSASNPROLEULYSASNPE 939
Db 481 ACAGATACAGAGATTGAATTTAGTGCAATTTTGGAAAAAACCCTCGAAAAAATCTTC 540
Qy 940 GLNGLNULEUSNLEUALAGLYASNARGVALYSERSEASPGLYTHRLEUALAPHEMETGLY 959
Db 541 CACGAGTTGAATTTGGCGGGAATCGTGAGAGATGATGATGATGATGATGATGATGATGAT 600
Qy 960 VALPHEGLUASNLEULYS 965
Db 601 GTATTGAGAACTTTAAG 618

RESULT 10
US-09-764-864-339
; Sequence 339, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 339
; LENGTH: 608
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (20)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE

```

; LOCATION: (23)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (26)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (86)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-339

Alignment Scores:
Pred. No.: 1,58e-140 Length: 608
Score: 1005.00 Matches: 189
Percent Similarity: 98.45% Conservative: 1
Best Local Similarity: 97.93% Mismatches: 3
Query Match: 18.41% Indels: 0
DB: 10 Gaps: 0

US-09-697-089-2 (1-1024) x US-09-764-864-339 (1-608)
QY 479 SerIleSerAspIleThrSerThrThrSerSerLeuLeuArgThrCysGlySerSer 498
DB 28 GCCATTTCGCCCATTCATCCACTATATACAGGCTGCTCCGGACACCTGTGGCTCATMT 87
QY 499 ValGluAlaThrArgAlaValMecIysHisLeuAlaAlaValTyrGlnHisGlyCysLeu 518
DB 88 GTGGAGGCCACCAAGGCTGTATGAAAGCCTCGCAGAGTGTATCAACACGCGCTCCCTT 147
QY 519 LeuGlyLeuSerIleAlaLysArgProLeuTyrPArgGlnGlnSerLeuGlnSerValLys 538
DB 148 CTCGGACTTTCATCCGCCAAGAGGCTCTCTGGAGACAGGAATCTTGGAAAGTGGAA 207
QY 539 AsnThrThrGlnGlnGlnIleLeuLysAlaAlaLeuAsnIleAsnSerPheValGluCysGly 558
DB 208 AACACACAGACAGAAAGAAATCTGAAGAGCATTAACATCAATTCCTTTAGAGTGTGC 267
QY 559 IleHisLeuTyrGlnGlnSerThrSerLysSerAlaLeuSerGlnGlnPheGluAlaPhe 578
DB 268 ATCCCTTTATATATCAAGAGAGTATCATCCAAATCAGCCCTGAGCCAGAAATTTGAAGCTTTC 327
QY 579 PheGlnGlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrIlePheAspPhe 598
DB 328 TTTCAGAGTAAAGCTTATATATATCACTACAGGAAACATCCCGATTAATTTGACTTC 387
QY 599 PheGlnHisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGly 618
DB 388 TTGGAACATTTGCCCAATTTGTCAAGTGTCTGGAAGTCAATTAACCTGACCTTTTATGGG 447
QY 619 GlyAlaMetAlaSerTyrGlnLysAlaAlaGluAspThrGlyGlyIleHisMetGlnGlu 638
DB 448 GGAGCATATGGCTTTCATGGGAAAGGCTGCAGAAACACAGAGYGAAATCCACATGGAAAGAG 507
QY 639 AlaProGlnThrTyrIleProSerArgAlaValSerLeuPheAsnThrPlyGlnGlu 658
DB 508 GCCCCAGAAACCTACATTTCCAGCAGGAGGCTGTATCTTGTCTCAACTGGAAGCAGAA 567
QY 659 PheArgThrLeuGluValThrLeuArgAspPheSerLys 671
DB 568 TTCAGAGACTGTGAGGTACACTCCGCGGATTCACGCAAG 606

RESULT 11
US-09-864-921-102
; Sequence 102, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Plo, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
```

```

; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
; FILE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use
; FILE REFERENCE: P-LI 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (277)...(744)
US-09-864-921-102

Alignment Scores:
Pred. No.: 1.24e-117 Length: 768
Score: 853.00 Matches: 154
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 15.63% Indels: 0
DB: 9 Gaps: 0

US-09-697-089-2 (1-1024) x US-09-864-921-102 (1-768)
QY 1 MetAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMecGlyMetThrValIle 20
DB 277 ATGAATTTATTAAGACATTAAGCCAGCCCTTATTCAAAGATGGGATGACTGTATA 336
QY 21 LysGlnIleThrAspAspLeuPheValTyrAsnValLeuAsnArgGluValAlaAsnIle 40
DB 337 AAGCAATACAGATGACCTATTGTATGGAATGTTCTGAATCCGCAAGATTAACATC 396
QY 41 IleCysCysGlnLysValGlnGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
DB 397 ATTTGCTGCAGAGAGGTGAGCAGATGCTGTAGAGGATCATTCATGATTTTGAA 456
QY 61 LysGlySerGlnSerCysAsnLeuPheLeuLysSerLeuLysGlnTyrAsnTyrProLeu 80
DB 457 AAGGGTTCAGAGTCTCTTAACCTCTTTTAAATCCCTTAAGAGATGGACTATCTCTTA 516
QY 81 PheGlnAspLeuAsnGlnSerLeuPheHisGlnThrSerGlnGlyAspLeuAspAsp 100
DB 517 TTTCAGAGCTGAATGAGCAAAAGTCTTTTCATCAGACATCAGAAAGAGACTTGGACAT 576
QY 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu 120
DB 577 TTGGCTCAGAGATTTAAAGACATTTGATACCATACCATCTTCTGAACTTTATATCCCTT 636
QY 121 GlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGlnProValLeuTyr 140
DB 637 GGTGAAGATATGACATTTATTTTAACTTGAAAAGACACTTTCACAGAACTGTCTGTGG 696
QY 141 ArgLysAspGlnHisHisHisArgValGlnGlnLeuThrLeu 154
DB 697 AGGAAGACCAACACCATACCGCGTGCAGACAGCTGACCTTA 738

RESULT 12
US-09-764-864-754
; Sequence 754, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
```

```

CURRENT APPLICATION NUMBER: US/09/764, 864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 754
LENGTH: 522
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (360)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (468)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (499)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (505)
OTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-754

```

APPLICANT: Lee, Sug-Hyung
APPLICANT: Oliveira, Vasco A.
APPLICANT: Hayashi, Hideki
APPLICANT: Pawlowski, Krzysztof
TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use
FILE REFERENCE: P-LJ 4752
CURRENT APPLICATION NUMBER: US/09/864,921
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 09/579,240
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/686,347
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 60/275,980
PRIOR FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 195
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 177
LENGTH: 261
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(261)
US-09-864-921-177

Alignment Scores:
Pred. No.: 3.37e-63 Length: 261
Score: 485.00 Matches: 87
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.88% Indels: 0
DB: Gaps: 0

US-09-697-089-2 (1-1024) x US-09-864-921-177 (1-261)

QY 1 MetasnhelllelyasapnsersarAlaleullelnargmetGlymetHValle 20
DB 1 ATGATATTCTAAAGGACATAGCCGAGCCCTTATTCAGAAAGGAGATGACTGTATA 60

QY 21 LysglIntlerhraspaapleupheValTrrpasnValleusnarvgIuglValAsnile 40
DB 61 AAGCAATTCACAGATGACCTTATTGTATGGATCTTCTGAATCCGAGAAAGTAACATC 120

QY 41 IllecysCysglulysValIuglnAspAlaAlaarglyllelleHsMetlleLeulys 60
DB 121 ATTGCGCGGAGAGGAGGAGAGATGCTGCTAGAGGATCATTCATCATTTTGAAA 180

QY 61 LysglSerGluserCysasnleupheleulysSerleulysgluITrrpasnTyrProleu 80
DB 181 AAGGATTCAGAGTCTCTTACCTTTCTTAAATCCCTTAAGGAGTGAATCATCTCTTA 240

QY 81 PheglAspleuAsnlyGln 87
DB 241 TTTCAGGACTTGAAATGACAA 261

RESULT 15
US-09-864-761-4236
Sequence 4236, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 4236
LENGTH: 421
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC011232.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HEEL, SIGNAL = 16
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
US-09-864-761-4236

Alignment Scores:
Pred. No.: 2e-55 Length: 421
Score: 435.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.97% Indels: 0
DB: Gaps: 0

US-09-697-089-2 (1-1024) x US-09-864-761-4236 (1-421)

QY 928 GlyAlaphepheclylYAsnProleulysAsnPhedngInleuAsnleuAlaGlyAsn 947
DB 181 GGTCATTTTGGAAAGAACCTCTCAAAAATCTCCAGCATTTTGCGCGGAAT 240

QY 948 ArgValSerSeraspGlyITrpleuAlaPhewetGlyValPhegluasnleulysGlnleu 967
DB 241 CGGTGAGCAGTGTATGATGGCTTCTCATGCGTATATTGGAATCTTAAGCAATTA 300

QY 968 ValPhepAspPheSerThrlysgluPheleuProAspProAlaLeuValArglyLeu 987
|||||

Db 301 GTGTTTTGACTTAGTACTAAGAAATTTCTACCTGATCCAGCATTTAGTCAGAAACTT 360
Qy 988 SerGlnValLeuSerLysLeuThrPheLeuGlnGluAlaArgLeuValGlyTrpGlnPhe 1007
|||||
Db 361 AGCCAAGTGTATCCAGTTAACTTTCTGCAAGAAGCTAGGCTTGTTGGTGGCAATTT 420

Search completed: January 31, 2003, 11:43:49
Job time : 154 secs

THIS PAGE BLANK (USPTO)

Mon Feb 3 14:11:37 2003

US-09-697-089-2.p2n.rapn

Pending Nucleic Acid and/or Pending Amino Acid database searches now generate two sets of results. These databases were split into to two parts to reduce the time needed to update the databases daily. The split freed up more machine time for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions, **.rnpn** and **.rapn**
Searches run against the Amino Acid Pending database produce two sets of results, with the extensions, **.rapn** and **.rapn**

The Pending database search results should not be left in the case because they contain data that is confidential.

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 31, 2003, 10:46:26 : Search time 5176 Seconds

(without alignments)
4974.093 Million cell updates/sec

Title: US-09-697-089-2

Perfect score: 5459

Sequence: 1 MNFKDNRSLIQLMGMTVI.....MQFDDDLSTVITGAFKLVTY 1024

Scoring table:

PAM120	4.0	Xgapext 12.0
Xgapop	4.0	Ygapext 12.0
Fgapop	6.0	Fgapext 7.0
Delop	6.0	Delext 7.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

```
-Q-MODEL-frame+_p2n.model -DEV-xlh  
-Q-/cgn2.1/USPFO.spool/US09697089/runat_29012003.092505_19190/app-query.fasta.1.1223  
-DB-pending_patents_NA_Main -QEMT-fastap -SUFFIX-p2n.rnrm -MINMATCH=0.1  
-LOOCL=0 -LOOEXT=0 -UNITS-bits -START=1 -END=1 -MATRIX-pam120  
-TRANS-human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE-LOCAL -OUTFMT=ptc -NORM-ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER-US09697089 -GCCN_1_1_3843 -runat_29012003.092505_19190  
-NCPU=6 -ICU=3 -NO_XIPXY -NO_MAP -LARGEQUERT -NEG_SCORES=0 -WAIT -LONGLOG  
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=4 -XGAPEXT=12 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=4 -YGAPEXT=12 -DELOP=6 -DELEXT=7
```

Database :

```
1: Pending Patents_NA_Main:*  
2: /cgn2.6/ptodata/2/pna/PCRUS.COMB.seq:*  
3: /cgn2.6/ptodata/2/pna/US06.COMB.seq:*  
4: /cgn2.6/ptodata/2/pna/US07.COMB.seq:*  
5: /cgn2.6/ptodata/2/pna/US08.COMB.seq:*  
6: /cgn2.6/ptodata/2/pna/US081.COMB.seq:*  
7: /cgn2.6/ptodata/2/pna/US083.COMB.seq:*  
8: /cgn2.6/ptodata/2/pna/US084.COMB.seq:*  
9: /cgn2.6/ptodata/2/pna/US085.COMB.seq:*  
10: /cgn2.6/ptodata/2/pna/US086.COMB.seq:*  
11: /cgn2.6/ptodata/2/pna/US087.COMB.seq:*  
12: /cgn2.6/ptodata/2/pna/US088.COMB.seq:*  
13: /cgn2.6/ptodata/2/pna/US089.COMB.seq:*  
14: /cgn2.6/ptodata/2/pna/US090.COMB.seq:*  
15: /cgn2.6/ptodata/2/pna/US091.COMB.seq:*  
16: /cgn2.6/ptodata/2/pna/US092.COMB.seq:*  
17: /cgn2.6/ptodata/2/pna/US093.COMB.seq:*  
18: /cgn2.6/ptodata/2/pna/US094.COMB.seq:*  
19: /cgn2.6/ptodata/2/pna/US095.COMB.seq:*  
20: /cgn2.6/ptodata/2/pna/US095B.COMB.seq:*  
21: /cgn2.6/ptodata/2/pna/US095C.COMB.seq:*  
22: /cgn2.6/ptodata/2/pna/US095D.COMB.seq:*  
23: /cgn2.6/ptodata/2/pna/US095E.COMB.seq:*  
24: /cgn2.6/ptodata/2/pna/US096.COMB.seq:*  
25: /cgn2.6/ptodata/2/pna/US096B.COMB.seq:*  
26: /cgn2.6/ptodata/2/pna/US096C.COMB.seq:*  
27: /cgn2.6/ptodata/2/pna/US096D.COMB.seq:*  
28: /cgn2.6/ptodata/2/pna/US097A.COMB.seq:*
```

Result		Query		Match		Length		DB		ID		Description	
No.	Score	Match	Length	DB	ID								
1	5459	100.0	3072	1	PCT-US00-29643-3							Sequence 3, Appl1	
2	5459	100.0	3072	27	US-09-697-089-3							Sequence 3, Appl1	
3	5459	100.0	3072	32	US-09-841-739-3							Sequence 3, Appl1	
4	5459	100.0	3133	1	PCT-US00-29643-1							Sequence 1, Appl1	
5	5459	100.0	3133	27	US-09-697-089-1							Sequence 1, Appl1	
6	5459	100.0	3133	32	US-09-841-739-1							Sequence 1, Appl1	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

7 5453 99.9 3075 41 US-10-156-733-1 Sequence 1, Appl 1
8 5453 99.9 3219 41 US-10-156-733-14 Sequence 23, Appl 1
9 5448 99.8 3213 42 PCT-US01-07143-23 Sequence 13, Appl 1
10 5448 99.8 3213 42 US-10-221-097-23 Sequence 23, Appl 1
11 5441 99.7 3260 1 PCT-US01-14826-66 Sequence 66, Appl 1
12 5441 99.7 3260 26 US-09-667-298-66 Sequence 66, Appl 1
13 5438 99.6 3396 33 US-09-864-921-96 Sequence 96, Appl 1
14 5438 99.6 3545 18 US-09-491-404-1319 Sequence 1319, Ap
15 5438 99.6 3545 34 US-09-922-279-1319 Sequence 1319, Ap
16 5438 99.6 3545 34 US-09-922-279A-1319 Sequence 1319, Ap
17 5425 99.4 3396 27 US-09-686-347-96 Sequence 96, Appl 1
18 5188 95.0 3612 27 US-09-687-089-6 Sequence 6, Appl 1
19 5188 95.0 3612 32 US-09-841-739-6 Sequence 6, Appl 1
20 5188 95.0 3615 1 PCT-US00-29643-4 Sequence 4, Appl 1
c 21 5188 95.0 3615 1 PCT-US00-29643-6 Sequence 6, Appl 1
22 5188 95.0 3615 27 US-09-697-089-4 Sequence 4, Appl 1
c 23 5188 95.0 3615 27 US-09-697-089-12 Sequence 12, Appl 1
24 5188 95.0 3615 32 US-09-841-739-4 Sequence 4, Appl 1
c 25 5188 95.0 3615 32 US-09-841-739-12 Sequence 12, Appl 1
26 4030 73.8 6012 22 US-09-557-676-911 Sequence 911, App
27 4030 73.8 6012 22 US-09-557-676-917 Sequence 917, App
28 4030 73.8 6012 38 US-10-042-938-911 Sequence 917, App
29 4030 73.8 6012 38 US-10-042-938-917 Sequence 917, App
30 4023 73.7 2343 22 US-09-578-789-15 Sequence 15, Appl 1
31 4023 73.7 2343 22 US-09-579-240-15 Sequence 15, Appl 1
32 4020 73.6 3018 22 US-09-577-408-3077 Sequence 3077, Ap
33 4019 73.6 2415 22 US-09-578-789-17 Sequence 17, Appl 1
34 4019 73.6 2415 22 US-09-579-240-17 Sequence 17, Appl 1
35 3950 72.4 2215 1 PCT-US01-07143-22 Sequence 22, Appl 1
36 3950 72.4 2215 42 US-10-221-097-22 Sequence 22, Appl 1
37 3785 69.3 3890 22 US-09-577-408-3078 Sequence 3078, Ap
38 3735 68.4 4098 22 US-09-557-676-906 Sequence 906, App
39 3735 68.4 4098 22 US-09-557-676-912 Sequence 912, App
40 3735 68.4 4098 38 US-10-042-938-906 Sequence 906, App
41 3735 68.4 4098 38 US-10-042-938-912 Sequence 912, App
42 3566 65.3 3435 80 US-60-360-207-4654 Sequence 4654, Ap
c 43 3543 64.9 2002 38 US-10-039-386-25135 Sequence 25135, A
44 3543 64.9 6900 22 US-09-578-789-73 Sequence 73, Appl 1
45 3543 64.9 6900 22 US-09-579-240-73 Sequence 73, Appl 1

ALIGNMENTS

RESULT 1
PCT-US00-29643-3
Sequence 3, Application PC/TUS0029643
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
FILE REFERENCE: 07334-136W01
CURRENT APPLICATION NUMBER: PCT/US00/29643
CURRENT FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/161, 822
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 3072
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US00-29643-3

Alignment Scores:

Pred. No.: 0 Length: 3072
Score: 5459.00 Matches: 1024
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-697-089-2 (1-1024) x PCT-US00-29643-3 (1-3072)

QY 1 Metaspheiletyaspasnserserargalaleuileglnargmetglmetthrvalle 20
DB 1 ATGATTTTCATAAAGGACAAATAGCGCCCTTATTCAAAGAAATGGGAATGACGTGTATA 60
QY 21 Lysglnliethrnpaspleuphevaltrpnsvalleuasnarglglvalasntle 40
DB 61 AAGCAAAACAGAGACCTATTTGTATGATGTCTGAAATCGGAGAAAGTAAACATC 120
QY 41 Ilecyssgylulysvalglnglnasplalaarglylleilehismetileuleus 60
DB 121 ATTTCCTCGAGAGAGTGGAGCAGGATCTCTGTAGAGGATCATTCATATTTTGA 180
QY 61 Lysglisergiusersyasnleupheuleusserleulysglutrpasntrypoleu 80
DB 181 AAGGTTACAGAGTCTGTAACTCTTCTTAATCCCTTAAGAGAGTGAATATCTCTTA 240
QY 81 Pheglaspheleasnlglnserleuphehnslntrhserrgluglyaspheuaspsp 100
DB 241 TTTCAGGACTTGAAAGCAAGAGTCTTTTCATCAGACATCAGAGGAGCTTGAGCAT 300
QY 101 Leualaglnaspleuylaspheutyrhistrproserpheleuasphetyrproleu 120
DB 301 TTGGCTCAGCATTTTAAAGACTTGACCATACCCATCTTTCTGAATTTATCCCTT 360
QY 121 Glylunaspleuaspleilepheasleuleusserthrphetrgluprovallleutrp 140
DB 361 GGTGAAGATATGACATTAATTTTAACTTGAAAGACCTTCACAGAACCTGCTCTG 420
QY 141 Argylsasrglnhshishisargvalglnglnleutrlleuasnglyleuleuglnla 160
DB 421 AGGAAGGACCAACACATCACCGCGTGAGAGCTGACCTGAAATGGCTCTCTGAGGCT 480
QY 161 Leuglnserprocyllleileglnglylsuerglylsygllysserthrleuleugln 180
DB 481 CTTCAGACCCCTGTATGATTAAGAGGGAATCTGGCAAGGCAAGTCACCTCTGAG 540
QY 181 Argllleamettretrgllyserglyscylsalsaleutrllyspheleupheval 200
DB 541 CGCATTCGCAATGCTCTGGGCGCTCGGAAAGTGCAAGGCTCGACCAATGTTAAATTC 600
QY 201 Phepheleuarglseuserargalaglnglyleupheglutrlleucysaspglnleu 220
DB 601 TTCTTCCTCCGCTCTAGAGAGGCGCCAGGCTGACTTTTGAACCTCTGTGATCACTC 660
QY 221 Leuasplleproglythrilearglysglnthrphemetalemetleuleusleuarg 240
DB 661 CTGCATATACCTGGCACAATCAGAGACATTCATGCGCATGCTGTAACCTGCGG 720
QY 241 Glnarvalleupheleuleuaspllytyrasngluupheylsproglnasnscysproglu 260
DB 721 CAGAGGGTCTTTCTCTCTTGATGGCTPACATGATGATTCAGCCCAAGCTGCCAGAA 780
QY 261 Ileglualaleuleileysgluasnhisargpheylsasmetvallevalthrthr 280
DB 781 ATCGAAGCCCTGATTAAGAAACACCGCTTCAGAAACATGGTCATCGTACCCATACC 840
QY 281 Thrglucysleuarghisileargglnpheglialaleutrhralagluvalglyaspket 300
DB 841 ACTGAGTCCGTGAGCACAATACGAGGAGTTGTGCTGCTGACTGCTGAGAGTGGGGAATG 900
QY 301 Thrgluaspserserlagnalaleuleileargglvalleuleileysgluleualaglucly 320
DB 901 ACAGAAAGACAGCGCCAGGCTCTCTCCGAGAAAGTCTGATCAGAGACTTGCTGAAGGC 960
QY 321 Leuleuleuglnilegllysserargcysleuarasleumetleuthrproleuphe 340
DB 961 TTGTGCTCCAAATTCACAAATCCAGGTGCTTGAGGAATCTCATGAAAGACCCCTCTCTT 1020
QY 341 Valvalliethrcysalaleileglmetgllylsuergluuphehnserrhistrglinthr 360
DB 1021 GTGGTCATCACTGTGTGCAATCAGATGGGTGAAGTGAATGATTCACATCTCACACAAACA 1080
QY 361 Thrleuphehistrphetyraspleuleuleileglnlysasnllyshislyshislysgly 380

|||||
Db 1081 ACCGCTTCACATCTTATGATCTGTGATACAGAAAAACAACAACTAAGGT 1140
QY 381 ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGly 400
Db 1141 GTGGCGCAAGGACCTTCCTGGACCTGGACACTGTGGACACTTCTGGAGGGGT 1200
QY 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420
Db 1201 GGTCTTCCACACAGTTTATTTCCAGCTGACAGATGTCTCCAGCTGATGAGATGTC 1260
QY 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440
Db 1261 CTGGCTGACAACTGGGCTCTCTGTAAATATACAGCTCAAGGTTCAAGCCAAAGTATATA 1320
QY 441 PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgLeuSerSerLeuLeuThr 460
Db 1321 TTCTTTCACAAAGTCATCTCAGAGGTACACAGCAGAGCAAGACTTCAGAGTTTATGAGC 1380
QY 461 SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480
Db 1381 TCTCATGACCGACAGAGGAGGTGACCAAGGGAGTGTACTTGCAGAAAAATGGTTCCATT 1440
QY 481 SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500
Db 1441 TCGGACATTAACATCCACTATACAGCTGCTCGGTACACCTGGGTGATCTGTGAA 1500
QY 501 AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly 520
Db 1501 GCCACAGGGGCTGTATGAGGACCTCGCAGCAGCTATCACACGCGTCCCTTCGGGA 1560
QY 521 LeuSerIleAlaLysArgProLeuThrPargGlnGluSerLeuGlnSerValLysAsnThr 540
Db 1561 CTTTCATGCGCCAAAGAGGCTCTCTGAGACAGGAATCTTGCAGAGTGGAACAAACCC 1620
QY 541 ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560
Db 1621 ACTGACACAGAAATCTGAAAGCCATAAACATCAATCTTGTGTAAAGTGGCACTCATT 1680
QY 561 LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln 580
Db 1681 TTATATCAAGAGAGTACATCCAAATCAGCCCTGACGCAAGAAATTTGAACTTCTTCAA 1740
QY 581 GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPheGlu 600
Db 1741 GGTAAAGCTTATATATCACTCAGGGAACATCCCGATTACTTATTTACCTTCTTGA 1800
QY 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyAla 620
Db 1801 CATTTCGCCAATTTGTCAGAGTCTCTGCACTTCATTAACTGGACTTTTATGGGGAGCT 1860
QY 621 MetAlaSerTyrGluLysAlaAlaGluAspThrGlyGlyIleHisMetGlnGluAlaPro 640
Db 1861 ATGGCTTCATGAGGAAAGGCTGACAGAGACACAGGTGAATCCACATGGAAGGAGCCCA 1920
QY 641 GluThrTyrIleProSerArgAlaValSerLeuPhePheAsnTyrLysGlnGluPheArg 660
Db 1921 GAAACCTACATTCACAGCGGCTGTATCTTGTCTTAACTGGAAGAGCAATTCAG 1980
QY 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu 680
Db 1981 ACTCTGAGAGTCACACTCGGGGATTTTCACAGAGTTGAATTAACCAATATCATATCTG 2040
QY 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700
Db 2041 GGGAAATATTCAGCTCTGCCAAGAGCCCTCAGGCTGCAATTAAGAGAGTCTGCTGTG 2100
QY 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu 720
Db 2101 GCTGGAAGCTCAGTGTGCTCTCAGACCTGTAAAGAAATTTATCTCTCATGGGGAA 2160
QY 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740
|||||

Db 2161 GCCAGTCCCTTCACCATAGAGATGAGAGCACATCATCTGTATAACAACTGAAACCC 2220
QY 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyIleuThrAspSerLeuGly 760
Db 2221 TTGAGTATTCATGACCTTACAGAAATCAAGCGCTCCGGGTGCTGTGACTCAGACGTTGGGT 2280
QY 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluAspAla 780
Db 2281 AACTTAAGACCTTCAAAAGCTCATATGATGATACATTAAGATGAATGAGAGATGCT 2340
QY 781 IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800
Db 2341 ATAAACATGCTGCAAGGCTGAAAAACCTGAAGAAAGATGTTATTTATTCATTGACCCAC 2400
QY 801 LeuSerAspIleGlyLysLeuLysMetAspTyrIleValLysSerLeuSerSerGluProCys 820
Db 2401 TTGCTGTGACATTTGGAAGGAAATGGATTCATATGATCAATGCTCTGTCAAGTGAACCTGT 2460
QY 821 AspLeuGluGluIleGlnLeuValSerCysLysSerAlaAsnAlaValLysIleLeu 840
Db 2461 GACCTTGAAGAAATTCATATTAATGATCTCTCTGCTTCTGTCCAAATCAGTGAACATCTTA 2520
QY 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860
Db 2521 GCTCAGAAATCTCACAAATTTGGTCAAACTGACGATTCCTTGATTTATCAGAAATTTACCTG 2580
QY 861 GluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGln 880
Db 2581 GAAAAAGATGGAATTAACCTCTTCATGAACTGATCGAAGATGAACCTGTAGAACAG 2640
QY 881 LeuThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900
Db 2641 CTCACCGCATGATGCTGCTGCGGCTGTGAGCTGACATGCAAGGACGCTGAGCACTGTGG 2700
QY 901 LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrPargLeuThr 920
Db 2701 AAACATTTGAGAGAGTCCACAACTGTCAGAGCTTGGGTGAAAAACCTGGAGACTCACA 2760
QY 921 AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940
Db 2761 GATACAGAGATTAAGAAATTTAGGTGATTTTGGAAACACCTCTGAAAAACCTCCAG 2820
QY 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrLeuAlaPheMetGlyVal 960
Db 2821 CAGTTGAATTTGGCGGGAATGCTGTGACACAGTATGATGCTTGCCTTCAATGGGTGTA 2880
QY 961 PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980
Db 2881 TTGGAAATCTTAAGCAATTAGTGTTTTGACTTATGACTTAAGAAATTTTCACTGAT 2940
QY 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla 1000
Db 2941 CCAGCATTTAGTCAGAAACCTTAGCCCAAGTGTATCCAACTTAACCTTCTGCAAGAGCT 3000
QY 1001 ArgLeuValGlyTyrGlnPheAspAspAspAspLeuSerValIleThrGlyAlaPheLys 1020
Db 3001 AGGCTTGTGGGGCAATTTGATGATGATCTCAGTGTATTAACAGCTGCTTTTAAA 3060
QY 1021 LeuValThrAla 1024
Db 3061 CTAGTACTGCT 3072

RESULT 2
US-09-697-089-3
; Sequence 3, Application US/09697089
; GENERAL INFORMATION:
; APPLICANT: Robison, John
; APPLICANT: Robison, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-136001
; CURRENT APPLICATION NUMBER: US/09/697,089
; CURRENT FILING DATE: 2000-10-26

PRIOR APPLICATION NUMBER: US 60/161,822
: PRIOR FILING DATE: 1999-10-27
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 3072
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-697-089-3

Alignment Scores:
Pred. No.: 0 Length: 3072
Score: 5459.00 Matches: 1024
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-697-089-2 (1-1024) x US-09-697-089-3 (1-3072)

QY 1 Metaspheilelyaspasnserrargalaleuileglnargmetglymethrvalile 20
DB 1 ATGATTTTCATTAAGACATATGCGGAGCCCTTATCAAGATGGAGATGCTTTATA 60
QY 21 Lysglnliethraspaspheulepheyvaltrpasmvalleuasnarvglugluvalasnlle 40
DB 61 AAGCAAAATCACAGATGACCTATTGTATGAGATGTTCGAATCGCGAAGAACTAAACATC 120
QY 41 Ilecyscsgluylvalgluglnasppalaiaargglyllelehismetlleuuls 60
DB 121 ATTCTCTCGAGAGAGTGGAGAGATGCTGCTAAGAGGATCATTCACATGATTTGAAA 180
QY 61 Lysgilyserglusercysasnleupheuleuylserrleuylsrlutrpasntrprouleu 80
DB 181 AAGGCTTCAGAGTCTCTTAACCTCTTCTTAATCCCTTAAGAGAGTGAACATATCCTCTA 240
QY 81 Pheglnasppleuasnglylnserleuphehisglntrsergluylasppleuaspp 100
DB 241 TTTCAGGACTTGATGGAAGAGTCTTTTTCATCAGACATCAGAGAGACTTGAGCAGT 300
QY 101 Leualaglnasppleuylasppleuylrhisrtrpserpheleuasppheleuylprouleu 120
DB 301 TTGGCTCAGAGATTTAAAGAGACTTGTACCATACCCCATCTTTTCTGAACCTTTATCCCTT 360
QY 121 Glylunasppilleaspillelepheasnleuylserrtrphefthgluprovalleutrp 140
DB 361 GGTGAAGATATTGACATATTTTTAACTTGAAGAACACCTTCACAGAACCTGCTCTGCG 420
QY 141 Arglyasppglnhisishisargvalgluglnleutheuasnglyleuendlnala 160
DB 421 AGGAAGAGACCAACACCATCACCGCTGGAGCAGCTGACCTGAATGGCTCTGACAGGCT 480
QY 161 Leuglnserprocyisleilegluglyluserglylsglylserrthreuleugln 180
DB 481 CTTGAGAGCCCTTGATCATTTGAAGGGAATGTGGCAAGGAATCCCATCTGCTGCAG 540
QY 181 Argillealmetleutrpgllyserglylscyslysalaaleutheulyspheyval 200
DB 541 CGCATTCGCATCTCTGGGGCTCCGGAAGTCAAGGCTCTGACCAAGTTCAAAATTCGTC 600
QY 201 Phepheleuarargleuserargalaglmglylleupheglutheuleucysasppgleu 220
DB 601 TTCTTCCCTCCCTCAGAGAGGCCAGGGTGGACTTTTGAAGCCCTCTGTGATCAACTTC 660
QY 221 Leuasppileproglythrilearglysglntrpmetalemetleuendleuylsuar 240
DB 661 CTGGATATACCTGCACATATCGAAGACAGACATTCATGGCCATCTGCTGAAGCTGCGG 720
QY 241 Glnarqvalleupheleuleuasppglytyrasngluupheylsproglinasncysprou 260
DB 721 CAGAGGGTCTTTCTCTTCTTGATGGCTACATGATTCATCAAGCCCAAGACAGCCAGAA 780
QY 261 Ileglnalaleuileylsgluasnhisargpheylsasmetvalilevalthrthrthr 280

DB 781 ATCGAAGCCCTGATTAAGAAACACCGCTTCAAGAACATGAGTCATGCCACATAC 840
QY 281 Thrglucysleuararghisillearglnpheglylaleutrralaglvalglyaspmet 300
DB 841 ACTGAGTCCCTGAGGACATATGGGAGTTGTGCTGCCCTGACTGCTGAGGTGGGGAATG 900
QY 301 Thrgluasppseralaglnalaleuilearggluvalleuileuylsglyleuadlaglucly 320
DB 901 ACAGAAAGACAGGCCGCCAGGCTCTCATCCGAGAAAGCTGATCAAGAGGACTTGGAAGGC 960
QY 321 Leuleuendglnlleglinlyserrargcysleuarargasnleumetlysthrprouphe 340
DB 961 TTGTGTCCCAAAATTCAGAAATCCAGGCTTGGAGGAATTCAGAGAACCCCTCTCTT 1020
QY 341 Valvaliethrcysalaileglnmetglylusergluphehisserhissthrglthr 360
DB 1021 GTGCTCATCACTTGTGCATTCAGATGGGTAAAGTGAAGTCCACTCTCACACACAAACA 1080
QY 361 Thrleuphehisrthrpheleuylasppheuleuileglnlysasnlyshislyshislysgly 380
DB 1081 ACGCTGTTCCATACCTCTATGATCTGTGATACGAAACAAACACAAACATTAAGGT 1140
QY 381 Valalaialaserasppheilleargserleuasphiscysglyasppheualaleuylucly 400
DB 1141 GTGGCTGCAAGTACTTCATTCGAGCCTGAGCACCTGTGAGACCTGATGCTGAGAGGT 1200
QY 401 Valpheaserhislyshisphaspphegluleuglnasppalasersevalasngluasppal 420
DB 1201 GTGTTCTCCCAACAGTTGATTTGCAACTGCAGAGATGTCTCACGCTGAATAGAGATCTC 1260
QY 421 Leuleuthrthrghlyleuleucyslysttythrallaglnargpheylsprolysttylys 440
DB 1261 CTGCTGACAACTGGGCTCTCTGTAAATATACAGCTCAAGGTTCAACCCAAAGATATAA 1320
QY 441 Phephehislysserpheglnglutrythrallaglyargyleuserseleuethr 460
DB 1321 TTCTTTCAAGTCAATTCAGAGAGTACACAGCAGACAGCAAGACTGAGATTTATGACG 1380
QY 461 Serhisgluproglylvalthrlysglyasnlytyrleuglnlysmetvalserille 480
DB 1381 TCTCATGAGCCAGAGAGAGTGCACAAAGGAGATGTTACTTGCAAAAGTGTTCATTT 1440
QY 481 Serasppilethrserrthryrserseleuethrarglytrhrcysglysersevalglu 500
DB 1441 TCGGACATTTACATCCATTAAGACGCTGCCGTACCTGGGTGCTATCTGTGGAA 1500
QY 501 AlaThrargalavalmetlyshisleuilaalavaltyrglnhisglycysleuendly 520
DB 1501 GCCACAGGCGCTGTATGAGACACCTCGAGAGGTATACACACAGGCTGCTCTTCGGA 1560
QY 521 Leuserillealalyasrproleutrparglngluserleuglnservallysasnthr 540
DB 1561 CTTTCATCGCCCAAGAGGCTCTCTGAGACAGGAATTTTGCAAAAGTGAACAAACGCC 1620
QY 541 Thrgluglngluilleuulysalalleasnleasnserphevalglucysglyllehis 560
DB 1621 ACTGAGCAAGAAATTCGAAAGCCATTAACATCAATCTCTTGTGAAGTGTGGATCCAT 1680
QY 561 Leutryglnluserthrseryseralaleuuserglnluphegluilaalphehegln 580
DB 1681 TTATATCAAGAGATACATCAAAATCACCCCTGAGCCCAAGATTTGAAGCTTCTTTCAA 1740
QY 581 Glylysserleuylrileasnserglysnlileproaspyrleupheasppheheglu 600
DB 1741 GGTAAACACTTATATATCACTCAGGGAACATCCCGATTTACTTATTTGACTTCTTTGAA 1800
QY 601 Hisleuproasnycysalaseralaleuasppheilleuylsleuasppheleuylglyala 620
DB 1801 CATTTGCCCAATTTGGCAAGTCTGTGACTTCAATTAACATGAGACTTTATAGGGGAGCT 1860
QY 621 Metaliasertrpgluylalalaglulaspthrghlyllehismetglugluapro 640

Db 1861 ATGGCTTCATGGGAAAAGGCTGCAGAGACACAGGTGGAATCCACATCGAAGAGGCCCA 1920
QY 641 GtUThrTyrlleProSerArgAlaValSerLeuPheAsnTrpIysGlnIupheArg 660
Db 1921 GAAACCTACATTTCCACGACGGGCTGATTTCTTCTTAACCTGGAAGACGAAATTCACG 1980
QY 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrlleu 680
Db 1981 ACTCTGGAGGTCACACCTCGGGATTTTCACCAAGTTGAATACAGATATCATATCTCG 2040
QY 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700
Db 2041 GGGAAATAATTACGCTTCGCCACAGCCCTCAGCTGCAAAATGAAGATGCTCGTGTCG 2100
QY 701 AlaGlySerLeuSerLeuValLeuSerTrpCysLysAsnIleLysSerIleuValGlu 720
Db 2101 GCTGGAGCCTCAGTTTGGTCTCTCAGCCCTGTAAAGAACATTTATCTCTCATGGGGAA 2160
QY 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740
Db 2161 GGCAGTCCCTCACCACATGAAGATGAGAGGCACATCACAATCTGTAAACAACCTGAAAAAC 2220
QY 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 760
Db 2221 TTGAGTATTCATGACCTACAGAAATCAACGGCTGCCGGGTGGTCTGACTGACAGCTTGGGT 2280
QY 761 AsnLeuLysAspLeuThrLysLeuIleMetAspAsnIleLysMetAsnGlnLysAla 780
Db 2281 AACCTTGAAAGAACCTTCAAAAGCTCATAAATGATTAACATGAATGAATGAATGAATGCT 2340
QY 781 IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800
Db 2341 ATAAAGACTAGCTGAAGGCTGAAAAACCTGAAGAGATGTGTTATTCATTGACCCAC 2400
QY 801 LeuSerAspIleGlyGlnGlyMetAspTrpIleValLysSerLeuSerSerGluProCys 820
Db 2401 TTGTCTGCATTTGAGAGGGAATGATGATACATAGTCAAGTCTCTGCAAGTGAACCTGT 2460
QY 821 AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840
Db 2461 GACCTTGAAAGAAATCATATGCTCTGCTGCTGCTGCTGCAAAATGCAAGTGAATTCCTA 2520
QY 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGlnAsnTrpLeu 860
Db 2521 GCTCAGAAATCTTCACAAATTTGGTCAAACTGACATCTTGATTTATCAGAAATATACCTG 2580
QY 861 GtUlysAspGlyAsnGlnAlaLeuHisGluLeuIleAspArgMetAsnValLeuGln 880
Db 2581 GAAAAAGATGGAAATGAAGCTCTTCATGAACATGATCGACAGCATGAAGCTGTACAGAC 2640
QY 881 LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeu 900
Db 2641 CTCACCGCACTGATCTGCTGCGGGCTGTGTGACGTGCAAGGAGGCTGAGCGCTGTG 2700
QY 901 LysHisLeuGluGlnValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThr 920
Db 2701 AAACATTTGGAGAGGAGTCCCAACTCGTCAAGCTTGGGTTGAAAACTGAGACTCACA 2760
QY 921 AspTrpGluIleArgIleLeuGlnAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940
Db 2761 GATACAGAGATTTGAATTTTGTAGCTCATTTTGTGAAGAACCCCTGTGAAAACTTCCAG 2820
QY 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyVal 960
Db 2821 CAGTTGAATTTGGCGGAAATCGTGTGACAGTGTGATGAGCTTGCTTCATGGGTGTA 2880
QY 961 PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980
Db 2881 TTTGAGATCTTAAACAAATTTAGTGTGTTTGTGACTTAGACTAAAGAAATTTCTACCTGAT 2940
QY 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnAla 1000
Db 2941 CCAGCATTTAGTCGAAAACTTAAAGCCAGGTGTTATCCAAAGTAACTTTTCTGCAAGAACCT 3000

QY 1001 ArgLeuValGlyTrpGlnPheAspAspAspLeuSerValIleThrGlyAlaPheLys 1020
Db 3001 AGCTTTGTTGGGTGGCAATTTGATGATGATGATCTCAGTGTATTATACAGGTCTTTTAA 3060
QY 1021 LeuValThrAla 1024
Db 3061 CTAGTAACTGCT 3072
RESULT 3
US-09-841-739-3
; Sequence 3, Application US/09841739
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/09/841,739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3072
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-841-739-3
Alignment Scores:
Pred. No.: 0 Length: 3072
Score: 5459.00 Matches: 1024
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 32 Gaps: 0
US-09-697-089-2 (1-1024) x US-09-841-739-3 (1-3072)
QY 1 MetAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetCylMetThrValIle 20
Db 1 ATGAATTTTCATAAAGACATAGCCGAGCCCTTATTCAAAGAAATGGAATGACTGTATATA 60
QY 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGlnValAsnIle 40
Db 61 AAGCAAAATCAGATGACCTATTTGTATGGAATGTTCTGAATCGCGAAGAAAGTAAACATC 120
QY 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
Db 121 ATTTCCTCGAAGAAAGCTGAGAGCATGCTGCTAGAGGATCATTCACATGATTTTGAATA 180
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTrpProLeu 80
Db 181 AAGGTTTCAGACTCCTGTAAACCTCTTCTTAAATCCCTTAAGAGATGGAACATATCCTTA 240
QY 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluLysAspLeuAspAsp 100
Db 241 TTTTCAGACTGATGAGCAAAAGCTTTTTCATTCAGACATCAGAAAGAGACTTGGACAT 300
QY 101 LeuAlaGlnAspLeuLysAspLeuTrpHisThrProSerPheLeuAsnPheTrpProLeu 120
Db 301 TTGGCTCAGAGATTTAAAGACTGTGACATACCCCATCTTTTCTGACATTTTATCCCTT 360
QY 121 GlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTrp 140
Db 361 GGTGAAGATATTGACATTAATTTTAACTTGAAMACACCTTCACAGAACTGTCTGTGG 420
QY 141 ArgLysAspGlnHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla 160
Db 421 AGGAAGGCAACACCATCACCGGCTGAGAGCAAGCTGACCTGTGAATGCTCTCTGAGGCT 480
QY 161 LeuGlnSerProCysIleIleGluGlyLysSerGlyLysSerThrLeuLeuGln 180

|||||
Db CTTAGAGCCCTGCATCATTTGAAGGGGAATCTGGCAAGCAAGCTCCACTGCTGCAG 540
Qy ArgileamelleupTpgLysSerGlyLysCysLysAlaLeuThrLysPheLysPheVal 200
Db CGCATGGCAATGCTCTGGGGCTCCGGAAAGTGCAGAGCTCTGCACCAAGTTAAATTCCTC 600
Qy PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 220
Db TTTCTTCCTCCGCTCAGCAGAGGGCCAGGGTGAGCTTTTGAACCCCTGTGATCAACTC 660
Qy LeuAspLlePheProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 240
Db CTGATATATACCTGGCAGCAATCAGGAAGCAGCAATTCAGGCAAGCTCTCAAGCTGGGG 720
Qy GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 260
Db CAGAGGGTCTTTTCCTTCCTTCGATGCGTACAAATGATTCAGGCCCAAGACTGCCAGAA 780
Qy IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr 280
Db ATCGAAGCCCTGATTAAGAAACACCGCTTCAAGAACATGATCATGCTCACCCTACC 840
Qy ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300
Db ACTGAGTCCCTGAGGCAATCAGGAGGAGTTGTGCTGCTGCTGAGCTGAGGAGTATG 900
Qy ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGlnGly 320
Db ACAGAAAGCAGCGCCCAAGGCTCTCATCCGAAAGATGCTGATCAAGAGACTTGCTTAAGC 960
Qy LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340
Db TTGTGTGCTCCAAATTCAGAAATCCAGGTGCTTGAAGAAATCATGAAGACCCCTCTCTT 1020
Qy ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr 360
Db GTGGTCATCACTGTGCAATCAGATGGGTGAAGTGAATGCTCCACTCCACACACAAACA 1080
Qy ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysGly 380
Db ACCGCTTCATCACTCTTATGATCTGTGATACGAAACAAACAAACATTAAGCT 1140
Qy ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGlnGly 400
Db GTGGTCGCAAGTCACTTCAATTCGAGGCTGAGCCACTGTGGAGACTGCTGTGAAGGT 1200
Qy ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420
Db GTGTTCCTCCACAACTTGTGATTTCCAACTGCAAGTGTGCTCAGAGGTGAATGAGATGCTC 1260
Qy LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440
Db CTGCTGCAACTGCGGCTCTCTCTGTAATATATACAGCTCAAAAGTTCAACCAAGTATTA 1320
Qy PhePheHisLysSerPheGlnGluThrIleArgAlaGlyArgArgLeuSerSerLeuLeuThr 460
Db TTTCTTTCACAAGTCACTTCAGAGATACACAGAGACAGCAAGACTGATTAATTTAGCG 1380
Qy SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480
Db TCTCATGAGCCAGAGAGAGTGCACAAAGGGAATGCTTACTTGCACAAATGGTTTCCATT 1440
Qy SerAspLleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500
Db TCGGACATTAATCACTTAATAGCAGCTGCTCGGTACCTGCGGTCACTCTGTGAA 1500
Qy AlaThrArgAlaValMetLysHisLeuAlaValTyrGlnHisGlyCysLeuLeuGly 520
Db GCCACAGAGGCTGTTATAGACACCTCGCAGCAGTATCAACAGGGTGCCTTCTCGGA 1560
Qy LeuSerIleAlaLysArgProLeuThrParGlnGluSerLeuGlnSerValLysAsnThr 540
|||||

Db CTTTCATCGCCAAAGGCTCTCTGAGACAGGAATCTTTGCAAGTGTGAAAAACACC 1620
Qy ThrGluGlnGluIleLeuValAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560
Db ACTGAGCAGAAATTTGAAAGCCATTAACATCAATTCCTTTGTAGATGTGGCATCAT 1680
Qy LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln 580
Db TTATATCAAGAGATACATCCAAATCAAGCCCTGAGCCCAAGAAATTTGAAGCTTCTTCAA 1740
Qy GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhePheGlu 600
Db GGTAAAGCTTATATATCACTCAGGGGAACATCCCGATTAATCTTATTTGACTTTTGA 1800
Qy HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyValAla 620
Db CATTTGCCCATTTGTGCAAGTGCCTGAGCTTCAATTAACAGGACTTTTATGGGGAGCT 1860
Qy MetLaserTpgLysAlaIleGluAspThrGlyGlyIleHisMetGluGluAlaPro 640
Db ATGCTTCATGGAAGGCTGAGAGACACAGGTGGAATCCACATGGAAGAGGCCCA 1920
Qy GluThrTyrLleProSerArgAlaValSerLeuPheAsnThrPylsGlnLupheArg 660
Db GAAACCTAATTCCTCAGCAGGGGCTGTATCTTGTCTTCAACTGGAAGCAGGAATTCAGG 1980
Qy ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspLleThrTyrLeu 680
Db ACTGTGAGGTCACACTCCGGGATTTGACAAAGTTGAATAGCAAGATATCACTATCTG 2040
Qy GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700
Db GGGAATAATATCACTCTGCCACAAAGCTCAGCTGCAAAATTAAGATGCTGCTGCTG 2100
Qy AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu 720
Db GCTGGAACCTCAGTGTGCTCAGCACCCTGTAAGAACTTATATCTCTATGAGTGA 2160
Qy AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740
Db GCCAGTCCCTCCACCATTAAGATGAGGAGGACATCACTGTGTAACAACTGAAACCC 2220
Qy LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 760
Db TTTGATATTCATGACCTCAAGATCAACGCGCTCGGGGTGCTGACTGACGACTGGGT 2280
Qy AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetLanGluLysAla 780
Db AACTTGAAGAACTTACAAAGCTCATATGATGAATGAATGAATGAAGAGATGCT 2340
Qy IleLysLeuAlaGlnGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800
Db ATAAACATAGCTGAAGGCTGAAAAACCTGAAGAAGATGTGTTATTTCAATTTACCCAC 2400
Qy LeuSerAspIleGlyGlnGlyMetAspTyrIleValLysSerLeuSerSerGluProCys 820
Db TTTGCTGACATTTGGAGAGGAATGATTAATACATAGCAAGTCTCTGCAAGTGAACCTGT 2460
Qy AspLeuGlnGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840
Db GACCTTGAAGAAATTCATTTGCTCTCGCTGCTGTCTGCAAAATGCAAGTGAATAATCTTA 2520
Qy AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860
Db GCTGGAATCTTTCACAAATTTGTCAAACTGAGCATTTGTGATTTATCAAGAAATTAACCTG 2580
Qy GluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGlnGln 880
Db GAAAGATGGAATGAAGGCTTTCATGACTGATCGCAGAGATGAAGAGCTGTAAGACAG 2640
Qy LeuThrAlaLeuMetLeuProTpgLysAspValGlnGlySerLeuSerSerLeuLeu 900
Db CTAACCGCACATGATGCTGCTCTGGGGCTGTGACGTGCAAGGCAAGCTGAGAGCTGTG 2700

QY 901 LYSHISLEUGLNUVALPROGLNLEUVALYSLLEUGLYLEUYSASNTTPARGLEUTHR 920
| | | | |
DB 2701 AAMCATTTGGAGAGAGTCCACACACTGCTACACTTGGGTGAAACCTGGAGACTACAC 2760
QY 921 ASPTHRGLULIENRGLILEUGLYALAPHEPHEGLYLSASNPROLEUYSASNPHEGLN 940
| | | | |
DB 2761 GATACAGAGATTGAAATTTAGTGCATTTTGGAAAGAACCTCTGAAACAACTTCCAG 2820
QY 941 GINLEUASNLEUALAELYSANARGVALSERSERASPGLYTRPLEUALAPHEMETGLYVAL 960
| | | | |
DB 2821 CAATTGAATTTGGCGGGAATCTGTGACACAGATGATGCGCTTCCATCAAGGGGTGA 2880
QY 961 PHEGLASNLEUYSGLNLEUVALPHEPHEASPHESERTHRYSGLUPHELEUPROASP 980
| | | | |
DB 2881 TTTGACAACTTACAGCAATTAAGTGTGTTTGGACTTACACTTACAAATTTTCACTGAT 2940
QY 981 PROALALEUVALARGYLSLEUSERGINVALLEUSERYLSLEUTHRPHLEUGINGUALA 1000
| | | | |
DB 2941 CCAGCATTTAGTCAGAAACTTACCAAGTGTATCCAAAGTTACTTTCTGCAAGAAGCT 3000
QY 1001 ARGLEUVALGLYTRPGINPHEASPAASPASPSEUSERYALLIETHRGYALAPHELYS 1020
| | | | |
DB 3001 AGCGTTGGTGGGGCAATTTGATGATGATCTCAGTGTATACAGTCTTTTAA 3060
QY 1021 LEUVALTHRALA 1024
| | | | |
DB 3061 CTGATCACTGCT 3072

RESULT 4
PCT-US00-29643-1
; Sequence 1, Application PC/TUS0029643
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-136W01
; CURRENT APPLICATION NUMBER: PCT/US00/29643
; CURRENT FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3133
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)...(3107)
PCT-US00-29643-1

Alignment Scores:
Pred. No.: 0 Length: 3133
Score: 5459.00 Matches: 1024
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-697-089-2 (1-1024) x PCT-US00-29643-1 (1-3133)

QY 1 MetASNPhelIElySAspAsnSerArgAlaLeuILEGLIARMeTcJLWETHRVAlIle 20
| | | | |
DB 36 ATGAATTTTATTAAGACAAATAGCCGAGCCCTTATTCCAAGATGGGAATGACTGTTATA 95
QY 21 LYSGLINLEIThrAspAspLeuPheValITRPASNVALLEUASNARGGLNUVALASNILE 40
| | | | |
DB 96 AAGCAATATCAGAGATCACTATTGTAATGTAATGTTCTGAATCGCAAGAGTAACATC 155
QY 41 IIECYSGCYGLULYSVALGLUNASPALAALARGLYIIEIIEHISMETIIELEULYS 60
| | | | |
DB 156 ATTGCTCGAGAGAGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGAA 215

QY 61 LYSGLYSERCIUSERCYSASNLEUPHELEULYSERLEULYSGLINTRPASNITRPROLEU 80
| | | | |
DB 216 AAGGCTTCAGAGTCCTGTATCACTCTTTCTTAATCCCTTAAGAGTGAATCTTACTTA 275
QY 81 PHEGLASNLEUASNGLINSERLEUPHEHISGLINTHRSEUGLUYSLPEUASNPASP 100
| | | | |
DB 276 TTTCAAGACTTGAATGACAAACTCTTTTTCATCAGACATCACAAGAGACTTGGAGAT 335
QY 101 LEUALAGLINASPLEUYSAPLEUTYRHSITHPROSERPHELEUASNPHETRYPROLEU 120
| | | | |
DB 336 TTGGCTCAGGATTAAAGCACTTGATCAATACCCACTTTTCTGAACTTTTATCCCTT 395
QY 121 GLYUASNPLEIIEPHEASNLEULYSERTHRPHEHGRUPROVALLEUTRP 140
| | | | |
DB 396 GGTGAAGATATTCATATTATTATTTAACTTGAAGACCTTCAACAGAACTGTCTGTGG 455
QY 141 ARGLYASPGLINHSHISHSIARGVALGLUGINLEUTHRDEUASNGLYLEUENGINALA 160
| | | | |
DB 456 AGGAAGGACCAACACATCAACCGGTGGAGCACTGACCTGAATGGCTCCTGCAAGCT 515
QY 161 LEUGINSETPROCYSILEIIEGLUGLYUSERYLSGLYLSERTHRILEUGIN 180
| | | | |
DB 516 CTTCAGAGCCCTGCATCATTTGAAGGGGAATCTGGCAAAAGGCCAAGTCCACTGTGCGAG 575
QY 181 ARGILEALMETLEUTHRPGIYSERYLYSCYSVALLEUTHRYSRPHLYSPHEVAL 200
| | | | |
DB 576 CGCATTTGCCATGCTCTGGGGCTCCGAAAGTGCAGAGCTGTGCACAAATTCATTCGTC 635
QY 201 PHEPHELEUARGYSEARARGALAGINGLYLEUPHEGLIUTHRUCYASPGINLEU 220
| | | | |
DB 636 TTTCTTCCTCGTCTCAGACAGGGCCCAAGGGTGGACTTTTGAACCTGTGTATCAACTC 695
QY 221 LEUASPIIEPROGLYTHRILEARGLYSGINTHPHEMETALMETLEULEULYSLEUARG 240
| | | | |
DB 696 CTGGATATACCTGGCAATCAGAGAGCAACATTCATGCGCCATGCTGTGAAGCTGCGG 755
QY 241 GINARVALLEUPHELEUENASPGIYTRYASNGLIUPHELYSPROGLINASNCPROGLIN 260
| | | | |
DB 756 CAGAGGGTCTTTCTCTTGTGATGGCTCAATGAATTCAGGCCCAAGAACTCCAGAA 815
QY 261 IIEGLUALALEULIIEGLYSGLUNSHIARGPHELYSASMETVALILEVALTHRTHRTHR 280
| | | | |
DB 816 ATCGAAGCCCTGATTAAGGAACCAACCGCTTCAAGACATGGTCTCATCGCACCACTACC 875
QY 281 THRGLUCYSLIENRGLHISILEARGGINPHEGLYALALEUTHRALAVALGLYASPMET 300
| | | | |
DB 876 ACTGAGTGCCTGAGGACATACGCGAGTTGGTGCCTGACTGAGGTGGGGGATATG 935
QY 301 THRGLUASPSERIALAGINLALEULIENRGLIENRGLIENRGLIENRGLIENRGLIENR 320
| | | | |
DB 936 ACAGAAAGACAGCCGCCAGGCTCTCATCCGAAAGTGTCTGATCAAGAGCTGTGTAAGGC 995
QY 321 LEULEULEUGINILEGINYSERARGCYSLIENRGLIENRGLIENRGLIENRGLIENRGLIEN 340
| | | | |
DB 996 TTGTTCTCCCAATTCAGAAATCCAGAGTGTGAGAAATCTCATGAAGACCCCTCTCTT 1055
QY 341 VALVALIIETHRCSYALALEGINMETGLYUSERYGLUPHEHISERTHRINRINTHR 360
| | | | |
DB 1056 GTGGTATCATCTGTCAATCCAGATGGGTGAAGATGATTCACACTCCACACACAAACA 1115
QY 361 THRLEUPHEHISTHRPHETRYRASPLEULEULIIEGLIYASNLSYHSISLYSGLY 380
| | | | |
DB 1116 ACCGCTTTCATACCTCTTCTATGATCTGTGATACAGAAAACAAACAAACATAAAGGT 1175
QY 381 VALALIASERASPHIIEARGSERLEUASPHISCYSGLYASPLEUALALEUGINGLY 400
| | | | |
DB 1176 GTGGCTGCAAGTACTTATTTGGAGCCGTGGACCACTGTGGAGACTTGTGGAGGGGT 1235
QY 401 VALPHESERTHISLYSPHEASPHIEGLIENRGLINASPYALSERSEYVALASNGIUNASPYAL 420
| | | | |
DB 1236 GTGTTCTCCACAAAGTTTATTTGAACTGCAAGGATGTCTCAGCGTGAATGAGATGTC 1295

Qy 421 LeuLeuThrThrGlyLeuLeuCysLysTyThrAlaGlnArgPheLeuProLysTyThrLys 440
Db 1296 CTGCTGACAACTGGGCTCTCTGTAAATATATACAGCTCAAGGTCACGCAAAAGTATAA 1355
Qy 441 PhePheHisLysSerPheGlnGluTyThrAlaGlyArgArgLeuSerSerLeuLeuThr 460
Db 1356 TTCCTTCCAAACTCATTCCAGAGATACACAGCAGCAGCAAGCTACGCTTATTTGACG 1415
Qy 461 SerHisGluProGlnGluValThrLysGlnLysGlnLysGlnLysMetValSerIle 480
Db 1416 TCTCATGAGCCAGAGAGAGGTGACCAAGGGAGTGGTACTTCCAGAAATGGGTTCCATT 1475
Qy 481 SerAspIleThrSerThrTyThrSerSerLeuLeuArgTyThrCysGlySerSerValGlu 500
Db 1476 TCGGACATTACATCCATTATGACAGCTGCTCGGTACACTGGGGTCATCTGTGGAA 1535
Qy 501 AlaThrArgAlaValMetLysHisLeuAlaAlaValTyThrGlnHisGlyCysLeuLeuGly 520
Db 1536 GCCACACAGGCGCTTATGACACCTCCAGCAGGTGTATCAACACGCGCTTCTCGGA 1595
Qy 521 LeuSerIleAlaLysArgProLeuThrArgGlnGlnSerLeuGlnSerValLysAsnThr 540
Db 1596 CTTTCCATGCGCCAGAGAGGCTCTGTGAGACAGAAATCTTCCAAAGTGTGAAAAACACC 1655
Qy 541 ThrGlnGlnGluIleLeuLysAlaIleAsnLysSerPheValGlnCysGlyIleHis 560
Db 1656 ACTGAGCAAGAAATCTGAAACCCATTAACATCATCTCTTGTAGAGTGGCATCCAT 1715
Qy 561 LeuTyThrGlnGlnSerThrSerLysSerAlaLeuSerGlnGlnPheGlnAlaPhePheGln 580
Db 1716 TTATATCAAGAGATACATCCAAATCAGCCCTGACGCAAGAAATTTGAAGCTTCTTCAA 1775
Qy 581 GlyLysSerLeuTyThrIleAsnSerGlnLysAsnIleProAspTyThrLysPhePhePheGln 600
Db 1776 GGTAAAGACTTATATATACACTCAGGAGAACATCCCGATTTCTTATTTGACTTCTTGA 1835
Qy 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyGlyAla 620
Db 1836 CATTTGCCCAATTTGCAAGTCTCTGACCTCATTTAAACCTGACCTTTTATGGGGAGCT 1895
Qy 621 MetAlaSerTrpGlnLysAlaAlaGlnAspThrGlyGlyIleHisMetGlnLysAlaPro 640
Db 1896 ATGGCTTATGGGAAAGGCTGCCAAGACACAGGTGGATCCACATGGAAAGAGGCCCA 1955
Qy 641 GluThrTyThrIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGlnPheArg 660
Db 1956 GAAACCTACATTTCCAGCAGGCGCTGATCTTTGTTCTTCACTGGAGCAGAAATTCAGG 2015
Qy 661 ThrLeuGlnValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyThrLeu 680
Db 2016 ACTGTGAGGTACACACTCGGAGATTTCAGCAAGTTGAATTAACAGATATCATATATCTG 2075
Qy 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700
Db 2076 GGGAAAAATATTCAGCTGTGCCAAGCCCTCAGGCTGCAATTAAGAGATGCTGTGTGG 2135
Qy 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyThrSerLeuMetValGlu 720
Db 2136 GCTGGAAGCTCAGTTGGTCTCTCAGCAGCTGTAAACATTTATTTCTCTCATGTGGGA 2195
Qy 721 AlaSerProLeuThrIleGlnAspGlnArgHisIleThrSerValThrAsnLeuLysThr 740
Db 2196 GCCAGTCCCTCCACATAGAAAGATGAGAGCAGATCATCTGTAAACAAACCTGAAAAACC 2255
Qy 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 760
Db 2256 TTGAGTATTCATGACCTACAGAAATACGCGCGCGGTGCTCATCAGCTTGGGT 2315
Qy 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGlnGlnAspAla 780
Db 2316 AACTTGAAAGAACCTTACAAAGCTCATATGATTAACATTAAGATGAATAAGAGATGCT 2375
Qy 781 IleLysLeuAlaGlnGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800

Db 2376 ATAAACTAGCTGAGAGGCTGAAAAACCTGAAGAGATGTGTTATTTCACTTGCACCAC 2435
Qy 801 LeuSerAspIleGlyGlnGlyMetAspTyThrIleValLysSerLeuSerSerGlnProCys 820
Db 2436 TTGCTGACATTTGAGAGGGAATGATTACATAGTCAAGTCTCTGTCAAGTGAACCCGTG 2495
Qy 821 AspLeuGlnGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840
Db 2496 GACCTTGAAGAAATTCATTACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2555
Qy 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGlnAsnTyThrLeu 860
Db 2556 GCTCAGAAATCTTCACAAATTTGGTCAACCTGAGACATTTCTGATTTATCAGAAATTAACCTG 2615
Qy 861 GlyLysAspGlyAsnGlnAlaLeuHisGlnLeuIleAspArgMetAsnValLeuGln 880
Db 2616 GAAAAAGATGGAATGAACCTCTTCATGATGATGATGATGATGATGATGATGATGATGATG 2675
Qy 881 LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900
Db 2676 CTCACCGCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2735
Qy 901 LysHisLeuGlnGlnValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThr 920
Db 2736 AAACATTTGGAGAGGTGCCACACACTGTCAGACTTGGGTTAAAAAAGTGAAGACTCACA 2795
Qy 921 AspThrGlnIleArgIleLeuGlnAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940
Db 2796 GATACAGAGATTAAGAAATTTAGTGCATTTTGGAAAGAACCCCTGTGAAAACTTCCAG 2855
Qy 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyThrLeuAlaPheMetGlyVal 960
Db 2856 CAGTTGAATTTGGCGGAATGCTGTGACAGATGATGATGATGATGATGATGATGATGATG 2915
Qy 961 PheGlnAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGlnPheLeuProAsp 980
Db 2916 TTGAGAAATCTTAACCAATTAAGTGTGTTTGTGACTTGAAGTAAAGAAATTTCTACTCAT 2975
Qy 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnLysAla 1000
Db 2976 CCAGCATTAAGTAGAAACTTAAGCAAGTGTATCCAGTTTAACCTTTCTGCAAGAGCT 3035
Qy 1001 ArgLeuValGlyTrpGlnPheAspAspAspAspLeuSerValIleThrGlyAlaPheLys 1020
Db 3036 AGCCTTGTGGGTGGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATG 3095
Qy 1021 LeuValThrAla 1024
Db 3096 CTAGTAACGTCT 3107
RESULT 5
; US-09-697-089-1
; Sequence 1, Application US/09697089
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 0734-136001
; CURRENT APPLICATION NUMBER: US/09/697,089
; PRIOR APPLICATION NUMBER: 2000-10-26
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FASTSEQ for Windows version 4.0
; SEQ ID NO 1
; LENGTH: 3133
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)..(3107)

US-09-697-089-1

Alignment Scores:

Pred. No.:	0	Length:	3133
Score:	5459.00	Matches:	1024
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	27	Gaps:	0

US-09-697-089-2 (1-1024) x US-09-697-089-1 (1-3133)

Qy 1 Metasnphelietysaspasnserrarglaleuileglnargmetglywethervalyle 20
Db ATGAATTTCAATAAGACAAATAGCCGAGCCCTTATTCAAGAAATGGAAATGACTGTATA 95
Qy 21 Lysglnliethrpsaspheuphevaltrpsnvalleunsnargluciuvalsnlle 40
Db AAGCAAAATCACAGATGACCTATTGTATGGAATGTTGAAATCGGAGAACTAAACATC 155
Qy 41 Ilecyscysglulysvalgluglnaspaiaaiaargglyllelhismetlleulelys 60
Db ATTCTCTCGAGAAAGGTGGAGCAGATGCTGCTAGAGGATCATTCACATGATTTTGANA 215
Qy 61 LysglserserGlusercysasnleupheuleysserleuylsultprasntrProleu 80
Db AAGGTTTCAGAGTCCCTGTAACTCTTTCTTAATCCCTTAAGAGATGGAAATATCTCTA 275
Qy 81 Pheglnaspleuasnglylserleuphehisglnthrsergluglylaspleunasp 100
Db TTTTCGGAGCTTGAAATGGACAAAGTCTTTTCATCAGACATCAGAGAGGACTTGAGCAT 335
Qy 101 LeuailaglnaspleuylaspheultrhisthrproserpheleunaspheultrProleu 120
Db TTGGCTCAGGATTTAAAGACTGTACCATACCCATCTTTTCTTAATCTTTATCCCTT 395
Qy 121 GlyluaspheileaspheilepheasnleuylserrthrPheulgluProvalleultrp 140
Db GGTGAAGATATTGACATATTATTTTAACTTGAAAGACACCTTCACAGAACTCTGCTGG 455
Qy 141 ArgylasarpGlnHisHisargvalglucglnleuthrleuasnglyleuleucnlaia 160
Db AGGAAGGACCAACACACATCACCCTGGAGACGCTGACCCCTGAAAGGCTCTCTGACGCT 515
Qy 161 LeuGlnserProCysIlelleuglulyserserlylsglyllyserrthreuleuGln 180
Db CTTCAGAGCCCTCATATGTAAGGGAATCTGGCAAGGCAAGTCCACTGTGCTGAG 575
Qy 181 ArgIlealemetleuTrpGlyserglylscylsalaaleuthrLysPheLysPheVal 200
Db CGCATGCGCATGCTCTGGGGCTCGGAAAGTGCAAGGCTCTGACCAAGTCAAAATTCGTC 635
Qy 201 PhePheleuargleuSerarglAglnglyleupheglulthrLeucysaspGlnleu 220
Db TTTCTTCCCTCCCTCAGAGGGCCAGGGTGGACTTTTGAAACCCTGTGATCAACTC 695
Qy 221 LeuaspIleProGlyThrIleargylsglnthrPheMetIlealeuileuileuylsleuarg 240
Db CTGATTAATCCTGGCACAATCGAAGACAGACATTCATGGCCATGCTGTGAAGCTGGGG 755
Qy 241 GlnarValleupheleuileuaspGlytyrasngluPheLysProGlnAsnCyProGlu 260
Db CAGAGGGTCTTTTCTCTTGTATGGCTACAAATGAATCAAGCCCAAGACTGCCAGAA 815
Qy 261 lleglualaleuileylsgluasnHisargPheLysasnMetValIleValIthrThrThr 280
Db ATCGAAGCCCTGATAAAGAAACCAACCGCTTCAGAAACATGTCATGCTGACCACTACC 875
Qy 281 ThrGluCysleuargHisIleargGlnPheglualaleuThrAlaGluValGlyspmet 300
Db ACTGATGCTCTGAGGCAATATACGCGATTTGGTGGCTGTACTGCTGAGGTGGGGAATNG 935
Qy 301 ThrGluasPserAlaGlnAlaleuilearggluValleuileylsglualeuagluGly 320

Db 936 ACAGAAAGACAGGCCAGGCTCTCATCCGAAAGTGTCTATCAGAGACTTCTGAGGC 995
Qy 321 LeuileuGlnIleGlnLysSerargCysleuargasnleuMetLysThrProleuphe 340
Db TTTTGTGCTCCAAATTCAGAAATCCAGGTCTCTGAGGAATCTCATGAAGACCCCTCTTT 1055
Qy 341 ValValIleThrCysAlaIleGlnmetGlyluserGluPheHisSerHisThrGlnThr 360
Db GTGGTCATCTTGTGCATTCAGATGGTGAAAGTGAATTCACCTCTCACACACAACTA 1115
Qy 361 ThrleupheHisThrPheTyraspleuileuileglnLysasnLysHisLysgly 380
Db ACGTGTTCATACCTTGTATGATCTGTGATACAGAAACAAACAAACATAAAGGT 1175
Qy 381 ValAlaIleaserAspPheleargserleuasphHisCysglylaspheualaileuGly 400
Db TTTTGTGCAAGTGAAGTCTCTTGGAGCCCTGGACCACTGTGAGACCTTACTCTGGAGGT 1235
Qy 401 ValPheSerHisLysPheaspPhegluleuGlnaspaIleSerSerValasnGluaspVal 420
Db TTTTCTCTCCACAAAGTTTATTTCCAGACTGCGAGATGTCTCCAGCTGTAATAGATGTC 1295
Qy 421 LeuethrThrGlyleuLeuLysTyrrhralaglnargPheLysProLysTyrrLys 440
Db CTGCTGACAACTGGGCTCTCTGTAATATACAGCTCAAAAGTTCAAGCCAAAGTATAA 1355
Qy 441 PhePheHisLysSerPheGlnGluTyrrhralaglylthargLysSerSerleuThr 460
Db TTTCTTTCACAAATGATTCATCCAGAGATACACAGACAGCAAGCACTGCAAGTTAATGAGC 1415
Qy 461 SerHisgluProGluGluValThrLysglLysasnGlyTyrrLeuGlnLysMetValSerIle 480
Db TTTCTATGAGCCAGAGAGGTGACCAAGGGGATGTACTTTCAGAAATGGTTTCCATTT 1475
Qy 481 SeraspIleerhSerThrTyrrSerSerleuLeuargTyrrThrCysglYserSerValGlu 500
Db TCGGACATATACATCCACTATAGACGCCCTGCCGTACACCTGGGGTCATCTGGANA 1535
Qy 501 AlaThrargAlaValMetLysHisleuAlaIleValTyrrGlnHisGlyLysleuengly 520
Db GCCACAGGGCTGTATATGAAGACCTCGCAGAGGTATCAACACGGCTCTTCGGGA 1595
Qy 521 LeuSerIleAlaLysargProleuTrpargGlnLysSerleuGlnSerValLysasnThr 540
Db CTTTCCATCGCCAAAGGCTCTCTGGAGACAGGAATCTTTCANAGTGTGAAAAACCC 1655
Qy 541 ThrGlnGlnLulileuLysAlaIleasnIleasnSerPheValGluCysglyIleHis 560
Db ACTGAGCAAGAAATTCGAAAGCCATAAACATCAATTCCTTGTAGAGTGGCATCCAT 1715
Qy 561 LeuTyrrGlnLysSerThrSerLysSerAlaLeuSerGlnLupheGluAlaPhePheGln 580
Db TTTTGTGCAAGAGATACATCCAAATCAGCCCTGAGCCAAAGAAATTTGAACCTTCTTCA 1775
Qy 581 GlyLysSerleuTyrrIleasnSerGlyasnIleProaspTyrrLeuPheaspPhePheGlu 600
Db GTTAAAGCTTATATATCACTCAGGAGACATCCCGATTAATTATGACTTCTTGAA 1835
Qy 601 HisleuProasnCysAlaSerAlaLeuaspPheIleLysleuaspPheTyrrGlyAla 620
Db CATTGGCCCAATGTGCAAGTGTCTGACCTCATTAACCTGAGCTTTATAGGGGAGGT 1895
Qy 621 MetAlaSerTrpGluLysAlaIleagLysPthrGlyGlyIleHisMetGluAlaPro 640
Db ATGGCTTATGGGAAAGGCTCAGAAAGACACAGGTGATCATCATGGAAGAGCCCCCA 1955
Qy 641 GluThrTyrrIleProSerargAlaValSerleuPheaspThrLysGlnLuphearg 660
Db GAAACCTATATTCACAGCGGGCTGATCTTGTCTTCACTGGAAGCGAATTCACAG 2015
Qy 661 ThrleuGluValThrleuargaspPheSerLysleuAsnLysGlnaspIleThrTyrrleu 680

Dh 2016 ACTGTGAGGTACACATCCGGGATTTTCAGCAAGTTGAATAAGCAATATCATATCTGT 2075
Qy 681 G1YLSIIEPHESESERAlAThrSerleuArgleuGlnIleuysARCYsAlaGlyVal 700
Dh 2076 GGGAAATATTCAGCTCTGCCACAGACCTCAGCTGCAGAAATAAGATGATGCTGTG 2135
Qy 701 AlAglSerleuSerleuValleuSerThrCYsLYsAsnIleYrSerleuMetValGlu 720
Dh 2136 GCTGGAAGCCTCAGTTGGTCTCCAGCACCTGTAAAGACATTTATCTCATGTGTGAA 2195
Qy 721 AlAserProleuthrIleGluAspGluArgHisIleThrSerValThrAsnleuysThr 740
Dh 2196 GCCAGTCCCTCCACCATAGAAGATGAGGCGACATCATCTGTGAACAACTGAAACC 2255
Qy 741 LeuSerIleHisAspLeuGlnAsnGlnArgleuProGlyGlyLeuThrAspSerleuGly 760
Dh 2256 TTGAGTATTCATGACCTACATCAATCAACGCTGCCGGGTGGTCTGACACAGCTTGGGT 2315
Qy 761 AsnleuysAsnleuThrIleuValleuMetAspAsnIleuysMetAsnGluAspAla 780
Dh 2316 AACTTGAAGAACCTTACAAACCTCATATGATGAATAAGATGAAGAAAGATGCT 2375
Qy 781 IleuysleuAlaGluGlyLeuIleuysAsnleuysLYsMetCYsleuPheHisleuThrHis 800
Dh 2376 ATAAACTAGCTGAAGGCTTAAAAAACCCTGAAGAGATGCTTTATTCATTTGACCCAC 2435
Qy 801 LeuSerAspIleGlyGluGlyMetAspTyrIleValLYsSerleuSerSerGluProCYs 820
Dh 2436 TTGTCTGACATTTGAGAGAGGAAATGATTAATGATCAAGTCTCTGTCAAGTGAACCTGT 2495
Qy 821 AspLeuGluGluIleGlnleuValSerCYsCYsleuSerAlaAsnAlaValLYsIleleu 840
Dh 2496 GACCTTGAAAGAAATTCATTAATGATCTCCGCTGCTGCTGCAAAATGACAGTAAATCCTA 2555
Qy 841 AlaGlnAsnleuHisAsnleuValLYsleuSerIleleuAspLeuSerGluAsnTyrleu 860
Dh 2556 GCTGAGATCTTCACAAATTTGGTCAAACTGAGCACTTCTTGATTTATCGAAATTAACCTG 2615
Qy 861 GluLYsAspGlyAsnGluAlaIleuHisGluIleuValleuAspArgMetAsnValleuGluGln 880
Dh 2616 GAAAAAGATGGAATGAAGCCTTCATGAACTGATCGACAGATGAAGAGTCTGAAACAG 2675
Qy 881 LeuThrAlaIleuMetleuProTyrPGLYCYsAspValGlnGlySerleuSerSerleu 900
Dh 2676 CTCACCGACTGATGCTGCCCTGGGGCTGTGACGTGCAAGCAGACCTGACAGCCTGTG 2735
Qy 901 LysHisleuGluGluValProGlnleuValLYsleuGlyLeuLYsAsnTyrArgleuThr 920
Dh 2736 AAACATTTGGAGAGGCTCCCAACACTGCTCAAGCTTGGGTTGAAAAAACTGAGACTCA 2795
Qy 921 AspThrGluIleArgIleleuGlyAlaPhePheGlyLYsAsnProleuLYsAsnPheGln 940
Dh 2796 GATACAGAGATTAAGAAATTTAGTGTCATTTTGGAAAGAACCTCTGAATAAACTCCAG 2855
Qy 941 GlnleuysnleuAlaGlyAsnArgValSerSerAspGlyTyrPLeuAlaPheMetGlyVal 960
Dh 2856 CAGTTGAATTTGGGGGAAATCGTGTGAGCATGATGATGCTTGGCTTCATGGGTGTA 2915
Qy 961 PheGluAsnleuLYsGlnleuValPhePheAspPheSerThrLYsGlnPheleuProAsp 980
Dh 2916 TTTTGAATCTTAAGCAATTAAGTCTTTTCTTACTTTACTTAAGAAATTTCTACCTGAT 2975
Qy 981 ProAlaIleuValArgLYsleuSerGlnValleuSerLYsleuThrPheleuGlnGluAla 1000
Dh 2976 CCACCATTAAGCAAAAACTTAAGCAAGTGTATTCACCAAGTTAACTTTCTCCAGAAACCT 3035
Qy 1001 ArgleuValGlyTyrPGLInPheAspAspAspAspSerleuSerValIleThrGlyAlaPheLYs 1020
Dh 3036 AGGCTTCTTGGGTGCAATTTGATGATGATGATCATGCTTATTATACAGGTCTTTTAA 3095
Qy 1021 leuValThrAla 1024
Dh 3096 CTAGTAAGTCT 3107

RESULT 6
US-09-841-739-1
: Sequence 1, Application US/09841739
: GENERAL INFORMATION:
: APPLICANT: Bertin, John
: TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH
: FILE REFERENCE: 07334-329001
: CURRENT APPLICATION NUMBER: US 09/841,739
: PRIORITY FILING DATE: 2001-08-29
: PRIOR APPLICATION NUMBER: US 09/697,089
: PRIOR FILING DATE: 2000-10-26
: PRIOR APPLICATION NUMBER: US 60/161,822
: PRIOR FILING DATE: 1999-10-27
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 3133
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (36)...(3107)
US-09-841-739-1
Alignment Scores:
Pred. No.: 0 Length: 3133
Score: 5459.00 Matches: 1024
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-09-697-089-2 (1-1024) x US-09-841-739-1 (1-3133)
Qy 1 MetAsnPheIleLYsAspAsnSerArgAlaIleuIleGlnArgMetGlyMetThrValIle 20
Dh 36 ATGATTTTCATTAAGAAAGCAATAGCCGAGCCCTTATTCAAAAGAAAGGGAATGACTGTATA 95
Qy 21 LysGlnIleThrAspAspLeuPheValIlePheAsnValleuAsnArgGluGluValAsnIle 40
Dh 96 AAGCAATACAGATGACCTATTTGTATGAGATGTCTGAATTCGGAAGAAAGTAAACATC 155
Qy 41 IleCYsCYsGluLYsValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLYs 60
Dh 156 ATTTGCTCGAGAAAGGTGAGCAGAGATGCTGCTGAGAGGAGATCATCATGATTTTGAA 215
Qy 61 LysGlySerGluSerCYsAsnleuPheleuLYsSerleuLYsGluTyrPAsnTyrProleu 80
Dh 216 AAGGTTTCAGAGTCTCCTGTAACCTCTTCTTAATCCCTTAAGGAGTGAACATATCTCTA 275
Qy 81 PheGlnAspLeuAsnGlyGlnSerleuPheHisGlnThrSerGluGlyAspLeuAspAsp 100
Dh 276 TTTCAAGACTTGAATGCAAAAGCTCTTTTCTATGACATAGAAAGAGACTTGAGACAT 335
Qy 101 LeuAlaGlnAspLeuLYsAspLeuTyrHisThrProSerPheleuAsnPheTyrProleu 120
Dh 336 TTGGCTCAGATTTAAAGACTTGTACCATACCCCATCTTTCTGAACTTTATCCCTT 395
Qy 121 G1YLSIIEPHESESERAlAThrSerleuArgleuGlnIleuysARCYsAlaGlyVal 700
Dh 396 GGTAGATTAATTAAGCAATTAAGTCTTTTCTTACTTTACTTAAGAAATTTCTACCTGAT 2975
Qy 141 ArgLYsAspGlnHisHisArgValGluGlnleuThrleuAsnGlyLeuLeuGlnAla 160
Dh 456 AGGAAGGACCAACACATCACCGGTGAGAGCACTGCAATGGCTCTCCAGAGCT 515
Qy 161 LeuGlnSerProCYsIleIleGluGlyGluSerGlyLYsSerThrleuLeuGln 180
Dh 516 CTTCAAGAGCCCTGCATCATTAAGAGGGAATCTGCAAAAGCAAGTCCACTCTGCTGAG 575
Qy 181 ArgIleAlaMetleuTyrPGLYSerGlyLYsCYsLYsAlaIleuThrLYsPheLYsPheVal 200

Dh 576 CGCATTCGCATCTCTCGGGGCTCCGGAAAGTCGAAGGCTCTGACCAGTTCMAATTCGTC 635
Qy 201 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 220
Dh 636 TTCTTCCTCCGCTTCAGCAGGGGCCAGGGTACCTTTTGAAACCTCTGTGATCAACTC 695
Qy 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 240
Dh 696 CTGATATACCTGGGCAACAATCAGGAAGCAGACATTCATGGCCATGCTCTGAAGCTGGGG 755
Qy 241 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnProGlu 260
Dh 756 CAGAGGGTCTTTCTCTTCGTGATGGCTACATGATTCAGGCCCAAGCTGCCCAAGAA 815
Qy 261 IleGluAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThrThr 280
Dh 816 ATCGAAGCCCTGATTAAGAAACCCAGCTTCAGAAACATGATGTCATGCCCTCAC 875
Qy 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300
Dh 876 ACTGAGTCCCTGAGGACATACGGCAGTTGGTGCCCTGACTGCTGAGAGTGGGGATATG 935
Qy 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 320
Dh 936 ACAGAAAGACAGCCGACGCTCTCATCCGAGAAAGTGTGATCAAGAGACTTGCTGAAGGC 995
Qy 321 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340
Dh 996 TTGTGTCCCAAAATTCACAAATCCAGGTGCTGAGAAATCTCATGAACACCCCTCTCTT 1055
Qy 341 ValValIleThrCysAlaIleGlnMetGlyLysSerGluPheHisSerHisThrGlnThr 360
Dh 1056 GTGGTCATCACTTGTGGCAATCAGATGGGTGAAGTGAATTCCTCCTCACACACAAACA 1115
Qy 361 ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGly 380
Dh 1116 ACGGTGCTCCATACCTCTATGATCTGTGTGATACAGAAACAAACACAAACATTAAGGT 1175
Qy 381 ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly 400
Dh 1176 GTGGTCGAAGTGAATTCATTCGGAGCCTGAGACCACTGTGAGACCTTGCTGAGAGGT 1235
Qy 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420
Dh 1236 GTGTTCTCCCAAGTTGATTGCACTGCAAGATGTCTCCAGCGTAAATGAGGATGTC 1295
Qy 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440
Dh 1296 CTGCTGACAACTGGGCTCTCTGTAAATATATACAGCTCAAAAGTTCAAGCCAAAGTATAA 1355
Qy 441 PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgLeuSerSerLeuLeuThr 460
Dh 1356 TTCTTTTCAAAAGTCAATTCAGAGATACACAGACAGCAACACTCAGAGTTTATTTGACG 1415
Qy 461 SerHisGluProGlnGluValThrLysGlnLysAsnGlyTyrLeuGlnLysMetValSerIle 480
Dh 1416 TCTCATGAGCCAGAGAGGATACCAAGGGGATGGTTACTTGACGAAATATGTTCCATT 1475
Qy 481 SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500
Dh 1476 TCGGACATTTACATCCACTTATAGCAGCTGCTCCGGTACACTGAGGGTCAATGTGAAA 1535
Qy 501 AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly 520
Dh 1536 GCCACACAGGGGTGTATTAACACCTCCGACAGTATTAACACGGGTGCTTCCTCGGA 1595
Qy 521 LeuSerIleAlaLysArgProLeuTyrArgGlnGlnSerLeuGlnSerValLysAsnThr 540
Dh 1596 CTTTCATACGCGCAAGAGGCTCTCTGGAGACAGGAATTTTGCAAAAGTGTAAACACCC 1655
Qy 541 ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560
Dh 1656 ACTGAGCAAAATTTCTGAAGCATTAAACATCAATTCCTTGTGTAGAGTGGCATTCAT 1715

Qy 561 LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln 580
Dh 1716 TTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCAAAGATTTGAAAGCTTTCTTTCAA 1775
Qy 581 GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhePheGlu 600
Dh 1776 GGTAAAGACTTATATATCACTCAGGAAACATCCCGGATTTACTTATTTGACTTCTTTGAA 1835
Qy 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyAla 620
Dh 1836 CATTGGCCCAATTTGGCAAGTCTCTGACATTAACCTGACATTTATATGGGGAGACT 1895
Qy 621 MetalSerTrpGluLysAlaAlaGlnAspThrGlyGlyIleHisMetGlnGluLapPro 640
Dh 1896 ATGGCTTATGGGAAAGGCTCCAGAGACACAGAGTGAATCCATGCAATGCAAGAGGCCCA 1955
Qy 641 GluThrTyrIleProSerArgAlaValSerLeuPheAsnTrpLysGlnGluPheArg 660
Dh 1956 GAAACCTACATTTCCAGCAGGCTGTATCTTGTCTTCACTGGAAGAGGAATTCAGG 2015
Qy 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu 680
Dh 2016 ACTGTGAGAGTCACACTCCGGGATTTCAAGATTAAGCAAGATATCATATCTCG 2075
Qy 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700
Dh 2076 GGGAAATATTTACGTCTGCCACAAAGCTCAGGCTGCAAAATTAAGATATGCTGTGGTG 2135
Qy 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu 720
Dh 2136 GCTGGAACCTCAGTGTGGTCTCGACACCTGTATGAACATTTATTTCTCATGTGGAA 2195
Qy 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740
Dh 2196 GCCAGTCCCTCACCATGAAAGATGAGAGGCACATCATCTGTGAACAACTGAAACCC 2255
Qy 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 760
Dh 2256 TTGATATTTCAATGACCTTCAGATATCAAGGCTCGGGGTGGCTGTACAGTGGCTGGGT 2315
Qy 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAla 780
Dh 2316 AACTTGAAGAACCTTACAAAGCTCATATGATATACATTAAGATATAAGAAAGATGCT 2375
Qy 781 IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800
Dh 2376 ATAAACTAGCTGAAGGCTGAAAAAAGCTGAAGAGATGTGTTATTTCAATTTGACCCAC 2435
Qy 801 LeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCys 820
Dh 2436 TTGCTGTACATTTGGAGAGGGAATGATTATACATAGCAAGTCTCTGTCAAGTGAACCCCTGT 2495
Qy 821 AspLeuGlnGluIleGlnLeuValSerCysLeuSerAlaAsnAlaValLysIleLeu 840
Dh 2496 GACCTTGAAGAAATTCATTTAGTCTCTGCTGCTGTGTGTGCAAAATGCAAGTGAATTCCTA 2555
Qy 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860
Dh 2556 GCTCAGATCTTCAACAATTTGGTCAAACTGAGACATTTGATTTATCGAAAAATTAACCTG 2615
Qy 861 GluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGlnGln 880
Dh 2616 GAAAAAGATGAAGAAAGCTTCTATACATGATCCAGAGATGAAGAGTCTGAAACAG 2675
Qy 881 LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900
Dh 2676 CTCACCGACATGATGCTGCTCGGGGCTGTGACGTGCAAGCAGCAGCTTACAGCAGCTGTG 2735
Qy 901 LysHisLeuGlnGluValProGlnLeuValLysLeuGlnLysLeuLysAsnTrpArgLeuThr 920
Dh 2736 AAACATTTGGAGAGGTCCCAACACTGTCGAAGCTTGTTGGTTGAAAAACTGAGAGACTCA 2795

Qy	461	SetHisGluProGluGluValThrIysGlyAsnGlyTyrLeuGlnLysMetValSerLe	480
Db	1381	TCTATATAGCGCAAGGAGGGGACCAAGGGGAAATGGTTACTTGCACAAAATGGTTCCAT	1440
Qy	481	SerAspIleThrSerPheTyrSerSerLeuAsnArgTyrThrCysGlySerSerValGlu	500
Db	1441	TCGGACATTACATCCACTTATACAGCCCTGCTCCGGTACACCTGTGGGTCAATCTGTGGA	1500
Qy	501	AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly	520
Db	1501	GCCACACGAGGCTGTATGAAGACACCTGCAGCAGATGATACACAGCGCTGCCTTCGGA	1560
Qy	521	LeuSerIleAlaLysArgProLeuTyrPargGlnGlnSerLeuGlnSerValLysAsnThr	540
Db	1561	CTTTTCCATCCCAAGGCGCTCTGTGGACAGAGAACTTTTGCAAAAGTGAACAAAACAC	1620
Qy	541	ThrGlnGlnLuuLeuLysAlaIleAsnIleAsnSerPheValGlyCysGlyIleHis	560
Db	1621	ACTGACGAAGAATTCGAAAGCCATAAACATCAATCTCTTGTGTAGAGTGGCATCCAT	1680
Qy	561	LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnLuuPheGluAlaPhePheGln	580
Db	1681	TTATATCAACAGAGTACATCCAAATCAGCCCTGCAGCAAGAAATTTGAAGCTTCTTCAA	1740
Qy	581	GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPheGlu	600
Db	1741	GGTAAAGCTTATATATCAACTGAGGAACATCCCGATTAATCTTATTTAGACTCTCTTGA	1800
Qy	601	HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyAla	620
Db	1801	CATTGGCCCAATTGTGCAAGTGCCTCGAGCATCAATTAACCTGACTTTATGGGGAGCT	1860
Qy	621	MetIleSerTrpLysAlaAlaGluAspThrGlyGlyIleHisMetGlnGluAlaPro	640
Db	1861	ATGGCTTCATAGGAAAGGCTGCGAAGACACAGGTGCAATCCACATGGAAGAGCCCA	1920
Qy	641	GluThrTyrIleProSerArgAlaValSerLeuPheAsnTrpLysGlnGluPheArg	660
Db	1921	GAACCTACATCTCCACAGAGGCTGTATCTTTGTTCTTCACTGGAACAGAAATTCAG	1980
Qy	661	ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu	680
Db	1981	ACTCTGGAGGTCACTCGCGGATTTTCACCAAGTTGAAATACCAAGAAATTCAGATATCTG	2040
Qy	681	GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal	700
Db	2041	GCGAAATATTCAGCTCTGCCACAAACCTCAGCGTGCAAATTAAGAGATGGCTGGTGTG	2100
Qy	701	AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu	720
Db	2101	GCTGGAGGCTCAGTTGGTCCCTCAGACACCTGTAGAACATTTATTTCTCATGTGTGAA	2160
Qy	721	AlaSerProLeuThrIleGluAspGluArgHisIlePheSerValThrAsnLeuLysThr	740
Db	2161	GCCAGTCCCTCCACCATAGAAATGAGAGGCAATCACAATCTGTATACAAACCTGAANAAC	2220
Qy	741	LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly	760
Db	2221	TTTGAGTATTCATAGCTACAGAAATCAACGCGTGCAGGGGAGTCTGACAGACGTTGGGT	2280
Qy	761	AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGlnGluAspAla	780
Db	2281	AACCTGGAAGACTTACAAAGGCTCATTAAGTATACATTAAGATTAATGAAGAAAGAGCT	2340
Qy	781	IleLysLeuAlaGlnGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis	800
Db	2341	ATAAACTAGCTAGAGGCGTGAACAAACCTCGAAGAGATGTGTTATTCATTGACCCAC	2400
Qy	801	LeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCys	820
Db	2401	TTTGCTGTACATTGTGAAGGAATGAGTTTCAATAGTCAAGTCTGTGTCAAGTGAACCTGT	2460

QY	821	AspleuGluGutIleGInleuValSerCySyleuSerAlaAsnAlaValLysIleLeu	840
Db	2461	GACCTTGAAGAAATTCATTAAATTAAGTCTCCTGCTGTGCTGCAAAAGCAGTGAATATCCTA	2520
QY	841	AlaGInAsnLeuHISaSnleuValLysLeuSerIleLeuAspLeuSerGlnAsnTyrlheu	860
Db	2521	GCTCAGAAATCTTCCAAATTTGGTCCAAACTGAGCATTTCTGATTTTATCCAGAAATTTACCTG	2580
QY	861	GluLysAspGlyAsnGluAlaLeuHISgluLeuIleAspArgMetAsnValLeuGluGln	880
Db	2581	GAATAAGATGGAATTAAGAACTCTTCATTAAGAACTGATGACAGATGAAGTGTGAACAG	2640
QY	881	LeuThrAlaLeuMetLeuProTrrpGlyCySAspValGlnGlySerLeuSerSerleuLeu	900
Db	2641	CTCACCCGCACTGATGCTGCCCTGGGGCTGTGACGTGCACAGCAGCCTGAGACGCTTGTG	2700
QY	901	LysHISleuGluGluValProGInleuValLysLeuGlyLeuLysAsnTrrpArgleuThr	920
Db	2701	AAACATTTTGGAGGGGATCCCAACAATCTGCACGCTTGGGTTAAAAAATCGAGACTACA	2760
QY	921	AspTrpGluIleArgIleLeuGlnAlaPhePheGlyLysAsnProLeuLysAsnPheGln	940
Db	2761	GATACAGAGATTAAGAAATTTAGTGTGATTTTTTGGAAAGAACCCCTGTGAAAAACTTCAG	2820
QY	941	GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrrpLeuAlaPheMetGlyVal	960
Db	2821	CAGTTGAATTTGGCGGGAATTCGTGTGACAGATGATGATGCTTGCCCTCATGGGTGTA	2880
QY	961	PheGlnAsnLeuLysGlnleuValAlaPhePheAspPheSerThrLysGluPheLeuProAsp	980
Db	2881	TTTATAGAACTTAAAGCAATTAAGTGTGTTTTGACTTTAGTACMAAGAAATTTCTACCTGAT	2940
QY	981	ProAlaLeuValAlaArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla	1000
Db	2941	CCACAGATTAGCAGAAAACCTTACCAAGTCTTATCCAAATTAACCTTTCTCGAAGAACT	3000
QY	1001	ArgLeuValGlyTrrpGlnPheAspAspAspLeuSerValIleThrGlyAlaPheLys	1020
Db	3001	AGGCTGTGGTGGCAATTTGATGATGATGATCTCAGTGTATTATACAGGTGCTTTTAA	3060
QY	1021	LeuValThrAla 1024	
Db	3061	CTAGTAACTGCT 3072	
RESULT 8			
US-10-156-733-14			
; Sequence 14, Application US/10156733			
; GENERAL INFORMATION:			
; APPLICANT: Alnemit, Emad S.			
; TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING			
; TITLE OF INVENTION: FACTOR			
; FILE REFERENCE: 480140, 477			
; CURRENT APPLICATION NUMBER: US/10/156,733			
; CURRENT FILING DATE: 2002-05-24			
; NUMBER OF SEQ ID NOS: 14			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 14			
; LENGTH: 3219			
; TYPE: DNA			
; ORGANISM: Homo sapIens			
US-10-156-733-14			
Alignment Scores:			
Pred. No.: 0			
Score: 5453.00			
Percent Similarity: 99.908			
Best Local Similarity: 99.90%			
Query Match: 99.89%			
DB: 41			
Gaps: 0			
Length: 3219			
Conservative: 1023			
Mismatches: 1			
Indels: 0			
US-09-697-089-2 (1-1024) x US-10-156-733-14 (1-3219)			
QY	1	MetasnhlelleuLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle	20

|||||
Db 145 ATGAATTCATTAAGGACAAATAGCCGAGCCCTTATTCAAGAAAGGGAGATGACTGTATTA 204
Qy LysGlnIleThrAspPheLeuPheValTyrPasnValIleAsnArgGluGluValAsnIle 40
Db 205 AAGCAAAATACAGATGACACTTATTGTATGATATGTTCTGAAATCGGAAAGAAAGTAAACATC 264
Qy IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
Db 265 ATTGGCTCCGGAAGGTGAGACAGGATGCTGTAGAGGAGCATTCACATGATTTTGAAA 324
Qy LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTyrPasnTyrProLeu 80
Db 325 AAGGTTTAGAGTCTGTAGACTCTTCTTAATCCCTTAAGAGATGGAACTATCTCTTA 384
Qy PheGlnAspLeuAsnGluGlnSerLeuPheHisGlnThrSerGluGluAspLeuAspAsp 100
Db 385 TTTCAGAGACTTGAAATGAGCAAAAGTCTTTTCATCAGACATCAGAGAGAGACTTGACAT 444
Qy LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu 120
Db 445 TTGGCTCAGAGATTAAAGACTTGTACCATCCCATCTTTCTGAACTTTATCCCTT 504
Qy GlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuThr 140
Db 505 GGTCAGATATTGACATTAATTTTACTTGAAGACCTTCACAGAACTGTCTCTGTGG 564
Qy ArgLysAspGlnHisHisHisArgValGluGlnLeuThrLeuAsnGluLeuLeuGlnAla 160
Db 565 AGGAAGAGCAACACCATCACCGGTGAGCAGCTGACCCGAAATGGCTCTCTGACAGCT 624
Qy LeuGlnSerProCysIleIleGluGluSerGlyLysGlyLysSerThrLeuLeuGln 180
Db 625 CTTGACAGCCCTGATATTGAAGGGGAAATCTGGCAAAAGCAATCCACTCTGCTGACG 684
Qy ArgIleAlaMetLeuThrGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 200
Db 685 CGAATGGCAATGCTCTGGGGCTCCGAAAGTGCAAGGCTGTGACCAATTCATAATTCCTC 744
Qy PhePheLeuArgLeuSerArgAlaGlnGlyLysLeuPheGluThrLeuCysAspGlnLeu 220
Db 745 TTCTTCCTCCGCTCAGCAGAGGGCCAGGCTGGACTTTTGAACCCCTGTGTGATCAACTC 804
Qy LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 240
Db 805 CTGGATATACCTGGCACAATCAGGAAGCAGACATTCATGGCCATCTCTGAGAGCTGGG 864
Qy GlnArgValIleuPheLeuAspGlyTyrAsnGluThrLysProGlnAsnProGlu 260
Db 865 CAGAGGGTCTTTCTCTGTATGGCTACAAATGAATTCAGCCCAAGACCTGCCCAAGAA 924
Qy IleGlnAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValIleThrThr 280
Db 925 ATCGAAGCCCTGATTAAGAAACACCGCTTCAGAAACATGTGTATGTCTCACCCCTAC 984
Qy ThrGluCysLeuArgHisIleArgGlnPheGluAlaLeuThrIleAlaGluValGlyAspMet 300
Db 985 ACTGAGTCTCGAGGACATACGCGAGATTGTGCTGCTGACTGCTGAGAGTGGGGATATG 1044
Qy ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 320
Db 1045 ACAGAAAGCAGCGCCAGGCTCTATCCGAAAGTGTGATCAAGGACTTGTCTGAAGGC 1104
Qy LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuThr 340
Db 1105 TTGTGCTCCCAATTCAGAAATCCAGGTGCTTGAGAAATCTCATGAAACCCCTCTCTTT 1164
Qy ValValIleThrCysAlaIleGlnMetGlyLysSerGluPheHisSerHisThrGlnThr 360
Db 1165 GTGTGATCACTGTGTGCAATCAGATGGGTGAAGTGAATTCACCTGCACACACAAACA 1224
Qy ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysGly 380
|||||

Db 1225 ACGCTGTTCCATACCTCTGTATGATCTGTGATACAGAAAAACAAACAAATTAAGCT 1284
Qy ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly 400
Db 1285 GTGGTGCAGATGACTTATTCGGAGCTGGACACACTGTGGAGACCTATGCTGTGAAGGCT 1344
Qy ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420
Db 1345 GTGTCTCCCAAGATTGATTTGAACTGCAAGATGTGTCCACGCTGGAATGAGAGATGTC 1404
Qy LeuLeuThrThrGlyLeuLeuCysLysTyrThrIleGlnArgPheLysProLysTyrLys 440
Db 1405 CTGCTGACAACTGGGCTCTCTGTAAATATACAGCTCAAAAGCTTCACCCAAATTAATA 1464
Qy PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgLeuSerSerLeuLeuThr 460
Db 1465 TTCTTTCACAAAGTATTCACAGAGATACACAGACAGACAGAAAGTATGAGCTTATGACG 1524
Qy SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480
Db 1525 TCTCATGAGCCAGAGAGATGACCAAGGGGAAATGTTACTTGCAAAAAATGGTTCATT 1584
Qy SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500
Db 1585 TCGACATTCATCCACTTATACAGCTGCTCCGATACACTGTGGCTCATCTGTGGAA 1644
Qy AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly 520
Db 1645 GCCACCAAGGCTGTTATGAAACACACTCGCAGCAGATGATCAACAGGCTGCTCTCGGA 1704
Qy LeuSerIleAlaLysArgProLeuThrParGlnGlnSerLeuGlnSerValLysAsnThr 540
Db 1705 CTTTCATCGCCCAAGAGGCTCTCTGAGACAGAAATCTTGGCAAAAGTGTAAAAACACC 1764
Qy ThrGluGlnGluIleLeuLysAlaIleAsnLysSerPheValGluCysGlyIleHis 560
Db 1765 ACTGAGCAAGAAATTCGAAAGCCATTAACATCAATTCCTTTGTAAGCTGTGGCATTCAT 1824
Qy LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln 580
Db 1825 TTATATCAAGAGATGACATTCAAATACAGCCCTGAGCCAAAGAAATTTGAAGCTTTCTTCA 1884
Qy GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhePheGlu 600
Db 1885 GGTAAACCTTATATCACTCAAGGCAATCCCGATCTCTTAATTTGACTCTTTGAA 1944
Qy HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyValAla 620
Db 1945 CATTGCCCCAATGTGCAAGTGCCCTGGACTTCATTAACGTGACCTTTATGTGGGGAGCT 2004
Qy MetaLaserTyrGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaPro 640
Db 2005 ATGGCTTATGGAAGAAAGCTGCGAAGAACACAGGTGGAATCCCATGGAAGAGGCCCA 2064
Qy GluThrTyrIleProSerArgAlaValSerLeuPheAsnTyrPlyGlnGluPheArg 660
Db 2065 GAAACCTCATCTCCAGCAGAGGCTGTATCTTTGTTCTTCACTGGAAGACAGAAATTCAG 2124
Qy ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu 680
Db 2125 ACTGTGAGGTCACACTCCGGGATTTTCAGAAATGGAATTAAGAAATGATGATCTGTG 2184
Qy GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGluVal 700
Db 2185 GGGAAATATTCAGCTCTGCCACAAAGCTCAGGCTGCAAAATTAAGAGATGTGCTGGTGTG 2244
Qy AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu 720
Db 2245 GCTGGAACCTCAGATTGCTGCTCAGCAGCTGTAAAGAACTTTATGCTCATGTGTGAA 2304
Qy AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740
Db 2305 GCCAGTCCCTCACCATAGAAAGATGAGAGGACATCATCTGTAAACAAACCTGAAAAAC 2364
|||||

QY 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyLeuThrAspSerLeuGly 760
|||||
Db 2365 TTGAGTATTCATGACCTCAGAAATCAAGCGCGGCTGCTGACAGCAGCTTGGGT 2424
QY 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluLysPhe 780
|||||
Db 2425 AACTGGAAGAACCTTACAAAGCTCTAATGCTAATACATTAAGATTAATGAGAAATGCT 2484
QY 781 IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800
|||||
Db 2485 ATAAACTAGCTGAGAGCGCTGAAAAAAGCTGAAAGAGATGTGTTATTCATTGACCCAC 2544
QY 801 LeuSerAspIleGlyGlyGlyMetAspTyrIleValLysSerLeuSerSerGluProCys 820
|||||
Db 2545 TTGCTGACATTGGAGAGGAGATGATTACATAGCAAGTCTCTGCAAGTCAAGTCAAGTCTG 2604
QY 821 AspLeuGluGluIleGluLeuValSerCysLeuSerSerAlaAsnAlaValLysIleLeu 840
|||||
Db 2605 GACCTGGAAGAAATTCATTAATCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2664
QY 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860
|||||
Db 2665 GCTCAGAAATCTTCAACAATTTGGTCAAACTGAGACATTTGATTTATCAGAAAAATTAACCTG 2724
QY 861 GluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGln 880
|||||
Db 2725 GAAAAAGATGGAATGAAAGCTTCTCATAGCTGAGATGAGAGATGAAAGCTGTAAGACAG 2784
QY 881 LeuThrAlaLeuMetLeuProTyrPglCysAspValGlnGlySerLeuSerSerLeuLeu 900
|||||
Db 2785 CTCACCGACATGATGCTCCTCGGCGCTGCTGACCTGCAAGCAGCAGCTGACAGCTGCTG 2844
QY 901 LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThr 920
|||||
Db 2845 AAACCTTTGGAGAGGCTCCCACTGCTCAAGCTTGGGTTGAAAAAACTGAGAGACTCACA 2904
QY 921 AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940
|||||
Db 2905 GATCAGAGATTAATATTTTGGTGCTATTTTGGAAAGAACCTTCTAAGAACTTCCAG 2964
QY 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrLeuAlaPheMetGlyVal 960
|||||
Db 2965 CAGTTGATTTGGCGGGAATCGTGAGCAGTGTGATGATGCTTGCCTTCATGGGTGTA 3024
QY 961 PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980
|||||
Db 3025 TTTGGAATCTTAAGCAATAGTGTGTTTTTGTACTTACTTAAAGAAATTTCTACTGAT 3084
QY 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla 1000
|||||
Db 3085 CCAGCATTAAGCAGAAAACTTAACCAAGCTGTTATCCAGTTAACTTTTCTGCAGAAACT 3144
QY 1001 ArgLeuValGlyTyrPglNpheAspAspAspAspLeuSerValIleThrGlyAlaPheLys 1020
|||||
Db 3145 AGCCTGTTGGGTGGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3204
QY 1021 LeuValThrAla 1024
|||||
Db 3205 CTAGTAACCTGCT 3216

RESULT 9

PCT-US01-07143-23
; Sequence 23, Application PC/TUS0107143
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.L.C.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50016
; CURRENT APPLICATION NUMBER: PCT/US01/07143
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06

;; PRIOR APPLICATION NUMBER: 60/236,874
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/188,916
;; PRIOR FILING DATE: 2000-03-13
;; PRIOR APPLICATION NUMBER: 60/237,846
;; PRIOR FILING DATE: 2000-10-03
;; NUMBER OF SEQ ID NOS: 52
;; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 3213
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-07143-23

Alignment Scores:
Pred. No.: 0 Length: 3213
Score: 5448.00 Matches: 1022
Percent Similarity: 99.90% Conservative: 1
Best Local Similarity: 99.80% Mismatches: 1
Query Match: 99.80% Indels: 0
Gaps: 0

US-09-697-089-2 (1-1024) x PCT-US01-07143-23 (1-3213)

QY 1 MetaSnpHeIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
:::|||||
Db 139 TTGAATTCATTAAGAAATGACATGCGAGCCCTTATTCAAAGATGGATGACGTGTTATA 198
QY 21 LysGlnIleThrAspAspLeuPheValTyrAsnValLeuAsnArgGluValAsnIle 40
|||||
Db 199 AAGCAATACACAGATGACCTTATTTCTATGAAATGTTCTGAAATCGGAAAGAAATGAACTC 258
QY 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
|||||
Db 259 ATTGCTCTCGAAGAGGTGAGCAGGATCTGCTAAGAGGATCATTCACATGATTTTGAAA 318
QY 61 LysGlySerGlySerCysAsnLeuPheLeuLysSerLeuLysGluTyrAsnTyrProLeu 80
|||||
Db 319 AAGGTTAGAGTCTCTGTAACCTCTTTCTTAAATCCCTTAAAGAGTGAATATCTCTTA 378
QY 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp 100
|||||
Db 379 TTTCAGAGCTTGAATGAGCAAAAGTCTTTTCATCAGACATCAGAAAGAGACTTGGAGAT 438
QY 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu 120
|||||
Db 439 TTGGCTCAGATTTAAAGACTTGTACCATCCCATCTTTTCTGAACTTTATCCCTT 498
QY 121 GlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuThr 140
|||||
Db 499 GGTGAGATTAATGACATTAATTTTAACTTGAAGAACCTTCAACAAAGCTGCTCTG 558
QY 141 ArgLysAspGlnHisHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla 160
|||||
Db 559 AGGAAGAGCAACACCATCACCAGCGGTGAGCAGCTGACCTCGAATGGCTCTCGAGAGCT 618
QY 161 LeuGlnSerProCysIleIleIleGluGlyLysSerGlyLysGlyLysSerThrLeuLeuGln 180
|||||
Db 619 CTTCAAGACCCCTGCATCATTAATGAAGGGAAATCTGGCAAGCAAGTCACACTCTCTGAG 678
QY 181 ArgIleAlaMetLeuTyrPglSerGlyLysCysLysAlaLeuThrLysPheLysPheVal 200
|||||
Db 679 CGAATTCGCAATGCTCTCGGCGCTCCGGAAGTGCAGAGGCTCTGACCAAGTTAAATTCGTC 738
QY 201 PhePheLeuArgLeuSerArgAlaGlnGlyLysLeuPheGluThrLeuCysAspGlnLeu 220
|||||
Db 739 TTCTTCCTCCGCTCAGAGAGGCCAGGCTGACCTTTTGAAGAACCTCTGATCAACTC 798
QY 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 240
|||||
Db 799 CTGATATTAATCCTGCACATATCAGAGAGCATTTACATGCGCATGCTGTAACCTCGCG 858
QY 241 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnGlyProGlu 260

D	859	CAAGAGGCTCTTTTCCCTTCTTGATGGCTACAAAGAAATTCAGCCCAAGAACTCCCAAGAA	918	D	1939	CATTGCCCAATTGTGCAGTGGCCCTGCAGCTTCATTAACTGGACTTTTATGGGGAGCT	1998
O	261	IIeGIAlAlaLeuIleIySGIuAsnHISArgPheIySAsnMetValIleValIThrThr	280	O	621	MetAlaSerTrpGIuIySAlaIaGIuAspThrIyGIyIleHISMetGIuIuAlaPro	640
D	919	ATGGAAACCCCTGATTAAGAAAAACACCCCTTCAGAGACATGGTCAATCGTCACACAGTACC	978	D	1999	ATGGCTTCATGGGAAAAAGGCTGCGAAGACACAGGGGGAATCCACATGGGAAGAGGCCCA	2058
O	281	ThrGIuIySLeuArghISIleArgGIuPheGIyAlaLeuThrAlaGIuValIyIyAspMet	300	O	641	GIuThrTyrIleProSerTrpAlaValSerIleuPhePheAsnTrpIySGIuIuPheArg	660
D	979	ACTGAGTGGCTGAGGACACATACGGCAGTTGGTCCCTGACTGCTGAGGGGGGATATG	1038	D	2059	GAACCTACATTCACAGCAGGGGCTGTATCTTTGTTTCACTGAGAGCAGGAATTCCAG	2118
O	301	ThrGIuAspSerAlaGlnAlaLeuIleArgGIuValLeuIleIySGIuIuAlaGIuIy	320	O	661	ThrLeuGIuValThrLeuArghAspPheSerIySLeuAsnIySGIuAspIleThrTyrIleu	680
D	1039	ACAGAAACAGCCGCCAGGCTCTCATCCGAGAACTGCTGATCAAGAGACTTGGCTGAAGGC	1098	D	2119	ACTCTGGAGGTCACTCCGGGATTCAGCAAGTTGAATAGACAGATATCAGATATCTG	2178
O	321	LeuIleuGIuIleGIuIySAsnArgCysLeuArghAsnIleuMetIySThrProIleuPhe	340	O	681	GIyIySIIePheSerSerAlaThrSerIleuArghLeuGIuIleIySArgCysAlaGIyVal	700
D	1099	TTGTGGTCCCAAAATTCAGAAATCCAGGTGCTTGAGGAAATCTCATGAAGACCCCTCTTT	1158	D	2179	GGGAAATATTCAGTCTGCGACACAGCTTCAGAGCTCCAAATAAAGAGATGCTGGTGG	2238
O	341	ValValIleThrCysAlaIleGIuMetGIyIuSerGIuPheHISerHIStrhGIuThr	360	O	701	AlaGIySerIleuSerIleuValIleuSerThrCysIySAsnIleThrSerIleuMetValGIu	720
D	1159	GTGGTATCATCTGTGCATTCAGATGGGTGAAGTAGATCCACTCTCACACACAAACA	1218	D	2239	GCTGGAAAGCTCAGTTGGTCTCTACACCTGTAAAGAACTTTATCTCATGTGGAA	2298
O	361	ThrIleuPheHIStrPheIyTrpAspLeuIleGIuIySAsnIySHISIySHISIySGIy	380	O	721	AlaSerProIleuThrIleGIuAspGIuArghISIIeThrSerValThrAsnIleuIySthr	740
D	1219	ACGCTGTTCCATACCTCTCTATGATCTGTATACAGAAAAACAACAAACATTAAGGT	1278	D	2299	GCCAGTCCCTCACCAATAGAAATGAGAGGCACATCATCTGTAACAAACCTGAAGAC	2358
O	381	ValAlaIaIaSerAspPheIleArghSerIleuAspHISerCysGIyAspLeuAlaIeGIuIy	400	O	741	LeuSerIIeHISAspLeuGIuAsnGIuIuArghLeuProGIyGIyLeuThrAspSerIeGIy	760
D	1279	GTGGCTCAAGTCACTTCATTCGAGACCTGACACACTGTGAGACCTCATAGCTGTGAGAGT	1338	D	2359	TTGAGATTCATGACCTACAGAAATCAACGGCTCCGGGTGGCTGTGACTGTGCACCTGGGT	2418
O	401	ValPheSerHISIySAspPheGIuIeGIuIuAspValSerSerValAsnGIuAspVal	420	O	761	AsnIleuIySAsnIleuThrIySLeuIleMetAspAsnIleIySMetAsnGIuIuAspAla	780
D	1339	GTGGTTCACCAAGATTGTGATTCGAACTGACAGATGTGTCCACCGCAATAGAGATGTC	1398	D	2419	AACTGGAAGACCTTCATAAAGCTCATATGATGATTAACATTAAGATGAATGAAGATGCT	2478
O	421	LeuIleuThrThrGIyLeuLeuCysIySThrThrAlaGlnArghIySProIySThrIyS	440	O	781	IIeIySLeuAlaGIuIyLeuIySAsnIleuIySAsnIleuIySAsnIleuIySAsnIleuIyS	800
D	1399	CTGCTGCAACCTGGCTCTCTGTAAATATACACTCAAGGTTCAAGGCCCAAGATATPAA	1458	D	2479	ATTAAGTACTGAGAGCCCTGAAGAAACCTGAGAGAGATGTTATTTATTCATTTGACCAC	2538
O	441	PhePheHISIySAspPheGIuIyTrpThrAlaGIyArghLeuSerSerIleuIleuThr	460	O	801	LeuSerAspIleGIyGIuIyMetAspTyrIleValIySAsnIleuSerIeGIuIuProCys	820
D	1459	TTCTTTCACAAGTATTCACAGAGTACACAGACAGAGAGACACACAGTTTATTGACG	1518	D	2539	TTGTCTACATTTGGAGGGAATGATTAATGATGTCAGACTGTGTCAACTGTGAACCTGT	2598
O	461	SerHISGIuProGIuIuValThrIySGIyAsnGIyTyrIleuGIuIyMetValSerIle	480	O	821	AspLeuGIuIuIleGIuIuValIleuIySAsnIleuIySAsnIleuIySAsnIleuIyS	840
D	1519	TCTATGAGCCAGAGAGGTACCAAGGGGATGTACTTGCAGAAATGGTTCCATTT	1578	D	2599	GACCTTAAGAAATTCATTATGTCCTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG	2658
O	481	SerAspIleThrSerThrIySAsnIleuArghTyrThrCysGIySerSerValGIu	500	O	841	AlaGIuIuAsnIleuHISAsnIleuValIySLeuSerIleuAspLeuSerGIuAsnTyrIleu	860
D	1579	TCGGAATTCATCCACTTATAGCAAGCTGCTCGGTACACCTGTGGGTCAATCTGTGAA	1638	D	2659	GCTGAGATCTTCACAAATTTGGTCAAACTGAGCATTTCTGATTTATCAGAAATTAACCTG	2718
O	501	AlaThrArghAlaValMetIySHISIleuAlaIaValTyrGIuHISGIyCysLeuIeGIy	520	O	861	GIuIySAspGIyAsnGIuIuAlaLeuHISGIuIleuIleAspArgMetAsnValIleuGIuIu	880
D	1639	GCCACACAGGCTGTATTAAGACACCTGCGACAGTATCAACAGGGTGCCTCTCGCA	1698	D	2719	GAAGAAATGGAATTAAGGCTTTCATGAATCTGACAGAGAAAGAACTGTGTAAGACAG	2778
O	521	LeuSerIleAlaIySArgProIleuTrpArgGIuIuSerIeGIuIuSerValIyAsnThr	540	O	881	LeuThrAlaLeuMetIeAsnProIleuGIyCysAspValGIuIySerIleuSerSerIleu	900
D	1699	CTTTCATCCAGCAAGAGCCCTCTGTGAGACAGAAATCTTGGCAAAAGTGTAAAAAACCC	1758	D	2779	CTCACCCGACTGATGCTGCCCTGGGGCTGTGACGTGCAAGGCAACCTGAGACGCTGTG	2838
O	541	ThrGIuGIuIuIleIeGIuIuAlaIleAsnIleAsnSerPheValGIuIyCysGIyIleHIS	560	O	901	IySHISLeuGIuIuValProGIuIuValIySLeuGIyIleuIySAsnTrpArgIleuThr	920
D	1759	ACTGAGCAAGAAATTCGAAAGCCATTAACATCAATTCCTTTGTAGAGTGTGGCATTCAT	1818	D	2839	AAACATTTGGAGAGGTCCCAACACTGCTCAAGCTTGGGTGAAGAAACTGAGACTCACA	2898
O	561	LeuTyrGIuIuIuSerThrSerIySAsnIleuSerGIuIuIuPheGIuIuAlaPhePheGIu	580	O	921	AspThrGIuIleArghIleIeGIuIuAlaPhePheGIyIySAsnProIleuIySAsnPheGIu	940
D	1819	TTATATCAAGAGAGATCACAAAATCAAGCCCTGAGCCAAAGATTTGAAGCTTTCTTCAA	1878	D	2899	GATACAGAGATTAAGAAATTTAGGTGCAATTTTGTGAAGAAACCTCTGGAAGAAATTCAG	2958
O	581	GIyIySAsnIleuTyrIleAsnSerGIyAsnIleProAspTyrIleuPheAspPhePheGIu	600	O	941	GIuIeAsnIleuValGIyAsnArghValSerSerAspGIyTrpIleuAlaPheMetGIyVal	960
D	1879	GGTAAAGCTTATATATCAACTCAGGGAAACATCCCGCATTTACTTATTTGACTTCTTTGAA	1938	D	2959	CAGTTGAATTTGGGGGAAACGCTGTAGCAGTATGATGATGCTTGGCTTCATGGGTGA	3018
O	601	HISleuProAsnCysAlaSerAlaLeuAspPheIleIySLeuAspPheTyrGIyValAla	620	O	961	PheGIuIuAsnIleuIySGIuIeValPhePheAspPheSerThrIySGIuIuPheIleuProAsp	980
D				D	3019	TTTGAGATCTTAAGCAATTAAGTGTGTTTGTGACTTTAGTACTTAAGAAATTTCTACCTGAT	3078

OY	461	SerHisGluProGluGluValThrIleuSGlyAsnGlyTyrLeuGlnLysMetValSerIle	480
Db	1519	TCGTATGACGACAGGAGGAGGACCAAGGGGAATGGTACTTCGCAGAAATGGTTCCATT	1578
OY	481	SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu	500
Db	1579	TCGGACATTTACATCCACTTTTATGACAGCTGCTCCGGTACACCTGGTGGGCATCTGTGGAA	1638
OY	501	AlaThrArgAlaValMetLysHisIleuAlaValTyrGlnHisGlyCysLeuLeuGly	520
Db	1639	GCCACACAGGGGTGTATGAAAGCACCTCGACAGCTATCAACAGCGCTGCTTTCGGA	1699
OY	521	LeuSerIleAlaLysArgProLeuTyrParGlnGluSerLeuGlnSerValLysAsnThr	540
Db	1699	CTTTCCATCGCCAAAGAGCGCTCTCTGGAGACAGGAATCTTTGCCAAAGTGTAAACACAC	1758
OY	541	ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis	560
Db	1759	ACTGAGACAGAAATTCGAAAGCCATTAACATCAATCTTTGTGTAGAGTGTGGCATCAT	1818
OY	561	LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPheGln	580
Db	1819	TTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCAAAGATTTGAACTTTCTTTGAA	1878
OY	581	GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPheGlu	600
Db	1879	GGTAAAGCTTATATATCAACTCAGGAAACATCCCGATCTTATTTGACTTTCGAA	1938
OY	601	HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAsnPheTyrGlyValAla	620
Db	1939	CATTTCGCCAATTTGTGCAAGTGGCCCTGAGCTTATTAACTGGACTTTATGGGGAGACT	1998
OY	621	MetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaPro	640
Db	1999	ATGGCTTCATATGGGAAAGGCTCGAGAAAGACACAGGTGGAAATCCACATGAAAGAGGCCCA	2058
OY	641	GluThrTyrIleProSerArgAlaValSerLeuPheAsnTrpLysGlnGluPheArg	660
Db	2059	GAACCTACATTTCCACACAGGCGCTGATCTTTTCTTCACTGAGGAGGGAATTCAGG	2118
OY	661	ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu	680
Db	2119	ACTCTGGAGGTCACACCCCGGATTCACAGCAATGTAATACAGAGATTCAGATATCTG	2178
OY	681	GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyAla	700
Db	2179	GGGAAATATTCACCTCTGCCACAGGCTCAGGCTCCAAATTAAGAGAGTGTCTGGTGTG	2238
OY	701	AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu	720
Db	2239	GCTGGAGGCTCATTTGGTGGTCCAGAGCCTGTAAACAACATTTATTCCTCATGGTGGAA	2298
OY	721	AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr	740
Db	2299	GCCAGTCCCCCTACACATAGAAAGATGAGAGCACATCACTTCGTAAACAAACCTGTAAAC	2358
OY	741	LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly	760
Db	2359	TTTGAGTATTCAGCTACACGAATCAACAGGCTCCGGGTGGTCTGATGATACAGCTTGGGT	2418
OY	761	AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAla	780
Db	2419	AACCTTGAAGAACCTTACAAAGCTCATTAATGATTAACATTAACATGATGAAGAAATGCT	2478
OY	781	IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis	800
Db	2479	ATAAACAAGCTGGAAGGCTCGAAACCTGAAAGAAATGTGTTTATTTCTATTGTGACAC	2538
OY	801	LeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCys	820
Db	2539	TTGTCTGACATGTGAGAGGGAATGATACATATGTCATCAATCTCTGTGCAAGTGAACCTGCT	2598
OY	821	AspLeuGluGluIleGlnLeuValSerCysLysLeuSerAlaAsnAlaValLysIleLeu	840

Db	2599	GACCTTGAAGAATTCATTAGTCTGCCGCTGCTGTCTGCATAATGCAG
Oy	841	AlaGlnAsnLeuHISAsnLeuValLysLeuSerIleLeuAspLeuSerG
Db	2659	GCTCGAATCTTCCACAAATTTGGTCAAACTGAGCAATCTTGATTTATCAG
Oy	861	GluLysAspGlyAsnGlnAlaLeuHisGluLeuIleAspArgMetAsnV
Db	2719	GAATAAGATGGAAATGAAGAGCTCTTCATGACTGATCGACAGATGACG
Oy	881	LeuThrAlaLeuMetLeuProTyrPclYcysAspValGlnGlySerLeuS
Db	2779	CTCACCGCATGATGCTCCCTGGGGGCTGTGACGTGCAGGACGAGCTGA
Oy	901	LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnT
Db	2839	AAACATTTTGGAGAGAGTCCCAACACTGCTCAAGCTTGGGTTGAAAAACT
Oy	921	AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuH
Db	2899	GATACAGAGATTAGAAATTTTAGTGTCAATTTTGGAAAGAACCCCTGGA
Oy	941	GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPLeuAlaP
Db	2959	CAGTTGAATTTGGCGCGGAAACGTGTGAGCAGTGTGATGGCTTGCCCT
Oy	961	PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluP
Db	3019	TTTGGAATCTTAAGCAATTAGTGTGTTTTTGTACTTTAATACTAAAGAAT
Oy	981	ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheL
Db	3079	CCAGCATTAAGTCAGAAAACTTAGCCACAGCTGTATCCAAAGTTAACTTTC
Oy	1001	ArgLeuValGlyTyrGlnPheAspAspAspLeuSerValIleThrG
Db	3139	AGCGTTGTTGGGTGGCAATTTGATGATGATGATCTCAAGTGTATTACAG
Oy	1021	LeuValThrAla 1024
Db	3199	CTAGTAAC TGCT 3210
Result 11		
PCT-US01-14826-66		
Sequence 66, Application PC/TUS0114826		
GENERAL INFORMATION:		
APPLICANT: HySeq, Inc		
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES		
FILE REFERENCE: 21272-103		
CURRENT APPLICATION NUMBER: PCT/US01/14826		
CURRENT FILING DATE: 2001-05-16		
PRIOR APPLICATION NUMBER: 09/577,408		
PRIOR FILING DATE: 2000-05-18		
PRIOR APPLICATION NUMBER: 09/677,298<151>		
PRIOR APPLICATION NUMBER: 09/695,781<151>		
PRIOR APPLICATION NUMBER: 09/715,869<151>		
PRIOR APPLICATION NUMBER: 09/775,330<151>		
NUMBER OF SEQ ID NOS: 864		
SOFTWARE: Custom		
SEQ ID NO 66		
LENGTH: 3260		
TYPE: DNA		
ORGANISM: Homo sapiens		
FEATURE:		
NAME/KEY: CDS		
LOCATION: (29) ..(3226)		
PCT-US01-14826-66		
Alignment Scores:		
Pred. No.:	0	Length: 3260
Score:	5441.00	Matches: 1020
Percent Similarity:	99.80%	Conservative: 2

Best Local Similarity:	99.61%	Mismatches:	2
Query Match:	99.67%	Indels:	0
DB:	1	Gaps:	0
US-09-697-089-2 (1-1024) x PCT-US01-14826-66 (1-3260)			
Qy	1	MetaspheileuAspAsnSerArgAlaLeuIleGlnArgMetCylMetThrValIle	20
Db	155	TTGAATTCATFAAGACATAGCCGAGCCCTTATTCAAGAATGGGATGACTATTATA	214
Qy	21	LysGlnIleThrAspAspLeuPheValTrrPasnValLeuAsnArgLugLValAsnIle	40
Db	215	AAGCAAAATCACAGATGACCTATTGTATGGAATGTTCTGAATCGGAGAAATTAACATC	274
Qy	41	IleCysCysGluLysValGluGlnAspAlaIleArgGlyIleIleHisMetIleLeuLys	60
Db	275	ATTTCCTCGAGAGAGGTGGAGCAGATGCTGTAGGGGATATTCACATGATTTTGAAA	334
Qy	61	LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrrPasnTrrProLeu	80
Db	335	AAGGTTCAAGAGTCCGTGAACCTCTTTCTTAATCCCTTAAGAGAGTGAACATCTCTA	394
Qy	81	PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnTrrSerGluGlyAspLeuAspAsp	100
Db	395	TTTTCAGGACTTGAATGGAACAAAGCTTTTTCATCAGACATCAGAAAGGAGACTTGGACAT	454
Qy	101	LeuAlaGlnAspLeuLysAspLeuTrrHisTrrProSerPheLeuAsnPheTrrProLeu	120
Db	455	TTGGCTCAGAGATTAAAGGACTTGTACCATCCCATCTTTCTGAACCTTTATCCCTT	514
Qy	121	GlyGlnAspIleAspIleIlePheAsnLeuLysSerTrrPheThrGluProValLeuTrrP	140
Db	515	GGTGAAGATATTGACATATTATTTTAACTTGAAAGACACCTTCACAGAACCTCTCTG	574
Qy	141	ArgLysAspGlnHisHisHisArgValGluGlnLeuTrrLeuAsnGlyLeuGlnAla	160
Db	575	AGGAAGGACCAACACATCACCGCGTGGAGCAGCTGACCCTGAATGGCCCTCTGCAGCT	634
Qy	161	LeuGlnSerProCysIleIleGlnGlyLysSerGlyLysGlyLysSerThrLeuGln	180
Db	635	CTTCAGAGCCCTGCATATTGAAGGGAATCGCAAGCAAGCAATCCACTGTGTCAG	694
Qy	181	ArgIleAlaMetLeuTrrGlySerGlyLysCysLysAlaLeuTrrLysPheLysPheVal	200
Db	695	CGAATGGCATGCTCTGGGGCTCCGGAAGTCAAGGCTCTACCAAGTCAAAATTCGTC	754
Qy	201	PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluTrrLeuCysAspGlnLeu	220
Db	755	TTCTTCCTCCGCTCAGAGGCGCCAGGGGTGACTTTTGAACCCCTGTGATCAACTC	814
Qy	221	LeuAspIleProGlyTrrIleArgLysGlnTrrPheMetAlaMetLeuLeuLysLeuArg	240
Db	815	CTGGATTAACCTGGCACATCAGGAAGCAGACATTCATGGCCATCTGTGAAGTGGCG	874
Qy	241	GlnArgValLeuPheLeuLeuAspGlyTrrAsnGluPheLysProGlnAsnCysProGlu	260
Db	875	CAGAGGCTTCTTCTCTCTGATGGCTACATGATTCAGAGCCCAAGAACTGCCAGAA	934
Qy	261	IleGlnAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValTrrThrThr	280
Db	935	ATCGAAGCCCTGATFAAGAAACACCGCTTCAGAAACATGGTCATCGTCAACCTACC	994
Qy	281	ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuTrrAlaGluValGlyAspMet	300
Db	995	ACTGAGTCCCTGAGGACATCGGAGATTGGTGGCTTCGACTGCTGAGAGTGGGATATG	1054
Qy	301	ThrGluAspSerAlaGlnAlaLeuIleArgGluValIleLysGluLeuAlaGluGly	320
Db	1055	ACAGAAGACAGCCCGCAGCTCTATCCGAGAAGTGTGATCAAGAGACTTGTCTAAGGC	1114
Qy	321	LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysTrrProLeuPhe	340
Db	1115	TTGTGTCTCCAAATTCAGAAATCCAGTGTGTTGAGGAATCTCATGAAACCCCTCTCTT	1174

Qy	341	ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnTrr	360
Db	1175	GTGGTCATCATCTTGTCATTCAGATGGGTGAAGATGATTCACCTTCACACAAACA	1234
Qy	361	ThrLeuPheHisThrPheTrrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGly	380
Db	1235	ACGCTGTCCATACCTTCTATGATCTGTGATACAGAAAAACAAACAAACATTAAGST	1294
Qy	381	ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly	400
Db	1295	GTGGCTGCAAGTACTTCTTCGAGCCCTGGACCACTGTGGAGACCTACTCTGGAGGCT	1354
Qy	401	ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal	420
Db	1355	GTGTTCCTCCACAAAGTTTATTTGATTCAGACTGCAGGATGTGTCCAGCTGATAGAGTGT	1414
Qy	421	LeuLeuTrrThrGlyLeuLeuCysLysTrrThrAlaGlnArgPheLysProLysTrrLys	440
Db	1415	CTGCTGACAACTGGGCTCTGTAAATATACAGCTCAAGGTTCAAGCCAAAGTATAA	1474
Qy	441	PhePheHisLysSerPheGlnGluTrrAlaGlyArgArgLeuSerSerLeuLeuTrr	460
Db	1475	TTCTTTCACAACTCATTCACAGAGTACACAGCAGAGCAAGACTCAGCTTAATGACG	1534
Qy	461	SerHisGluProGluGluValThrLysGlyAsnGlyTrrLeuGlnLysMetValSerIle	480
Db	1535	TCTCATGAGCCAGAGAGGTGACCAAGGGGAATGTACTTCCAGAAATGGTTTCCATT	1594
Qy	481	SerAspIleThrSerTrrLysSerSerLeuLeuArgTrrThrCysGlySerSerValGlu	500
Db	1595	TCGACATTACATCCACTATAGACAGCTGCTCCGGTACACCTGGTGGTCACTGTGGAA	1654
Qy	501	AlaThrArgAlaValMetLysHisLeuAlaAlaValTrrGlnHisGlyCysLeuLeuGly	520
Db	1655	GCACACAGGCGTATTATGAAGCACCTCGCAGCAGTATCAACAGCGCTCTTCGGA	1714
Qy	521	LeuSerIleAlaLysArgProLeuTrrArgGlnGluSerLeuGlnSerValLysAsnTrr	540
Db	1715	CTTTCATGCGCCAGAGGCGCTCTGTGAGACAGGAATCTTCCAAAGTGTGAAAAACCC	1774
Qy	541	ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis	560
Db	1775	ACTGAGCAAGAAATTCGTGAAGCCATAACATCAATCTCTTGTAGAGTGGCATCCAT	1834
Qy	561	LeuTrrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGlnAlaPhePheGln	580
Db	1835	TTATATCAAGAGATACATCCAAATCACCCCTGAGCCCAAGAAATTTGAACCTTCTTCAA	1894
Qy	581	GlyLysSerLeuTrrIleAsnSerGlyAsnIleProAspTrrLeuPheAspPhePheGlu	600
Db	1895	GGTAAAGCTTATATATCAACTCAGGGAACATCCCGGATACTTATTTGACTCTTTGAA	1954
Qy	601	HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTrrGlyAla	620
Db	1955	CATTTGCCCAATTTGTGCAAGTCCCTGACTTCATTTAACTGGCTTTATGGGGAGCT	2014
Qy	621	MetAlaSerTrrGluLysAlaAlaGluAspThrGlyGlyIleHisMetCylGluAlaPro	640
Db	2015	ATGGCTTCATGGGAAAGGCTCGAAGACACAGGTGGAATCCACATGGAGAAGGCCCA	2074
Qy	641	GluTrrTrrTrrIleProSerArgAlaValSerLeuPhePheAsnTrrPylsGlnLysPheArg	660
Db	2075	GAACCTTCATATCCACAGAGGCTATCTTTGTTCTTCACTGGAAGCAGGAATTCAGG	2134
Qy	661	ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTrrLeu	680
Db	2135	ACTCTGAGGTACACCTCGGAGATTTCAGCAAGTTGAATACCAAGATATCGAATATCG	2194
Qy	681	GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal	700
Db	2195	GGGAAAAATATTCAGCTCTGCCACAAGCCTCAGGCTGCAAAATFAAGATGTCTGTGTG	2254


```

QY 701 AlAGlSerLeuSerLeuValLeuSerThrcyslysasniletyrSerLeuMetValGlu 720
| | | | |
Db 2255 GCTGAAGACCTCAGTTGGTCTCCAGCAGCCTGTAAAGACATTTATTCCTCATGGTGGAA 2314
QY 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740
| | | | |
Db 2315 GCCAGTCCCTCCACCATAGAAAGATGAGAGGCACATCATCTGTAAACAACTGAAAAAC 2374
QY 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 760
| | | | |
Db 2375 TTGAGTATTCATGACCTACCAATCAACAGCGCTGCCGGGTGGTCTGACAGACCTTGGGT 2434
QY 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGlnAspAla 780
| | | | |
Db 2435 AACTTGAAGAACCCTTACAAACCTCATATGGATAAACATAAAGATGAAGAAGATGCT 2494
QY 781 IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisIleuThrHis 800
| | | | |
Db 2495 ATAAAACTAGCTGAAGGCTTAAAAAAGCTGAAGAGATGTATTATTCATTTGACCCAG 2554
QY 801 LeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCys 820
| | | | |
Db 2555 TTGCTGCATCTGAGAGAGGAGATGATTACATAGTCAAGTCTCTCTCAAGTGAACCTCTGT 2614
QY 821 AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840
| | | | |
Db 2615 GACCTTGAAGAAATTCATATGATCTCCCTGCTGCTGTGCAAAATGACAGTGAATTCCTA 2674
QY 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860
| | | | |
Db 2675 GCTCAAGATCTTCACAAATTTGGTCAAACTGAGACATCTTGTATTTATGAAAAATTAACCTG 2734
QY 861 GluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGln 880
| | | | |
Db 2735 GAAAAAGATGAAATGAAAGCTCTTCATGACTGATCGACAGATGAAGAGTGGTCTGAAGAG 2794
QY 881 LeuThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900
| | | | |
Db 2795 CTCACCCGACATGATGCTCCCTCGGGGCTGTGACGTGCAAGCAGCCTGAGCAGCCTGTG 2854
QY 901 LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThr 920
| | | | |
Db 2855 AAAACATTTGGAGAGAGCTCCCAACCTGTCAGACCTTGGGTGAAAACTGGAGACTCACA 2914
QY 921 AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940
| | | | |
Db 2915 GATACAGAGATTAGAAATTTAGTGTCATTTTGGAAAAAACCCCTGAAAAAAGCTTCCAG 2974
QY 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPheAlaPheMetGlyVal 960
| | | | |
Db 2975 CAGTTGAATTTGGCGGGAATCGTGAGCAGTGAATGGCTTGCCTTCATGGGTGTA 3034
QY 961 PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980
| | | | |
Db 3035 TTTGAGAAATCTTAACCAATTTAGTGTTTTGAACCTTAAGTAAAGAAATTTCTACTCTAT 3094
QY 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGlnAla 1000
| | | | |
Db 3095 CCAGATTAAGTCAGAAAACTTAAGCCAAGTGTATCCAGTTAACTTTCTCGAANAACCT 3154
QY 1001 ArgLeuValGlyTyrGlnPheAspAspAspAspLeuSerValIleThrGlyAlaPheLys 1020
| | | | |
Db 3155 AGGCTTGTGGGTGGCATTTGATGATGATGATCTCACTGTATTATACAGTGCTTTTAAA 3214
QY 1021 LeuValThrAla 1024
| | | | |
Db 3215 CTAGTAACCTGCT 3226

```

RESULT 12
 US-09-667-298-66
 ; Sequence 66, Application US/09667298
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Y. Tom

```

: APPLICANT: Liu, Chenghua
: APPLICANT: Zhou, Ping
: APPLICANT: Asundi, Vinod
: APPLICANT: Ren, Feiyan
: APPLICANT: Zhao, Qing A.
: APPLICANT: Zhang, Jie
: APPLICANT: Xue, Aidong J.
: APPLICANT: Wang, Jidan-Rui
: APPLICANT: Chen, Rui-hong
: APPLICANT: Drmanac, Radoje T.
: TITLE OF INVENTION: Novel Nucleic Acids and
: FILE REFERENCE: Polypeptides
: CURRENT APPLICATION NUMBER: US/09/667,298
: PRIOR APPLICATION NUMBER: 09/577,408
: PRIOR FILING DATE: 2000-05-18
: NUMBER OF SEQ ID NOS: 178
: SOFTWARE: pt_fl_genes Version 2.0
: SEQ ID NO 66
: LENGTH: 3260
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (29)..(3229)
: US-09-667-298-66

Alignment Scores:
Pred. No.: 0 Length: 3260
Score: 5441.00 Matches: 1020
Percent Similarity: 99.80% Conservative: 2
Best local Similarity: 99.61% Mismatches: 2
Query Match: 99.67% Indels: 0
DB: 26 Gaps: 0

US-09-697-089-2 (1-1024) x US-09-667-298-66 (1-3260)
QY 1 MetaSnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
| | | | |
Db 155 TTGATATTTCATTAAGAGCAATATGCGAGCCCTTATTCAAAGATGGGATACATATATA 214
QY 21 LysGlnIleThrAspAspLeuPheValTyrAsnValLeuAsnArgGluGluValAsnIle 40
| | | | |
Db 215 AAGCAAAATCACAGATGACCTATTGTATGGAATGTTCTGAATCCCGAAGAGTAAACATC 274
QY 41 IleCysGlyGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
| | | | |
Db 275 ATTGCTCGGAAGAGGTGAGCAGAGATGCTGTAGGGGATCATTCACATGATTTTGAA 334
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTyrPasnTyrProLeu 80
| | | | |
Db 335 AAGGTTTACAGTCTCTGTAACTCTTCTTAAATCCCTTAAGAGTGGAACTATCCCTGA 394
QY 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp 100
| | | | |
Db 395 TTTCAAGACTTGAATGACAAAGCTTTTTCATCAGACATCAGAAAGAGACTTGGAGCAT 454
QY 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu 120
| | | | |
Db 455 TTGGCTCGGATTTTAAAGACTTGTACCATACCCCATCTTTTCGAACTTTTATCCCTT 514
QY 121 GlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuThrP 140
| | | | |
Db 515 GGTGAAGATATTGACATTTATTTTAACTTGAAGAACACCTTCACAGAAACCTGCTGTGG 574
QY 141 ArgLysAspGlnHisHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla 160
| | | | |
Db 575 AGGAAGAGCAACAACACATCACCGGTGAGCAGCTGACCTCGAATGGCTCTCGAGAGCT 634
QY 161 LeuGlnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeuLeuGln 180
| | | | |
Db 635 CTTCAAGACCCCTGCTCATCTGTAAGGGGAATCTGCAAGGCAAGTCCACTCTGCTGAG 694

```


OY	181	ArgIlealAmelLeuTrpGlySerGlyScyValaLeuThrLysPheVal	200
Db	695	CGAANTGCAACGCTCTGGGGCTCCGGAAATGCAAGCTCTGACCAAGTTCAAAATTCGTC	754
OY	201	PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuScyAspGlnLeu	220
Db	755	TTCTTCCCTCCGCTCCACACAGGGCCCGAGGGGACCTTTTGAACCCCTGTGATCACTC	814
OY	221	LeuAspLeuProGluThrThrLeuArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg	240
Db	815	CTGATATTACCTGGCACAAATCAGGAAGCAGACATTCATGCGCATCTGCTGAAGCTGGG	874
OY	241	GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGluAsnCyProGlu	260
Db	875	CAGAGGGTTCTTTCTTCTTGTATGGCTACAAATGAATTAACGCCACAGACTGCCACAA	934
OY	261	IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr	280
Db	935	ATCGAAGCCCTGATAAAGAAACCAACCGTTCAAGACATGTCATGTCACCACTACC	994
OY	281	ThrGluScyLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet	300
Db	995	ACTGATGCTCCAGGAGCACAACGCGAGTTTGTCCTGACTGCTGAGGTGGGGATATG	1054
OY	301	ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGlnGly	320
Db	1055	ACAGAGACACGCCCGAGGCTCTCATCCGAAAGTCTATCAAGACCTGCTGAAGGC	1114
OY	321	LeuLeuLeuGlnIleGlnLysSerArgCyLysArgAsnLeuMetLysThrProLeuPhe	340
Db	1115	TTGTGTCCTCAAAATTCAGAAATCCAGGTGCTTGAGAAATCTCATGAAGCCCTCTCTT	1174
OY	341	ValValIleThrCySalalIleGlnMetGlyLysSerGluPheHisSerHisThrGlnThr	360
Db	1175	GTGGTCATCACTTGTGCAAATCCAGATGGGAAAGTGAATTCACCTCCACACAAACA	1234
OY	361	ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysGly	380
Db	1235	ACGCTGTTCCATACCTCTCTATGATCTGTTGATACAGAAACAAACACAAACATTAAGT	1294
OY	381	ValAlaAlaSerAspPheIleArgSerLeuAspHisCyGlyAspLeuAlaLeuGluGly	400
Db	1295	GTGGCTGCAAGTGACTTCATTCGGAGCCCGAACAACCTGCGAGACTGACTGAGGGCT	1354
OY	401	ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal	420
Db	1355	GTGTCTTCCACAAAGTTTGATTTGCAATCCAGAGATGTGTCCAGCGTAAATGAGGATGC	1414
OY	421	LeuLeuThrThrGlyLeuLeuCyLysTyrThrAlaGlnArgPheLysProLysTyrLys	440
Db	1415	CTGGTGACAACTGGGCTCCCTGTAAATATACAGCTCAAAAGGTCAACCCAAAGATATAA	1474
OY	441	PhePheHisLysSerPheGlnGlnLysTyrThrAlaGlyArgArgLeuSerSerLeuLeuThr	460
Db	1475	TTCTTTCAACAAGTCATATCCAGAGAGTACACAGCAGGACGAAAGCTGACAGATTATGACG	1534
OY	461	SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle	480
Db	1535	TCTCATAGCGCAGAGGAGGAGCACAAGGGGAATGTGTACTTCGCAAAATGTTTCCATT	1594
OY	481	SerAspLeuPheSerThrTyrSerSerLeuLeuArgTyrThrCyGlyLysSerValGlu	500
Db	1595	TTCGACATTACATCCACTTATACACACTGTGCTCCGGTACACTGTGGGCTACATGTGGAA	1654
OY	501	AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCyLeuLeuGly	520
Db	1655	GCCACACAGGGCTGTTATGAAGCAGCCTCCGACAGCAGTGATACAAACAGGCTGCTCGGA	1714
OY	521	LeuSerIleAlaLysArgProLeuThrPargGlnGluSerLeuGlnSerValLysAsnThr	540
Db	1715	CTTTTCATTCGCAAGAGCCTCTCTGGAACAGGAATCTTTGCAAGGTGTAACAAACAC	1774

QY	541	ThGtGtngtngtllleuLysAlaIleasnIleasnSerPheValGlcysGlyIleHis	560
Db	1775	ACTGGCAAGAAATTCGTGAAGCCATTAACATCAATTCCTTGATGAGTGGCATCAT	1834
QY	561	LeuYrGngtngtSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPheGln	580
Db	1835	TTAATTCAGAGAGTACATCCAAATCCAGCCCTTAGCCAAAGAAATTCGAACCTTCCTTAA	1894
QY	581	GlyLysSerLeuYrIleasnSerGlyAsnIleProAspTyrLeuPheaspPheGlu	600
Db	1895	GGTAAACCTTATATATCACTCACTGAGGACATCCCGGATTAATTATTAAGCTCTTTGAA	1954
QY	601	HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysIleuAspPheTyrGlyAla	620
Db	1955	CATTGGCCCAATTGTGCAAGTGGCCCTGAGCTTCATTAACCTGGGCTTTATGGGGAGCT	2014
QY	621	MetAlaSerTrrpgLysAlaAlaGluAspThrGlyGlyIleHisMetGlnAlaPro	640
Db	2015	ATGGCTTCATGGGAAAAGCGTCGAGAAGACACGGTGGATCCACATGGAAAGGCCCA	2074
QY	641	GluTrrTyrIleProSerArgAlaValSerLeuPheAsnTrrLysGlnGluPheArg	660
Db	2075	GAACCTCATATTCCTCCACAGGGCTGTATCTTGTCTTCACTGGAAGCAGCAATTCAGG	2134
QY	661	ThrLeuGlnValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu	680
Db	2135	ACTCGAGAGTCACACCTCGGGATTTTCAGCAATTAATACCAAGATATACGATATCG	2194
QY	681	GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyAla	700
Db	2195	GGGAAATATTCACACTCTGCCACAGGCTCAGGCTCCAAATTAAGATGTGCTGTTGTG	2254
QY	701	AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu	720
Db	2255	GCTGGAAACCTCACTATTTGGTCTCAGACCTGTAAACAAATTATATCTCTCATGGTGAA	2314
QY	721	AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuYsThr	740
Db	2315	GCCAGTCCCTCACCATTAAGAAGATGAGGCAATCATCATCTGTAAACAACCTGAAACC	2374
QY	741	LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly	760
Db	2375	TTTGAGTATTCATGTGACCTACAGAAATCAACGGCTGCCGGGTGGTCTACACAGCTTGGGT	2434
QY	761	AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGlnGluAspAla	780
Db	2435	AACCTTGAAGAACCTTACAAAGCTCATTAATGATTAACATTAAGATGAAGAAGATGCT	2494
QY	781	IleLysLeuAlaGlnGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis	800
Db	2495	ATTAACACTAGCTGAAGGCTGGAAAACCTGAAGAAATGTGTTTATTTTCATTGTGACCAAC	2554
QY	801	LeuSerAspIleGlyGlnGlyMetAspTyrIleValLysSerLeuSerSerGlnProCys	820
Db	2555	TTTGCTGTCAATTGGAGAGGGAATGATTCATATGTCATCAATCTCTGTCAAGTGAACCCGT	2614
QY	821	AspLeuGlnGlnIleGlnLeuValSerCysCysLeuSerSerAlaAsnAlaValLysIleLeu	840
Db	2615	GACCTTGAAGAAATTCATTATAGTCTCTGCTGCTTGTCTGCAAAATGACGTGAATAATCTTA	2674
QY	841	AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGlnAsnTrrLeu	860
Db	2675	GCTCAGATCTTCACATTTTGGTCAAACTGACGATTCCTTGATTTTACGAAAATTAACCTG	2734
QY	861	GluLysAspGlyAsnGlnAlaLeuHisGluLeuIleAspArgMetAsnValLeuGlnGln	880
Db	2735	GAATAAGATGGAATTAAGACCTCTTCATTAAGAACTGATGACAGGATGAACGTGCTGAGACAG	2794
QY	881	LeuThrAlaLeuMetLeuProTrrpgLysAspValGlnGlySerLeuSerSerLeuLeu	900
Db	2795	CTCACCGCACTGAGTGGCCCTTGGGCTGTGAGCTGCAAAGGACGCTTACAGCCCTTGTG	2854
QY	901	LysHisLeuGlnGlnValProGlnLeuValLysLeuGlyLeuLysAsnTrrArgLeuThr	920

```

Db 2855 AACATTTGGAGAGGCTCCACAACTGTCAGACTTGGGTTGAAAACTGGAGACTCACA 2914
QY 921 AspThrGluIleArgIleLeuGIYAlaIaphepGlyLysAsnProLeuLysAsnPhegin 940
Db 2915 GATACAAAGATTGAATTTTAAAGTGTGCAATTTTGGAAAGAACCCCTCTGAAAACTTCCAG 2974
QY 941 GluLeuAsnLeuIaGIYAsnArgValSerSerAspGIYTriPheuAlaPheMetGIYAla 960
Db 2975 CAGTGAATTTGGGGGGAATTCGTGTGACGAGTCAGATGAGTGGCTTCCCTTCATGGGTGTA 3034
QY 961 PheGIYAsnLeuLysGIYAsnLeuValIpheAspPheSerThrLysGIYIuPheLeuProAsp 980
Db 3035 TTTGAGATCTTAAGCAATTAAGTGTTTTGTGACTTAAAGAAATTTCTACCTGAT 3094
QY 981 ProAlaLeuValIaGIYLysLeuSerGIYAlaLeuSerLysLeuThrPheLeuGIYAla 1000
Db 3095 CCACCAATTAGTCAGAAAACTTACCAAGTGTATCCAAAGTAACTTTCTGCAGAAAGCT 3154
QY 1001 ArgLeuValGIYTPGIYAsnPheAspAspAspLysLeuSerValIleThrGIYAlaPheLys 1020
Db 3155 AGGCTGTGTGGGGGCAATTGATGATGATGATCAAGTGTATTACAGGTCTTTTAAA 3214
QY 1021 LeuValIleAla 1024
Db 3215 CTACTACTGCT 3226

RESULT 13
US-09-864-921-96
: Sequence 96, Application US/098644921
: GENERAL INFORMATION:
: APPLICANT: Reed, John C.
: APPLICANT: Pio, Frederick F.
: APPLICANT: Godzik, Adam
: APPLICANT: Stehlik, Christian
: APPLICANT: Damiano, Jason S.
: APPLICANT: Lee, Sug-Hyung
: APPLICANT: Oliveira, Vasco A.
: APPLICANT: Hayashi, Hideki
: APPLICANT: Pawlowski, Krzysztof
: TITLE OF INVENTION: Novel Card Domain Containing
: FILE REFERENCE: P-1J 4752
: CURRENT APPLICATION NUMBER: US/09/864,921
: CURRENT FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 09/579,240
: PRIOR FILING DATE: 2000-05-24
: PRIOR APPLICATION NUMBER: US 09/686,347
: PRIOR FILING DATE: 2000-10-10
: PRIOR APPLICATION NUMBER: US 60/275,980
: PRIOR FILING DATE: 2001-03-14
: NUMBER OF SEQ ID NOS: 195
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 96
: LENGTH: 3396
: TYPE: DNA
: ORGANISM: Homo sapien
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (277)...(3348)
US-09-864-921-96

Alignment Scores:
Pred. NO.: 0 Length: 3396
Score: 5438.00 Matches: 1021
Percent Similarity: 99.80% Conservative: 1
Best Local Similarity: 99.71% Mismatches: 2
Query Match: 99.62% Indels: 0
DB: Gaps: 0

US-09-697-089-2 (1-1024) x US-09-864-921-96 (1-3396)
QY 1 MetAsnPhelIeLysASPAsnSerArgAlaLeuIleGlnArgMetGIYMetInValIle 20

```

Dp	277	ATGAATTTCTAATAAGACAAATAGCCGAGCCCTTATTCTAAAGAAAGGGAATGACGTTATA	336
Qy	21	LYGSLILIEHTRSPSPLEUPHEVALTRPASNVALIEASNAARGLUGLIVALASLILE	40
Dp	337	AAGCAATFCACAAATACCTATTGTTATGGAATGTTTCGAATCCCGAAGAAATTAACATC	396
Qy	41	ILECYSGLSLUDYSVALGLUGLINSAPLAAALARGYLILEIEHISMETILEULYS	60
Dp	397	ATTTCGCGAGAGAGGTGAGACAGATGCTGCTAAGAGGACATTCACATGATTTTGAAA	456
Qy	61	LYSGLYSERGLUSERCYSANLEUPHEULYSSERLULYSGLUTPASITTYPROLEU	80
Dp	457	AAGGTYCAGAGTCCTGTAACCTTTCTTAAATCCCTTAAGAGATGAACTATCCCTTA	516
Qy	81	PHGLINASPHEUNSLYGLINSERLEUPHEHISGLINTRSERGLUGLYASPHEUNSPASP	100
Dp	517	TTTCGAGACTTGTAATGGACAAAGTCTTTTTCATCAGACATCAGAAAGGAGACTTGACGAT	576
Qy	101	LEUALGLINASPHEULYSAPLEUTYRHSITRPROSERPHELEASNPHYTYPROLEU	120
Dp	577	TTTGCTCAGGATTTTAAAGGACCTTGACATCCATCCCATCTTTCGAATTTATCCCTT	636
Qy	121	GLYGLUSPLLEASPLLEIEPHEASNLEULYSSETRHPHEHGLIPROVALLEUTRP	140
Dp	637	GGTAACATATTTGACATTAATTTTAACTTGAAAGACACTTCACAGAACATATCTGCG	696
Qy	141	ARGLYSAPGLINHSHSHISARGVALGLUGLILEUPHTRLEUNSGLYLEULUGLINAL	160
Dp	697	AGGAAGACCAACACCATCCCGCTGGAGACGTGACCTGAATAGGCTCTCGAGGCT	756
Qy	161	LEULINSERPROCYSTILEIEGLUGLYGLUSERGLYSGLYLVYSETRHLEULENGIN	180
Dp	757	CTTGAGAGCCCTCGACATCTGAAGGGGAATCGGAAGGCAAGCACTCTGCTGCAG	816
Qy	181	ARGILEAMETLEUTRPGLYSERGLYSCYLSYSALEUTRHPHELYSPHEVAL	200
Dp	817	CGCATTCGCATGCTCTGGGCTCGGAAAGTGGAAGGCTCTGACCAAGTCAAAATTCGTC	876
Qy	201	PHEPHELEUPARGLEUSERARGALAGINGLYGLYLEUPHEGLUTRHPHECYSAPGLINLEU	220
Dp	877	TTTCTCTCCGCTGCACAGAGGCCGAGGGGTGGACCTTTTGAAGAACCTCTGTGATCAATC	936
Qy	221	LEUNSPLEIPEPOGLYTRHIEARGLYSGINTRHPHEVALAMETLEULYSLEUARG	240
Dp	937	CTGGATATACCTGGCACAAATCAGAAAGCAGACATTATGCGCATCTGCTGAAGTGGG	996
Qy	241	GLINARGVALLEUPHELEUNASPGLYTYRASNGULPHELYSPROGLINASNCSPROGLU	260
Dp	997	CAGAGGGTCTTTTCTTCTTGATGGCTCAATGAATTCMAAGCCCAACATGCCGACGAA	1056
Qy	261	ILEGLUALALEULIELYSGULASNHISARGPHELYSASMEVALILEVALIHTHTR	280
Dp	1057	ATCGAAGCCCTGATTAAGAAAGAAACCCGCTTCAGAACATGATGTCATGCCACTRACC	1116
Qy	281	THRGLUCYSEUARGHSISIEARGINPHEGLVALALEUTRHALAGLIVALGLIYSPMET	300
Dp	1117	ACTGATGCTCGAGAGCACATACGGCAGTTTGGTCCCTGACATGCTGAGGTGGGGATATG	1176
Qy	301	THRGUSPSERLAGINALALEULIEARGLIVALLEULIELYSGULEUNLAGLUGLY	320
Dp	1177	ACAGAAAGCACGCCGCGAGCTCTCATCCGAGAAAGTCTGATCAAGAGACTTGCCTGAAGC	1236
Qy	321	LEULEULENGINLEGLINYSSEARGCYSEUARGASULEMETLYSTRPROLEU	340
Dp	1237	TTTGTCCTCCAAATTCAGAAATCCAGGTGCTTGAGAAATCTATGACAGCCCTCTCTT	1296
Qy	341	VALVALIETHRCYSAALIEGLINMETGLYGLUSEGLIPHEHISSETHISHTRGLINTR	360
Dp	1297	GGGGCATACACTTGTGCATACAGATGGGGAAGGTGACCTCACCTCACACACAACAA	1356
Qy	361	THTRLEUPHEHISITRHPHYTRASPHEULILEGLINLYSASNLYSHISLYSHISLYSGLY	380

Dh 1357 ACGCTGTTCCATACCTCTGATGATCTGTTGATACAGAAAAACAAACAAACATTAAGGT 1416
Qy 381 VALAIAAIAASerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaIleuGluGly 400
Dh 1417 GTGGCTGCAAGGACTTCAATTCGGAGGCTGGACCCAGCCGAGGAGACTTACTCTGAGGGT 1476
Qy 401 VALPheSerHisLysPheAspPheGluLeuGluAsnAspValSerSerValAsnGluAspVal 420
Dh 1477 GTGTTCTCCCAACAGTTGATTTCCAACTGCAGATGTCGACGCGTGATGATGAGATGTC 1536
Qy 421 LeuLeuThrThrGlyLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 440
Dh 1537 CTGCTGACAACTGGGCTCCTCTGTAATATATACAGCTCAAGGTTCAAGCCAAAGATATAA 1596
Qy 441 PhePheHisLysSerPheGluGluGlyThrAlaGlyArgGlyLeuSerSerLeuLeuThr 460
Dh 1597 TTCCTTCCAAAGTCAATTCAGAGATACAGACAGACAGACAGACAGACAGACAGATTAATGACG 1656
Qy 461 SerHisGluProGluGluValThrLysGlyAsnGlyLysGlyLeuGluLysMetValSerIle 480
Dh 1657 TCTCATGAGCCAG 1716
Qy 481 SerAspIleThrSerThrLysSerSerLeuLeuArgLysThrCysGlySerSerValGlu 500
Dh 1717 TCGGACATTAACATCCACTTATAGCAGCTGCTCCGTTACACCTGTGGGTCAATCTGGAA 1776
Qy 501 AlaThrArgAlaValMetLysHisLeuAlaAlaValLysGluHisGlyCysLeuLeuGly 520
Dh 1777 GCCACCAAGGCTGTATAGACACTCGACAGAGTATCAACACAGGCGCTTCGGA 1836
Qy 521 LeuSerIleAlaLysArgProLeuThrParGluGluSerLeuGluSerValLysAsnThr 540
Dh 1837 CTTTCATCGCCAGAGAGGCTCTCTGAGACAGAGATCTTTGCAAAAGTGTGAAAAACAC 1896
Qy 541 ThrGluGluGluLysLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560
Dh 1897 ACTGAGCAAGAAATCTGAAGCCATAAACAATCAATCTTGTGTAGATGTGGCATCCAT 1956
Qy 561 LeuThrGluGluSerThrSerLysSerIleLeuSerGluGluGluPheGluAlaPhePheGlu 580
Dh 1957 TTATATCAAGAGATACATCCAAATACAGCCCTGAGCCAAAGAAATTTGAAGCTTCTTCA 2016
Qy 581 GlyLysSerLeuThrIleAsnSerGlyAsnIleProAspLysLeuPheAspPhePheGlu 600
Dh 2017 GGTAAACACTATATATCACTCAAGGAAACATCCCCGATTTACTTTTGACTCTTTGAA 2076
Qy 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheThrGlyAla 620
Dh 2077 CATTTGCCCAATTTGCAAGTGCCCTGGACTTCAATTAACAGTGAATTTATGGGGAGCT 2136
Qy 621 MetAlaSerTPGulLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaPro 640
Dh 2137 ATGGCTTATGGGAAAGGCTGACAGAAACAGAGGTGAATCCAAATGAAGAGGCCCA 2196
Qy 641 GluThrThrLysIleProSerArgAlaValSerLeuPheAsnThrLysGluGluPheArg 660
Dh 2197 GAAACCTCAATTCACAGAGGCTGTATCTTTGTTCTTCACTGACAGACAGAAATTCAGG 2256
Qy 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGluAspIleThrThrLeu 680
Dh 2257 ACTGTGAGGTGCACACTCCGGGATTTCAAGAAATTGAATGAACAAAGATATCAGATATCTG 2316
Qy 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGluIleLysArgCysAlaGlyAla 700
Dh 2317 GGGAAATAATTCAGCTTCCCAACAGCTCAGGCTGCAAAATGAAGATGTGCTGTGTGTG 2376
Qy 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleLysSerLeuMetValGlu 720
Dh 2377 GCTGGAACCTCAAGTTGGTCTCTGACAGCCTGAAGAATTAATTTATCTCATGTGTGAA 2436
Qy 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740
Dh 2437 GCCAGTCCCTTCACCATAGAGATGAGAGGACATCATCTGTAAACAACTGAAAC 2496

Qy 741 LeuSerIleHisAspLeuGluAsnGluArgLeuProGlyGlyLeuThrAspSerLeuGly 760
Dh 2497 TTGAGTATTCAGACCTTACAGATACAGGCTGGCGGGGTGTCTACTACAGCTTGGGT 2556
Qy 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAla 780
Dh 2557 AACCTTGAAACCTTACAAAGCTCATATGATTAACATTAAGATGATTAACAGAAAGTCT 2616
Qy 781 IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800
Dh 2617 ATAAACATGCTGAAGGCTGAAAAACCTGAAGAAGATGTGTTATTTCAATTTGACCCAC 2676
Qy 801 LeuSerAspIleGlyGluGlyMetAspLysThrIleValLysSerLeuSerSerLysProCys 820
Dh 2677 TTGCTGACATTTGAGAGGAGATTAATCAATATGATCAATCTCTGTCAAGTGAACCTGT 2736
Qy 821 AspLeuGluGluIleGluLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840
Dh 2737 GACCTTGAAAGAAATTCATTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2796
Qy 841 AlaGluAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnThrLeu 860
Dh 2797 GCTCAGAAATCTTCACAATTTGGTCAAACTGACAGCATTTGTATTCAGAAAAATTACCTG 2856
Qy 861 GluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlu 880
Dh 2857 GAAAAAGATGAATGAAGCTTTCATGAACATGATCGACAGAGATACAGTGTATACACAG 2916
Qy 881 LeuThrAlaLeuMetLeuProThrProGlyCysAspValGluGlySerLeuSerSerLeuLeu 900
Dh 2917 CTGACCGGACATGATCTGCTCGGCGGTGTGACGTCAGCAAGGCTGAGCGCTGTGTTG 2976
Qy 901 LysHisLeuGluGluValProGluLeuValLysLeuGlyLeuLysAsnThrArgLeuThr 920
Dh 2977 AAACATTTGGAGAGAGCTCCACACACTGTCAGAGCTTGGGTGAAAAACGTGGAGACTACA 3036
Qy 921 AspThrGluIleArgIleLeuGluAlaPhePheGlyLysAsnProLeuLysAsnPheGlu 940
Dh 3037 GATACAGAGATTAAGATTTAGTGCATTTTGTGAAAAACCCCTGTGAAAAACTTCCAG 3096
Qy 941 GluLeuAsnLeuValAlaGlyAsnArgValSerSerAspGlyThrLeuAlaPheMetGlyVal 960
Dh 3097 CAGTTGAATTTGGCGGGAATGTGTGACAGATGATGATGCTGCTGATGATGCTGATG 3156
Qy 961 PheGluAsnLeuLysGluLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980
Dh 3157 TTTGAGAAATCTTAACCAATTAAGTGTGTTTGTGACTTACTTAAGAAATTTCTACTGAT 3216
Qy 981 ProAlaLeuValArgLysLeuSerGluValLeuSerLysLeuThrPheLeuGluGluAla 1000
Dh 3217 CCAGCATTAAGTCAAAAACTTAAGCCAAAGTTATCAAGTTAACTTTCTGCAAGAGCT 3276
Qy 1001 ArgLeuValGlyThrGluPheAspAspAspAspLeuSerValIleThrGlyAlaPheLys 1020
Dh 3277 AGCGTTGTGGGTGGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3336
Qy 1021 LeuValThrAla 1024
Dh 3337 CTAGTAACCTGCT 3348

RESULT 14
US-09-491-404-1319
; Sequence 1319, Application US/09491404
; GENERAL INFORMATION:
; APPLICANT: Tang, Yuanhua T.
; APPLICANT: Tillinghast, John
; APPLICANT: Sinku, Ankura
; APPLICANT: Liu, Chenghua
; APPLICANT: Dimanac, Radjoje T.
; TITLE OF INVENTION: Novel Contigs Obtained
; TITLE OF INVENTION: From Various Libraries
; FILE REFERENCE: 785

;; CURRENT APPLICATION NUMBER: US/09/491.404
;; CURRENT FILING DATE: 2000-01-27
;; NUMBER OF SEQ ID NOS: 3796
;; SOFTWARE: PL_SP_genes Version 1.0
;; SEQ ID NO 1319
;; LENGTH: 3545
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: sig_peptide
;; LOCATION: (781)...(916)
;; OTHER INFORMATION: this location contains the signal peptide sequence,
;; OTHER INFORMATION: MIMSGCKALTKFVFFLRLSRAQGLFETLQDLIDPQTR, Run with SignalP
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (679)...(3279)
;; OTHER INFORMATION: similar to g13688110 in the genepept database release 114,
;; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
US-09-491-404-1319

Alignment Scores:

Pred. No.:	0	Length:	3545
Score:	5438.00	Matches:	1021
Percent Similarity:	99.71%	Conservative:	0
Best Local Similarity:	99.71%	Mismatches:	3
Query Match:	99.62%	Indels:	0
DB:	18	Gaps:	0

US-09-697-089-2 (1-1024) x US-09-491-404-1319 (1-3545)

QY 1 MetAsnPhelIeLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
DB 232 ATGATTTTCATTAAGACAAATAGCCGAGCCCTTATTCMAAATGGGAATGACTGTATATA 291
QY 21 LysGlnIleThrAspAspLeuPheValTyrPasnValLeuAsnArgGluGluValAsnIle 40
DB 292 AAGGAATATCAGATGACCTATTGTATGAAATGTTCGAATCCGGAAGAGTAAACATC 351
QY 41 IleCysGylLysValGluGlnAspAlaIleArgIleIleIleHsMetIleLeuLys 60
DB 352 ATTTGCGCGAGGAAGGTGAGACAGATGCTCTAGAGGAGATTCACATATTTTGAA 411
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTyrPasnTyrProleu 80
DB 412 AAGGTTTCAGAGTCTGTAACCTCTTCTTAATCCCTTAAGGAGTGAATATCTCTTA 471
QY 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluLysAspLeuAsp 100
DB 472 TTTCAGACCTTGAAATGACAAAGTCTTTTTCATCAGACATCAGAAAGGAGACTTGACGAT 531
QY 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProleu 120
DB 532 TTGGCTCGAGATTAAAGGACTTGACCATACCCCATCTTTTCGAACTTTTATCCCTT 591
QY 121 GlyLysAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTyr 140
DB 592 GGTAAAGATATGACATTAATTTTAACCTTGAAAGCACCTTCACAGAACCTGCTCTGG 651
QY 141 ArgLysAspGlnHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla 160
DB 652 AGGAAGGACACACACATCACCGGTGGAGCAGTGCAGATCGAATGGCTCTCGAGGCT 711
QY 161 LeuGlnSerProCysIleIleGluGluSerGlyLysGlyLysSerThrLeuLeuGln 180
DB 712 CTTGAGAGCCCTGCATCATATTGAAGGGGAATCTGGCAAAAGCAAGTCCACCTGCTGAG 771
QY 181 ArgIleAlaMetLeuTyrPglySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 200
DB 772 CGCATTCCCAAGCTCTCTGGGGCTCCGGAAGAGTCAAGGCTCGACCAAGTTCAAAATTCGTC 831
QY 201 PhePheLeuArgLeuSerArgAlaGlnGlyLysLeuPheGluThrLeuCysAspGlnLeu 220
DB 832 TTCTTCTCTCCGCTCAGAGGAGGCCAGGGTGGACTTTTGAACCTCTGTGATCAACTC 891

QY 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 240
DB 892 CTGATATTAACCTGGCACAAATCAGAGACAGACATTAATGGCCATGCTGCAAGCTCGG 951
QY 241 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 260
DB 952 CAGAGGGTCTTCTTCTCTGATGGCTACAAATTAATCAAGCCCAAGTCCAGAA 1011
QY 261 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThr 280
DB 1012 ATCGAAGCCCTGATTAAGAAAGAACACCCGCTTCAGAAATGTCATGTCACCACTACC 1071
QY 281 ThrGluLysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300
DB 1072 ACTAGATGCTCGAGGACACATTCGCGCAGTGTGCTCCCTGACTGCTGAGGTGGGGAATG 1131
QY 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 320
DB 1132 ACAGAAAGACAGCCGCCAGGCTCTCATCCGAAAGTGTGATCAAGAGACTTGTGAAGGC 1191
QY 321 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340
DB 1192 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTGAGGAATTCATGAAGACCCCTCTCTT 1251
QY 341 ValValIleThrCysAlaIleGlnMetGlyLysSerGluPheHisSerHisThrGlnThr 360
DB 1252 GTGGTCATCACTTGTGCATTCACATCGGTGAAGTGAATGATTCACATCCACACAAACA 1311
QY 361 ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysGly 380
DB 1312 ACGCTGTTCCTACCTTCTATGATCTGTGATACGAAAAACAACCAACATAAAGT 1371
QY 381 ValAlaIleSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly 400
DB 1372 GTGGCTGAAAGTCACTTCATTCGAGGCTGGAGCCAGCTGTGATACCTGATGCTGAGAGGT 1431
QY 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420
DB 1432 GTGTTCTCCCAAGATTGATTTGCAACTGCAGATGTCACACGGAATGAGAGATGTC 1491
QY 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440
DB 1492 CTGCTGACAACTGGCTCTCTGTAATATACACCTCAAAAGTTCAAGCCAAATATAAA 1551
QY 441 PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgLeuSerSerLeuLeuThr 460
DB 1552 TTCTTTTCAAGATCATTCACGAGGTACACAGCAGAGCAAGACTCAGCAGTTTATTGACG 1611
QY 461 SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480
DB 1612 TCTCATGAGCCAGAGGAGGTGACCAAGGGGAATGTTACTTCGAAATGTTTCCATY 1671
QY 481 SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500
DB 1672 TCGGACATTAATCATCTTAATAGAGGCTGCTCGGTAACACCTGTGGGTCAATCTGTGAA 1731
QY 501 AlaThrArgAlaValMetLysHisLeuAlaValTyrGlnHisGlyCysLeuLeuGly 520
DB 1732 GCCACCAAGGCTGTTATGAACACACCTGCGACAGATGATCAACACGGCTGCTTCTGGA 1791
QY 521 LeuSerIleAlaLysArgProLeuTyrArgGlnLysSerLeuGlnSerValLysAsnThr 540
DB 1792 CTTTCATCGCCAGAGAGGCTCTCTGAGACAGAAATCTTTCGAAAGTGAATAAACACC 1851
QY 541 ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560
DB 1852 ACTGAGCAAGAAATTCGAAAGCCCATTAACATCAATTCCTTTGTAAGGTGGCATCAT 1911
QY 561 LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln 580
DB 1912 TTATATCAAGAGATACATCCAAATTCAGCCCTGAGCCCAAGATTTGAACTTTTCTTCAA 1971

```

QY 581 GlySerLeuTyrIleAsnSerGlyAsnIleProAspTyrIleuPheAspPhehecu 600
    |||
Db 1972 GGTAAACCTATATATCACTCAGAGAAACATCCCGATTTCTTGTGACTTCTTTGAA 2031
QY 601 HisLeuProAsnGlyAlaSerAlaLeuAspPheIleIleuAspPheTyrGlyAla 620
    |||
Db 2032 CATTTGCCCAATTTGGCAAGGCTCTGCACTTCATTAACGGCTTTTATGGGGAGCT 2091
QY 621 MetalaserTPGluValAlaGluAspThrGlyIleHisMetGluGluValPro 640
    |||
Db 2092 ATGGCTTCATGGAAAGAGGCTGCGAGACACAGAGGTGAATCCACATGGAAGAGGCCCA 2151
QY 641 GluThrTyrIleProSerArgAlaValSerLeuPheAsnTrpLysGluIleuPheArg 660
    |||
Db 2152 GAAACCTCATCTCCAGCAGGAGGCTGTATCTTGTCTTCATCGAAGCAGGAATTCAGG 2211
QY 661 ThrLeuGluValIleThrLeuArgAspPheSerLysLeuAsnLysGluAspIleThrTyrLeu 680
    |||
Db 2212 ACTCTGGAGGTCACTCCGGGATTTTCAGCAAGTTGAATTAAGCAAGATATCAGATATCTG 2271
QY 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGluIleLysArgCysAlaGlyVal 700
    |||
Db 2272 GGGAAATATTCAGCTCTGCGCAACAGCTCAGGCTGCAATTAAGAGATGTGCTGTG 2331
QY 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu 720
    |||
Db 2332 GCTGGAACTCATCTGCTGCTCCTCAGCAGCTGTAAAGCAATTTATCTCTCATGCTGGA 2391
QY 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740
    |||
Db 2392 GCCAGTCCCTCCACCATTTGAAGATGAGAGCACAATCATCTGTAAACAACTGAAAC 2451
QY 741 LeuSerIleHisAspLeuGluAsnGluArgLeuProGlyLysLeuThrAspSerLeuLys 760
    |||
Db 2452 TTGACTATTCATGACCTCAACAATCAACGCGCTCGGCTGTGACTGACAGACTTGCGCT 2511
QY 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAla 780
    |||
Db 2512 AACTTGAAGAACCTTACAAACCTCATATGATTAACATAAAGATGAATGAAGAAGATGCT 2571
QY 781 IleLysLeuAlaGluGlyLysLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800
    |||
Db 2572 ATAAACACTAGCTGAAGGCTGAAACCTGAAAGAGATGTTTATTCATTTGACCCAC 2631
QY 801 LeuSerAspIleGlyLysLeuMetAspTyrIleValLysSerLeuSerSerGluProCys 820
    |||
Db 2632 TTGCTGACATTTGAGAGGAGGATGATTAACATGCAAGCTCTCTCAAGGAAACCTGT 2691
QY 821 AspLeuGluGluIleGluLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840
    |||
Db 2692 GACCTTGAAGAAATTCATTTAGTCTCTCGCTGCTTGTCTGCAAAATGCAAGTGAAGAA 2751
QY 841 AlaGluAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860
    |||
Db 2752 GCTCAGAAATCTTCACAAATTTGTCAAACTGAGCAATTTCTTGAATTAATCAGAAATTA 2811
QY 861 GluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluIle 880
    |||
Db 2812 GAAAGAGTGAAGAAATGAACTCTTCATGAACTGATGCAAGAGATGAACGCTCTGAAACAG 2871
QY 881 LeuThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900
    |||
Db 2872 CTCACCGACATGATGCTCCCTCGGGCGTGTGACGTGCAAGCAGCAGCTGAGCCTGTG 2931
QY 901 LysHisLeuGluGluValProGluLeuValLysLeuGlyLysLeuLysAsnTrpArgLeuThr 920
    |||
Db 2932 AAAATTTGGAGAGGTGCCCACTGCAAGCTTGGGTTGAAAGAACTGAGACTGACA 2991
QY 921 AspThrGluIleArgGlyIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940
    |||
Db 2992 GATACAGAGATTAAGAAATTTTGTGTCATTTTGTGAAAGAAACCTCTGAAAGAACTTCAG 3051
QY 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyVal 960

```

```

Db 3052 CAGTTGAATTTGGCGGAAATCGTGTGAGCAGTGTGATGGCTTGCCTCATGGGTGA 3111
QY 961 PheGluAsnLeuLysGluLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980
    |||
Db 3112 TTTGGAATCTTTAAACCAATTTAGTGTTTTGTGCTTATGACTTAAAGAAATTTCTACCTGAT 3171
QY 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGluGluAla 1000
    |||
Db 3172 CCAGCATTAAGCAGAAACCTTAAGCCAACTGTATTCAGATTACTTTTCTGCAAGAACT 3231
QY 1001 ArgLeuValIleGlyTrpGluPheAspAspAspAspLeuSerValIleThrGlyAlaPheLys 1020
    |||
Db 3232 AGCGTTGTGGGTGSCAAATTTGATGATGATGATCTCAGTGTATATACAGGTGCTTTTAA 3291
QY 1021 LeuValThrAla 1024
    |||
Db 3292 CTAGTAACTGCT 3303

RESULT 15
US-09-922-279-1319
: Sequence 1319, Application US/09922279
: GENERAL INFORMATION:
: APPLICANT: Tang, Yuanhua T.
: APPLICANT: Tillinghast, John
: APPLICANT: Slinku, Ankura
: APPLICANT: Liu, Chenghua
: APPLICANT: Drmanac, Radote J.
: TITLE OF INVENTION: Novel Contigs Obtained
: TITLE OF INVENTION: From Various Libraries
: FILE REFERENCE: 785
: CURRENT APPLICATION NUMBER: US/09/922, 279
: PRIOR FILING DATE: 2001-08-03
: PRIOR APPLICATION NUMBER: 09/491,404
: PRIOR FILING DATE: 2001-01-25
: NUMBER OF SEQ ID NOS: 3796
: SOFTWARE: PL_SP_genes Version 1.0
: SEQ ID NO 1319
: LENGTH: 3545
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: sig_peptide
: LOCATION: (781)...(916)
: OTHER INFORMATION: this location contains the signal peptide sequence,
: OTHER INFORMATION: MIMSGCKALKTKFFFLRSRAQGGFLFLLCDQLDIPETIR, Run with Signal
: NAME/KEY: misc_feature
: LOCATION: (679)...(3279)
: OTHER INFORMATION: similar to g13688110 in the genepept database release 114,
: OTHER INFORMATION: Run with FASTX 3.3000, default parameters
US-09-922-279-1319

Alignment Scores:
Pred. No.: 0 Length: 3545
Score: 5438.00 Matches: 1021
Percent Similarity: 99.71% Conserves: 0
Best Local Similarity: 99.71% Mismatches: 3
Query Match: 99.62% Indels: 0
DB: 34 Gaps: 0

US-09-697-089-2 (1-1024) x US-09-922-279-1319 (1-3545)
QY 1 MetAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
    |||
Db 232 ATGATTTTCATTAAGGACAAATAGCCGACCTTATTCAAAGAAATGGGAATGACTGTATA 291
QY 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle 40
    |||
Db 292 AAGCAATACAGATGACCTATTTGTATGAGATGTTCTGAATCCGAAAGATGAATCAATC 351
QY 41 IleCysGlyLysValGluGluAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
    |||
Db 352 ATTTGCTCGGAAGAGGTGAGACAGAGATGCTCTGAGAGGAGATTCACATGATTTTGAA 411

```

OY	61	LysGIysSerGIusErCysAsnLeuPheLysSerLeuLysGIuTrpAsnTrpProLeu	80
Db	412	AAGGTCCTAGAGTCTCTGTAACTCTTCTTAAATCCCTTAAGAGAGTGAACATATCTCTTA	471
OY	81	PheGIAsnPheAsnGnGIyGInSerLeuPheHISGIuTrpSerGIuLysPheAspSP	100
Db	472	TTTCAGAGCTTGAAATGGACAAAGCTTTTTCATCAGACATCAGAAAGAGACTTGGACAT	531
OY	101	LeuAlaGInAsnPheLysAsnPheLysTrpHisTrpSerPheLeuAsnPheTrpProLeu	120
Db	532	TTGGCTCAGGATTTTAAAGAGACTGTGTACATACCCCACTTTCTGTCACTTATCCCTT	591
OY	121	GIyGIuAsnPIAsnPIIeIIPheAsnLeuLysSerTrpPheTrpIuProValLeuTrp	140
Db	592	GCTGAGATATTGCATATTATTTTAACTTGAAGAACCTTCACAGAACCTGTCTGTGG	651
OY	141	ArgLysAspGInHisHISArgValGIuGInLeuTrpLeuAsnGIyLeuLeuGInIa	160
Db	652	AGGAAGGACCAACATCAACCGGTGTGAGACACTGACCTGTAAATGGCTCTCGACAGCT	711
OY	161	LeuGInSerProCysIIeIIGluGIyGIuSerGIyLysGIyLysSerTrpLeuGIn	180
Db	712	CTTGAGACCCCTCATCATTTGAAGGGGAACTGTGGAAAGGCAGCAAGTCCATCTGTGTAG	771
OY	181	ArgIleAlaMeIeUTrpGIySerGIyLysCysLysAlaLeuTrpHisPheLysPheAl	200
Db	772	CGCATGTGCATGCTCTGGGGCTCGGAAAGTGTGAAGGCTGTGACCAAGTCCAAATTCGT	831
OY	201	PhePheLeuArgLeuSerArgAlaGInGIyGIyLeuPheGInTrpLeuCysAspGInLeu	220
Db	832	TTTCTTCCTCCCTCACACAGGGCCAGGGGAGACTTTTGAACCTCTGTATCACTG	891
OY	221	LeuAspIleProGIyTrpIleArgLysGIuTrpPheMetAlaMeIeULeuLysLeuArg	240
Db	892	CTGATATACCTGGCACAAATCAGAAAGCAACATCATGTGCCATGCTGTGAAGCTGGG	951
OY	241	GIuArgValLeuPheLeuLeuAspGIyTrpAsnGIuPheLysProGInAsnCysProGIu	260
Db	952	CAGAGGGTCTTTTCTTCTTGTGATGGTCAAAAGAAATTCAGGCCCAAGTCCAGTCCCA	1011
OY	261	IleGIuAlaLeuIleLysGIuAsnHISArgPheLysAsnMeValIleValTrpTrpTr	280
Db	1012	ATCGAAGCCCTGATTAAGGAAGAAACCCGCTTAAAGACATGGCTATGTCAACCCTAAC	1071
OY	281	ThrGIuCysLeuArgHISIleArgGInPheGIyAlaLeuTrpAlaGIuValGIyAspMet	300
Db	1072	ACTGATGCTCTGAGGACATACGGCAAGTTGTGGCCCTGACTGTGAGGTGGGGATATG	1131
OY	301	ThrGIuAspSerArgAlaGInAlaLeuIleArgGIuValLeuIleLysGIuLeuAlaGIuGIy	320
Db	1132	ACAGAAAGCACGGCCAGGGCTCTATCCGAAAGTCTGTATCAAGGACGTTCTCTAAGCC	1191
OY	321	LeuLeuLeuGInIleGInLysSerArgCysLeuArgAsnMeUeLysTrpProLeuPhe	340
Db	1192	TTGTGTCCTCAAAATTGAGAAATCCAGGTGCTTAGGAATCTATGAAGACCCCTCTCTT	1251
OY	341	ValValIleThrCysAlaIleGInMetGIyLysErGIuSerGIuPheHISerHISThrGIuTr	360
Db	1252	GTGGTCATCACTTGTCAAATCCAGATGGGGAAGGTGAGTCCACTCTCACACACAAACA	1311
OY	361	ThrLeuPheHISThrPheTrpAsnPheLeuIleGInLysAsnLysHISLysHISLysGIy	380
Db	1312	ACGGTGTCCATTACTTCTATGATCTGTGTATACAAAAAACAAACAAACATTAAGGT	1371
OY	381	ValAlaAlaSerAspPheIleArgSerLeuAspHISCysGIyAspLeuAlaLeuGIuGIy	400
Db	1372	GTGGCTGCAAGTGACTTCATTCGAGGCTGTGACACTGTGATACCTACTGTGAGAGGT	1431
OY	401	ValPheSerHISLysPheAspPheGIuLeuGInAspValSerSerValAsnGIuAspVal	420
Db	1432	GTGTTCCTCCCAAGATTGTGATTTCGAATGTGACAGATGTGTCCAGCTGTAAATGAGATGTC	1491

QY	421	LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLeuProLysTyrLys	440
Db	1492	CTGGCGAACACTGGGGCTCTCTGTAAATATACAGCTCAAGAGTTTCAAGCCAAAGATATAA	1551
QY	441	PhePheHisLysSerPheGlnGluTyrThrAlaGlyValArgLysLeuSerLeuLeuThr	460
Db	1552	TTCCTTACCAAGTCATTCTCCAGNATTACACGACGAGCAAGNACTCAGAGTTATTAGAG	1611
QY	461	SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle	480
Db	1612	TCCTATGAGCCACAGAGAGAGTACCAAGGGAAATGGTTACTTTCAGAAAATGGTTTCCATT	1673
QY	481	SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu	500
Db	1672	TGGGCACTTACATTCACACTTATAGCAAGCTCTCGCGTACACCTGTGGGCATCTGTGGAA	1733
QY	501	AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly	520
Db	1732	GGCACACAGGGCTGTTATGAACACCTCGACAGTGTATATCAACAGCGGTCCCTTCGGA	1799
QY	521	LeuSerIleAlaLysArgProLeuThrArgGlnGlnSerLeuGlnSerValLysAsnThr	540
Db	1792	CTTTTCATCGCCCAAGAGGCGCTCTGGAGACAGAACTTTGGAAAGTGTAAGAAAAACAC	1851
QY	541	ThrGlnGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis	560
Db	1852	ACTGAGCAAAAAATTCGSAAGCCATTAACATCAATTCTTTAGAGTGTGGCATCATC	1911
QY	561	LeuTyrGlnGlnSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln	580
Db	1912	TTATATTCAGAGAGTACATCCAAATCAGCCCTGAGCCAAATAATTGAACCTTCTTTCAA	1973
QY	581	GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPheGlu	600
Db	1972	GGTAACACTTATATATCAACTCAGGGGAACATCCCGATTACTTATTGACTCTTTGGA	2033
QY	601	HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyGlyAla	620
Db	2032	CATTTGGCCCAATGTGCAGAGGCTCTGACTTATTAATGAATGGGCTTTATGTGGGAGCT	2091
QY	621	MetAlaSerTrpGluLysAlaAlaGlnAspThrGlyGlyIleHisMetGluLysLysPro	640
Db	2092	ATGGGTTATATGGAAAGAGCGTCGCAAGACACACAGTGGAAATCCACATGGAAAGGCCCA	2151
QY	641	GluThrTyrIleProSerArgAlaValSerLeuPheAsnTrpLysGlnGluPheArg	660
Db	2152	GAACCTCAATTTCCACAGAGGGCGTATCTTTGTCTTCAACCTGGAAAGCAGCAATTTCAAG	2211
QY	661	ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu	680
Db	2212	ACTCTGGAGGTACACCTCGGGATTTACGAAAGTTGAATAGCAAAATTTCCAGATATCTCG	2273
QY	681	GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal	700
Db	2272	GGGAAATATTCAGCTCGCCACAGGCTCAGGCTGCAATAAAGAGATGCTCGTGTGG	2333
QY	701	AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu	720
Db	2332	GCTGGAAACCTCAGTTGGTCTTCGACCTGTGAAGAACCTTTATTTCTCTCATGTGGGA	2391
QY	721	AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr	740
Db	2392	GGCACTCCCTCACCATTAAGAAGATGAAGCACATCATCTGTATACAAACCTGAAAAC	2451
QY	741	LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly	760
Db	2452	TTGAGTATTTCATGACTACACAAATCAACAGGCTCGCGGTGGTCTGACTACAGCTTGGGT	2511
QY	761	AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluLysAla	780
Db	2512	AACCTTGAAGAACCTTACAAAGCTATATATGATATACATTAAGATGAATGAAGACAGTCT	2573
QY	781	IleLysLeuAlaGluGlyLeuLysAsnLeuLysMetCysLeuPheHisLeuThrHis	800

```
Db 2572 ATAAACTAGCTGAAGCCCTGAAAAACCTGAAGAGATGTGTTATTCATTGACCCAC 2631
QY 801 LeuSerAspIleGlyGluGlyMetAspTyrIleValIysSerLeuSerSerGluProCys 820
Db 2632 TTGTCGACATTGGAGAGGAAATGATGATACATAGCAAGTCTCTGCAAGTGAAACCTGT 2691
QY 821 AspleuGIuGIleGIleuValSerCysCysLeuSerAlaAsnAlaValIysIleLeu 840
Db 2692 GACCTTGAAAGAAATTCATTAGTCTCCCTGCTGCTGCTGCTGCAAAATGCAGTGAATACTTA 2751
QY 841 AlaGlnAsnLeuHisAsnLeuValIysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860
Db 2752 GCTCAGATCTTCACAAATTTGGTCAAACTGAGACATTTTGATTTATCAGAAAATATACCTG 2811
QY 861 GluIysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGln 880
Db 2812 GAAAAAGATGGAATGAAATGAACTTTCATGAACTGAACTGAACTGAACTGAACTGAACTG 2871
QY 881 LeuThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900
Db 2872 CTCACCGCAGCTGATGCTCCCTGGGGCTGTGACGTGCAAGCGACGCTGAGCAGCTGTG 2931
QY 901 LysHisLeuGluGluValProGlnLeuValIysLeuGlyLeuLysAsnTyrArgLeuThr 920
Db 2932 AAACATTGGAGAGAGGTCCCACTGCTCAAGCTTGCGTTGAAATACTGGAGACTCACA 2991
QY 921 AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940
Db 2992 GATACAGAGATTAGAAATTTAGTGCATTTTGGAAAGAACCCCTGAAAAACTTCCAG 3051
QY 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPheAlaPheMetGlyVal 960
Db 3052 CAGTTGAATTTGGCGGGAATCGTGTGACAGATGATGATGATGATGATGATGATGATGATG 3111
QY 961 PheGlnAsnLeuLysGlnLeuValPhePheAspPheSerThrIysGluPheLeuProAsp 980
Db 3112 TTTGAGATCTTAAGCAATTAGTGTGTTTGTGACTTACTAAGAAATTTCTACTGAT 3171
QY 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla 1000
Db 3172 CCACCATTTAGTCAGAAAACTTACGCCAAGTGTATCCAAAGTTAACTTCTGCCAAGAACT 3231
QY 1001 ArgLeuValGlyTyrGlnPheAspAspAspAspLeuSerValIleThrGlyAlaPheLys 1020
Db 3232 AGGCTTGTTGGGTGGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATG 1024
QY 1021 LeuValThrAla 1024
Db 3292 CTAGTAACTGCT 3303
```

Search completed: January 31, 2003, 13:16:41
Job time : 5276 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 31, 2003, 08:55:41 : Search time 310 Seconds
(without alignments)
4026.925 Million cell updates/sec

Title: US-09-697-089-2
Perfect score: 5459
Sequence: 1 MNFIKNSRALIQMGMTVI.....MQPDDDLSTVITGAFKLVTA 1024

Scoring table:
PAM120
Xgapop 4.0, Xgapext 12.0
Ygapop 4.0, Ygapext 12.0
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2500250 seqs, 609544256 residues
Total number of hits satisfying chosen parameters: 5000500

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+p2n,model-DEV-xlh
-O=/cgn2_1/USPRO.spool/US09697089/funat_29012003.092506_19212/app_query.fasta.1.1223
-DB=Pending_Patents_NA_New-OFMT-fastap-SUFFIX=p2n.rnpn-MINMATCH=0.1
-LOOPCL=0-LOOPEXT=0-UNITS-bits-START=1-END=1-MATRIX=pam120
-TRANS=human40.cdi-LIST=45-DOCALIGN=200-THR SCORE=pct-THR MAX=100
-THR MIN=0-ALIGN=15-MODE=LOCAL-OUTFMT=plo-NORM=ext-HEAPSIZE=500-MINLEN=0
-MAXLEN=2000000000-USER=US09697089-ECGN_1_1_114-ETUNAT_29012003.092506.19212
-NCPU=6-ICPU=3-NO_XLPHY-NO_MMAP-LARGEQUERY-NEG_SCORES=0-WAIT-LOG=LOG
-DEV.TIMEOUT=120-WARN.TIMEOUT=30-THREADS=1-XGAPOP=4-XGAPEXT=12-FGAPOP=6
-FGAPEXT=7-YGAPOP=4-YGAPEXT=12-DELOP=6-DELEXT=7

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5453	99.9	3075	1	PCT-US02-21946A-1
2	5453	99.9	3219	1	PCT-US02-21946A-14
3	5438	99.6	3545	6	US-10-276-781-111
4	435	8.0	421	6	US-10-203-138A-4307
5	391	7.2	220	6	US-10-203-138A-9429
6	279	5.1	5984	6	US-10-285-408-2
7	279	5.1	6133	5	US-09-949-002-84
8	279	5.1	6133	5	US-09-949-002-125
9	279	5.1	60194	5	US-09-949-002-656
10	279	5.1	60195	5	US-09-949-002-697
11	270	4.9	3210	5	US-09-724-676-6819

12	270	4.9	3210	5	US-09-724-676A-6819	Sequence 6819, Ap
13	270	4.9	3597	5	US-09-724-676-6801	Sequence 6801, Ap
14	270	4.9	3597	5	US-09-724-676A-6801	Sequence 6801, Ap
15	270	4.9	4143	5	US-09-724-676-6810	Sequence 6810, Ap
16	270	4.9	4143	5	US-09-724-676A-6810	Sequence 6810, Ap
17	270	4.9	4259	5	US-09-724-676-6816	Sequence 6816, Ap
18	270	4.9	4259	5	US-09-724-676A-6816	Sequence 6816, Ap
19	270	4.9	4268	5	US-09-724-676-6824	Sequence 6824, Ap
20	270	4.9	4268	5	US-09-724-676A-6824	Sequence 6824, Ap
21	270	4.9	4280	5	US-09-724-676-6818	Sequence 6818, Ap
22	270	4.9	4280	5	US-09-724-676A-6818	Sequence 6818, Ap
23	270	4.9	4646	5	US-09-724-676-6798	Sequence 6798, Ap
24	270	4.9	4646	5	US-09-724-676A-6798	Sequence 6798, Ap
25	270	4.9	4667	5	US-09-724-676-6800	Sequence 6800, Ap
26	270	4.9	4667	5	US-09-724-676A-6800	Sequence 6800, Ap
27	270	4.9	5189	5	US-09-724-676-6815	Sequence 6815, Ap
28	270	4.9	5189	5	US-09-724-676A-6815	Sequence 6815, Ap
29	270	4.9	5192	5	US-09-724-676-6807	Sequence 6807, Ap
30	270	4.9	5192	5	US-09-724-676A-6807	Sequence 6807, Ap
31	270	4.9	5210	5	US-09-724-676-6817	Sequence 6817, Ap
32	270	4.9	5210	5	US-09-724-676A-6817	Sequence 6817, Ap
33	270	4.9	5213	5	US-09-724-676-6809	Sequence 6809, Ap
34	270	4.9	5213	5	US-09-724-676A-6809	Sequence 6809, Ap
35	270	4.9	5576	5	US-09-724-676-6797	Sequence 6797, Ap
36	270	4.9	5576	5	US-09-724-676A-6797	Sequence 6797, Ap
37	270	4.9	5597	5	US-09-724-676-6799	Sequence 6799, Ap
38	270	4.9	5597	5	US-09-724-676A-6799	Sequence 6799, Ap
39	270	4.9	6122	5	US-09-724-676-6806	Sequence 6806, Ap
40	270	4.9	6122	5	US-09-724-676A-6806	Sequence 6806, Ap
41	270	4.9	6143	5	US-09-724-676-6808	Sequence 6808, Ap
42	270	4.9	6143	5	US-09-724-676A-6808	Sequence 6808, Ap
43	96	1.8	601	5	US-09-949-002-3101	Sequence 3101, Ap
44	96	1.8	601	5	US-09-949-002-3981	Sequence 3981, Ap
45	94	1.7	916	5	US-09-724-676-19376	Sequence 19376, A

ALIGNMENTS

RESULT 1
PCT-US02-21946A-1
Sequence 1, Application PC/TUS0221946A
GENERAL INFORMATION:
APPLICANT: Thomas Jefferson University
TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING
FILE REFERENCE: 480140.477PC
CURRENT APPLICATION NUMBER: PCT/US02/21946A
CURRENT FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 3075
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(3075)
PCT-US02-21946A-1

Alignment Scores:
Pred. No.: 0
Score: 5453.00
Percent Similarity: 99.90%
Best Local Similarity: 99.90%
Query Match: 99.89%
DB: 1
Gaps: 0

US-09-697-089-2 (1-1024) x PCT-US02-21946A-1 (1-3075)

Qy 1 MetaphoricallySASPasSerArgAlaLeuIcglAtgMetClyMethrValile 20
|||||
Db 1 ATGATTTCATTAAGGACATATGCGAGCCCTTATTCAAGAATGGAATGACTTTATA 60
|||||

Length: 3075
Matches: 1023
Conservative: 0
Mismatch: 1
Indels: 0

QY	21	LysGlnIleThrAspAspLeuPheValITrpAsnValLeuAsnArgGluGluValAsnIle	40
Db	61	AAGCAAAATCACAGCATGACCTATTGTGATGGAATGTTCTGAATCGCGAAGAGTAACATC	120
QY	41	IleCysCysGluLysValGluGlnAspAlaIleArgGlyIleIleHisMetIleLeuLys	60
Db	121	ATTGCTCTCGAAGGAAAGTGGAGCAGAGATGCTGGTAGGGGATCATATTCACATGATGTTTTGAA	180
QY	61	LysGlySerGlnSerCysAsnLeuPheLeuLysSerLeuLysGluITrpAsnTyrProLeu	80
Db	181	AAGGTTTCAGAGTCTCTTAACCTCTTTCTTAAATCCCTTAAGAGATGGAATCTCTTA	240
QY	81	PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp	100
Db	241	TTTCAGAGCTGTGAATGAGCAAAAGCTCTTTTTCATCAGACATCAGAAAGAGACTTGAGCAT	300
QY	101	LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu	120
Db	301	TTGGCTCAGGATTTAAAGGACTGTACACATACCCCATCTTTCTCAACTTTATCCCTT	360
QY	121	GlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTrp	140
Db	361	GCTGAAGATATATGACATATATTTTAACTTGAAAAGACCTTTCACAGAAACTGTCTGTGG	420
QY	141	ArgLysAspGlnHisHisAsnArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla	160
Db	421	AGGAAGGACCAACACCATATCCCGCTGGAGACAGCTGACCCCTGAATGGCCTCTGAGGCT	480
QY	161	LeuGlnSerProCysIleIleGluGluGlnSerGlyLysGlyLysSerThrLeuLeuGln	180
Db	481	CTTCAGAGCCCCCTGCATCATTTGAAGGGGAAATCTGGCAAAAGGCAATCCACTCTGCTGAG	540
QY	181	ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal	200
Db	541	CGAATTGCATGCTCTTGGGCTCCGGAAAGTCAGACGCTCTGACCAAGTTCAATGCTC	600
QY	201	PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu	220
Db	601	TTCTTCCTCCGCTGCACAGAGGCCAAGGGTGACCTTTTGAAAACCTCTGTGATCAACTC	660
QY	221	LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg	240
Db	661	CTGCAATATACCTGGCACAAATCAGGAAGCAGACATTCATGGCATGCTGCTGAAGCTCGG	720
QY	241	GlnArgValLeuPheLeuLeuAspGlyTyrAsnGlnPheLysProGlnAsnCysProGlu	260
Db	721	CAGAGGGTCTTCTTCTCTTGATGGCTCAAAATGAATTTAAACCCCAAGAACTGCCAATA	780
QY	261	IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr	280
Db	781	ATCAGAGCCCTGATAAAGGAAGAACACCCGTTCAAGACATGTCATGTCACCACTACC	840
QY	281	ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet	300
Db	841	ACTGATGCTCCGAGAGCACAATACGGAGTTGGTGGCCCTGACGTGAGAGTGGGGATATG	900
QY	301	ThrGlnAspSerAlaGlnAlaLeuIleIleArgGluValLeuIleLysGluLeuAlaGluGly	320
Db	901	ACAGAGACACAGCCCGAGGCTCTCATCCGGAAGTCTCATGAAGAGACTTGTCTGAAGCC	960
QY	321	LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe	340
Db	961	TTGTGCTCCCAATTCAGAAATCCAGGTGCTTGAGGAATCTGATAGAAGCCCTCTCTTT	1020
QY	341	ValValIleThrCysAlaIleGlnMetGlyGlnSerGluPheHisSerHisThrGlnThr	360
Db	1021	GTGGTCATCACTTGTGCATACAGATGGGGAAAGTGAATTCCTCACTGCACACAAACA	1080
QY	361	ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysLysGly	380
Db	1081	ACGGTGTTCATACCTCTTGATCTGTGATTCACAAAACAAACACAAACATTAAGGT	1140

QY	381	ValAlaIaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGlnGly	400
Db	1141	GTGGGTGCAAGTGCATTTCATTCGGAGCCCTGGACCACTGGAGAGACTGCTCGAGAGCT	1200
QY	401	ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal	420
Db	1201	GTGTCTCCCAAGATTGATTTGATTCGAACTGCAAGATGTGTCCAGCGGTAAATGAGAGATGTC	1260
QY	421	LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys	440
Db	1261	CTGGCAACAACCTGGCCCTCCCTGTAATATATATACAGCTCAAAAGTTCAACCAAGCAATATAAA	1320
QY	441	PhePheHisLysSerPheGlnGlnTyrThrAlaGlyArgGlyLeuSerSerLeuLeuThr	460
Db	1321	TTCTTTTCCAAAGTATCTCCAGGAGTACACAGACGACGCAAGCACTGCAGATTTCATTCACG	1380
QY	461	SerHisGlnProGlnGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle	480
Db	1381	TCTCATGTGACCAAGGAGGAGGAGACCAAGGGGAATGGTTACTTGCAGAAATAGTTTCATT	1440
QY	481	SerAspIleLeuSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu	500
Db	1441	TTCGACATTCATTCCTACTTTACAGCGCTGCTCGGTACACCTGGTGGGTCACTGTGTGAA	1500
QY	501	AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly	520
Db	1501	GCCACACAGGCGCTTATGAAAGCACCTCGCAGCAGTGTATCAACACGCGCTTCCTCGGA	1560
QY	521	LeuSerIleAlaLysArgProLeuTyrPArgGlnGluSerLeuGlnSerValLysAsnThr	540
Db	1561	CTTTCATTCGCCAAAGAGCGCTCTCTGGAGCACGAAATCTTTCCAAAGTGTGAAANACCC	1620
QY	541	ThrGlnGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis	560
Db	1621	ACTGACGAGAAATTCGAAAGCCATTAACATCAATCTCTTGTAGATGTGGCATCAT	1680
QY	561	LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln	580
Db	1681	TTATATTCAGAGAGTACATCCAAATCAGCCCTGACGCAAGAAATTGGAAGCTTCTTTCAA	1740
QY	581	GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhePheGlu	600
Db	1741	GGTAAACCTTAATATATCAACTCAGGAGCAATCCCGATTACTGTATTTGACTCTTTGAA	1800
QY	601	HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyValAla	620
Db	1801	CATTGGCCCAATTGTGCAAGTGGCCCTGGACTTCATTAACTGTGACTTTATATGGGGAGCT	1860
QY	621	MetAlaSerTyrGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluAlaPro	640
Db	1861	ATGGCTTCATGGGAAAGGCTGCGAGAAACACAGGTGGAATCCATGAGAGAGAGCCCA	1920
QY	641	GluThrTyrIleProSerArgAlaValSerLeuPheAsnThrLysGlnGluPheArg	660
Db	1921	GAAACCTACATTTCCACACAGGCGTGTATCTTTGTTCTTCACTGACAGCAAGAAATTACG	1980
QY	661	ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu	680
Db	1981	ACTGTGAGGTCACTCCCGGATTTCCAGCAAGTTGATATAGCAAGATATAGATATCTG	2040
QY	681	GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal	700
Db	2041	GGGAAATATTCACCTCTGGCCACACGCTCAGGCTGCAATTAAGATGTGTGTGTGTG	2100
QY	701	AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu	720
Db	2101	GCTGGAACCTCACTTTGTGCTCCTCACACCTGTAAAGAAATTTATCTCTATGTGTGAA	2160
QY	721	AlaSerProLeuThrIleGluAspGluAspHisIleThrSerValThrAsnLeuLysThr	740
Db	2161	GCGAGTCCCTCCACCATAGAGATGAGAGGCAATCACTCTGTATACAAACCTAANAACC	2220
QY	741	LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly	760

```
|||||
Db 2221 TTGAGTATCTGACCTACACAAATACACGCGTCCGGGTGGTCTGACTGACAGCTTGGGT 2280
Qy 761 AsnLeuYsAsnLeuThrLysLeuIleMetAspAsnIleYsMetAsnGluGluAspAla 780
Db 2281 AACTGGAAGACCTTACAAACCTCATATGATGATTAACATAAAGATGAATGAAGAAGATGCT 2340
Qy 781 IleYsLeuAlaGluGlyLeuLeuYsAsnLeuYsLysMetCysLeuPheHisLeuThrHis 800
Db 2341 ATAAACTAGCTGAAGGCTGAAAAACCTGAAGAAGATGTTTATTTCAATTTGACCCAC 2400
Qy 801 LeuSerAspIleGlyGluGlyMetAspTyrIleValIlysSerIleSerSerGluProCys 820
Db 2401 TTGCTCTGACATTCGAGAGGAGGAAATGATTAATGATCAAGCTCTCTGCAAGTGAACCTTGT 2460
Qy 821 AspleuGluGluIleGluLeuValSerCysLeuSerAlaAsnAlaValIlysIleLeu 840
Db 2461 GACCTTGAGAAATTCATATGATGCTCCGTGCTGCTGCAAAATGCAAGTGAATCCCTA 2520
Qy 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrIleu 860
Db 2521 GCTCAGATCTTCACAAATTTGGTCAACCTGAGCATTTCTTGAATTAATCAGAAATTAACCTG 2580
Qy 861 GluYsAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGln 880
Db 2581 GAAAAAGATGGAATGAAGCTCTTCATGAACTGATCGACAGATGAACGTGCTAGAACAG 2640
Qy 881 LeuThrAlaLeuMetLeuProTyrPglyCysAspValGlnGlySerLeuSerSerLeuLeu 900
Db 2641 CTCACCCACATGATGCTGCCCTGGGGCTGTGACGTGCAGACGACCTGACAGACCTGTTG 2700
Qy 901 LysHisLeuGluGluValProGluLeuValLysLeuGlyLeuYsAsnTyrArgLeuThr 920
Db 2701 AAAATTTTGGAGGAGGCTCCCAACCTGCTCAAGCTTGGGTGAAAAACCTGAGACTCACA 2760
Qy 921 AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuYsAsnPheGln 940
Db 2761 GATACAGAGATTAAGATTTTATGTCATTTTGTGAAAGAACCTCTGAAAAACCTCCAG 2820
Qy 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPleuAlaPheMetGlyAla 960
Db 2821 CAGTTGAATTTGGGGGGAATCGTGTGAGCATGTATGATGATGGCTTGCCTTATGGGTGTA 2880
Qy 961 PheGluAsnLeuYsGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980
Db 2881 TTTGAGATCTTAAGCAATTAAGTGTTTTGTACCTTACTTAAGAATTTCTACCTGAT 2940
Qy 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla 1000
Db 2941 CCACCATTAATCAGAAAAATCAGCCAGTGTATCCAAAGTTAACTTTCTGCAGAAAGCT 3000
Qy 1001 ArgLeuValGlyTyrPglInPheAspAspAspLeuSerValIleThrGlyAlaPheLys 1020
Db 3001 AGGCTTGTGGGTGGCAATTTGATGATGATGATCTCACTGTATTAACAGTGTCTTTAAA 3060
Qy 1021 LeuValThrAla 1024
Db 3061 CTAGTAACCTGCT 3072

RESULT 2
PCT-US02-21946A-14
; Sequence 14, Application PC/TUS0221946A
; GENERAL INFORMATION:
; APPLICANT: Thomas Jefferson University
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING
; TITLE OF INVENTION: FACTOR
; FILE REFERENCE: 480140.477PC
; CURRENT APPLICATION NUMBER: PCT/US02/21946A
; CURRENT FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
```

```
; LENGTH: 3219
; TYPE: DNA
; ORGANISM: Homo sapiens
; PCT-US02-21946A-14

Alignment Scores:
Pred. No.: 0
Score: 5453.00
Percent Similarity: 99.90%
Best Local Similarity: 99.90%
Query Match: 99.89%
DB: 1
Gaps: 0

US-09-697-089-2 (1-1024) x PCT-US02-21946A-14 (1-3219)

Qy 1 MetAsnPheIleYsAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
Db 145 ATGATATTTCATAAAGAGACATAGCCGAGCCCTTATTCAAAGATGGAATGACCTGTATA 204
Qy 21 LysGlnIleThrAspAspLeuPheValTyrAsnValLeuAsnArgGluGluValAsnIle 40
Db 205 AAGCAATCACAAGATGACCTATTGTATGAAATGTTCTGAATCGCGAAGAAAGTAAACATC 264
Qy 41 IleCysGluYsValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuYs 60
Db 265 ATTGCTCGAGAAAGGTGAGCAGAGATCTCTAGAGGAGATTCATCATGATTTTGAA 324
Qy 61 LysGlySerGluSerCysAsnLeuPheLeuYsSerLeuYsGluTyrAsnTyrProLeu 80
Db 325 AAGGTTCAAGATCCTGTAAACCTCTTCTTAATCCCTTAAGAGATGAGATATCCCTCTA 384
Qy 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp 100
Db 385 TTTCAGGACTTGAATGGAAGCAAAAGTCTTTTCAATCAGAAATCAGAAAGGAGACTTGGACGAT 444
Qy 101 LeuAlaGlnAspLeuYsAspLeuTyrHisThrProSerPheLeuAspPheTyrProLeu 120
Db 445 TTGGCTCAGATTTAAAGAGCTGTATACCATACCATCTTTTCTGAACTTTATCCCTT 504
Qy 121 GlyGluAspIleAspIleIlePheAsnLeuYsSerThrPheThrGluProValLeuTyr 140
Db 505 GGTGAAGATTAATGACATTAATTTTAACTTGAAGAACCTTCACAGAACCTGCTCTGGG 564
Qy 141 ArgYsAspGlnHisHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla 160
Db 565 AGGAGGACCAACACATACCGCGGTGAGAGCTGAGCCGTGAATGGCTCTGTGAGGCT 624
Qy 161 LeuGlnSerProCysIleIleGluGlyLysSerGlyLysGlyLysSerThrLeuLeuGln 180
Db 625 CTTCAGAGCCCTCGATCATTTGAAGGGGAATCTGGCAAAAGGCAAGTCCACTGCTGAG 684
Qy 181 ArgIleAlaMetLeuTyrPglySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 200
Db 685 CGAATTCGATGCTCTGGGGCTCCGGAAAGTCAAGGCTTCGACCAAAATTCCTC 744
Qy 201 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 220
Db 745 TTCTTCTCCGCTCAGAGGAGGCCAGGGGTGACTTTTGAACCTCTGTGATCAACTC 804
Qy 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuYsLeuArg 240
Db 805 CTGATATACCTGGGACAAATCAGAGACGACATTCATGAGGCAATGCTCTGAGAGTGGG 864
Qy 241 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 260
Db 865 CAGAGGGTCTTTCTCTTCTGATGGCTACAAATGATTAAGCCCAACATGCCCCAACA 924
Qy 261 IleGluAlaLeuIleYsGluAsnHisArgPheLysAsnMetValIleValThrThrThr 280
Db 925 ATCGAAGCCGTGATTAAGAAACCAACCGCTTCAAGAAACATGTCATCCACCACTAC 984
Qy 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300
```

Db 985 ACTGAGTCCTGAGGACATACGGCAGTTTGGTCCCTGACTGCTGAGGTGGGGATATG 1044
QY 301 ThrGluAspSerAlaGlnAlaLeuIleargLValLeuIleuysGluLeuAlaGluGly 320
|||||
Db 1045 ACGAAGACAGCGCCCGGCTCTCATCCGAAAGTGTGTATCAAGAGGCTTGGCGAAGGC 1104
QY 321 LeuLeuLeuGlnIleGlnIysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340
|||||
Db 1105 TTGTGCTCCCAATTCAGAAATCCAGGTGCTTGAGAAATCTCATGAAGACCCCTCTCTT 1164
QY 341 ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr 360
|||||
Db 1165 GTGGTATCTCTGTGAAATCCAGATGGGTGAAGTAGTTCACACTCTCCACACCAACA 1224
QY 361 ThrLeuPheHisThrPheThrAspLeuLeuIleGlnIysAsnLysHisLysLysGly 380
|||||
Db 1225 ACCGTGTCCATACCTCTCTGTATCTGTATACGAAAAACAACAAACATAAAGGT 1284
QY 381 ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly 400
|||||
Db 1285 GTGGCTGCAAGTACCTTCATTCGGAGCCGTGACCACTGTGAGACCTAGCTCTGAGAGGT 1344
QY 401 ValPheSerHisLysPheAspPheGlnLeuGlnAspValSerSerValaGlnIuAspVal 420
|||||
Db 1345 GTGTCTCCACACAGTTTGATTCGAACTGACGATGTTCACGCTGATGAGAGATGTC 1404
QY 421 LeuLeuThrThrGlyLeuLeuCysLysTyThrAlaGlnArgPheLysProLysTyLys 440
|||||
Db 1405 CTGCTGACAACTGGGCTCCCTGTGAATATACAGCTCAAGGTTCAAGCCAAATATATA 1464
QY 441 PhePheHisLysSerPheGlnGluTyThrAlaGlyArgArgLeuSerSerLeuLeuThr 460
|||||
Db 1465 TTCTTTCACAAAGTCATTCACGAGGTACACAGACGAGCAAGACACTCAGCTTATTACG 1524
QY 461 SerHisGluProGlnGluValIleThrGlyAsnGlyTyLeuGlnLysMetValSerIle 480
|||||
Db 1525 TCTCATAGCCGACGAGGAGGTGACCAAGGGAGATGTTACTTGCGAATAAGTGTTCATTT 1584
QY 481 SerAspIleThrSerThrTyThrSerSerLeuLeuArgTyThrCysGlySerSerValGlu 500
|||||
Db 1585 TCGGACATTTACATCCACTTTATAGCAGCGCTCGGTACACCTGTGGGTACTCTGTGAA 1644
QY 501 AlaThrArgAlaValMetLysHisLeuAlaAlaValTyGlnHisGlyCysLeuLeuGly 520
|||||
Db 1645 GCCACGAGGGCTGTATGAAAGCACCTCGACAGCTGTATCAACACGCGCTCTCTCGGA 1704
QY 521 LeuSerIleAlaLysArgProLeuTrpArgGlnIuSerLeuGlnSerValLysAsnThr 540
|||||
Db 1705 CTTTCCATCCGCCAAGAGGCTCTCTGAGACAGAAATCTTTGCCAAAGTGTGAAAAACAC 1764
QY 541 ThrGlnGlnIuIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560
|||||
Db 1765 ACTGAGCAAGAAATTCGAAAGCCATTAACATCAATTCCTTTGTATGAGTGTGCATCCAT 1824
QY 561 LeuTyGlnGlnIuSerThrSerLysSerAlaLeuSerGlnIuPheGlnIuAlaPhePheGln 580
|||||
Db 1825 TTTATATCAAGAGATACATCCAAATACGCCCTGAGCCCAAGAAATTTGAAGCTTCTTCAA 1884
QY 581 GlyLysSerLeuTyIleAsnSerGlyAsnIleProAspTyIleuPheAspPhePheGln 600
|||||
Db 1885 GGTAAAGGCTTATATCACTCACTCGAGGACATCCCGCATTTACTTATTTGATTTCTTTGAA 1944
QY 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyGlyAla 620
|||||
Db 1945 CATTGTGCCAATTTGCAAGGCGCTGTGACTTCATTAACGAGCATTTTATAGGGGAGCT 2004
QY 621 MetLaserTrpGluLysAlaAlaGluAspPheGlyIleHisMetGlnGluAlaPro 640
|||||
Db 2005 ATGGCTTCATGGAAGGCTGCGAAGACACAGGTGAATCCACATGGAAGAGGCCCA 2064
QY 641 GluThrTyIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnIuPheArg 660
|||||
Db 2065 GAAACCTACATTCACAGCAGGGCTGTATCTTTGTTCTTCAACTGGAACGAGGAATTCAGG 2124

QY 661 ThrLeuGluValIleThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyLeu 680
|||||
Db 2125 ACTGTGAGGTGTCACTCCCGGATTTTCAGCAAGTTTGAAAGCAATATACAGATTTCTG 2184
QY 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700
|||||
Db 2185 GGGAAAAATATTCAGCTCTGCGACAAAGCTTCAGCTGCAAAATTAAGATGTGCTGGTGTG 2244
QY 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTySerLeuMetValGlu 720
|||||
Db 2245 GCTGGAAGCTCAGTTTGGTCTCAGCAGCCTGTGAAGAACTTTATCTCTCATGGTGGAA 2304
QY 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValIleAsnLeuLysThr 740
|||||
Db 2305 GCCAGTCCCTCACCATAGAAAGTAGAGGACATCACTCATCTTAACAAACCTGAAACC 2364
QY 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyLysLeuThrAspSerLeuGly 760
|||||
Db 2365 TTGAGTATTCATGACCTTACAGAAATCAACGGCTCGGGGTGCTGTGACTGACAGCTTGGGT 2424
QY 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGlnIuAspAla 780
|||||
Db 2425 AACTTGAAGAACCTTACAAAGCTCATATATGATTAACATTAAAGATGAAGAAGATGCT 2484
QY 781 IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisIleThrHis 800
|||||
Db 2485 ATAAACTACCTGAAAGCCCTGAAAAACCTGAAAGATGTGTTATTTACTTTGACCCAC 2544
QY 801 LeuSerAspIleGlyGlnGlyMetAspTyIleValLysSerLeuSerGluProCys 820
|||||
Db 2545 TTGTCTACATTTGAGAGGGAATGATACATATGTCATGTCATCTGTCATGAAGAACCTGT 2604
QY 821 AspLeuGlnGluIleGlnLeuValSerCysLysSerAlaAsnAlaValLysIleLeu 840
|||||
Db 2605 GACCTTGAAGAAATTCATTAATAGTCTCCTGCTGTGCTGCTGCAAAATGCAAGAAATCTTA 2664
QY 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyLeu 860
|||||
Db 2665 GCTCAGAAATCTTCACAAATTTGGTCAAACTGAACTGAACTTCTTATATTCAGAAATTTACTCTG 2724
QY 861 GluLysAspGlyAsnGlnIuAlaLeuHisGlnLeuIleAspArgMetAsnValIleGluGln 880
|||||
Db 2725 GAAAAAGATGGAATTAAGAGCTTTCATGAACATGATTCACAGATGAACGTGCTTAAGAACAG 2784
QY 881 LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900
|||||
Db 2785 CTCACCGCAGTGAATGCTGCTGGGCTGTGAGCTGCAAGGACGCTGAGCAGCCTGTGTG 2844
QY 901 LysHisLeuGlnGluValIleProGlnLeuValLysLeuIleLysLeuAsnTrpArgLeuThr 920
|||||
Db 2845 AAACATTTGGAGGAGGTCCCAACCTGTCAAAGCTTGGAAGAACTGGAAGCTGACAC 2904
QY 921 AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940
|||||
Db 2905 GATACAGAGATTAAGATTTTAAGTGCATTTTGTGAAGAAACCTCTGAAAAACTTCCAG 2964
QY 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyIleuAlaPheMetGlyVal 960
|||||
Db 2965 CAGTTGAATTTGGCGGGAATTCGTGTAGCAGTATGATGAGTGGCTTGCCTCATGGGTGA 3024
QY 961 PheGluAsnLeuLysGlnLeuValIlePhePheAspPheSerThrLysGlnPheLeuProAsp 980
|||||
Db 3025 TTTTGAATCTTAAGCAATTAAGTGTTTTGTGACTTGTAGTCTTAAGAAATTTCTACCTGAT 3084
QY 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnIuAla 1000
|||||
Db 3085 CCAGCATTTAGTCAAAAACTTAAGCAGTGTATCAAGTTAACTTTTCTGCAAGAAAGCT 3144
QY 1001 ArgLeuValGlyTrpGlnPheAspAspAspAspLeuSerValIleThrGlyAlaPheLys 1020
|||||
Db 3145 AGGCTGTGGTGGCATTTGATGATGATGATGATCATGATGTATATACAGGTGCTTTAAA 3204

Oy 1021 LeuValThrAla 1024
|
Db 3205 CTAGTAAGTCT 3216

RESULT 3
US-10-276-781-111
; Sequence 111, Application us/10276781
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-018 (785 conf19)
; CURRENT APPLICATION NUMBER: us/10/276,781
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/491,404
; NUMBER OF SEQ ID NOS: 2018
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 111
; LENGTH: 3545
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-781-111

Alignment Scores:
Pred. No.: 0 Length: 3545
Score: 5438.00 Matches: 1021
Percent Similarity: 99.71% Conservative: 0
Best Local Similarity: 99.71% Mismatches: 3
Query Match: 99.62% Indels: 0
Gaps: 0

US-09-697-089-2 (1-1024) x US-10-276-781-111 (1-3545)

Oy 1 MetAsnPhelIeLysAspAsnSerArgAlaLeuIleGlnArgMetClyMetThrValIle 20
Db 212 ATGATTTTCATTAAGAGCAATAGCGAGCCCTTATTCAAGAAATGGAAATGACTGTATA 291

Oy 21 LysGlnIleThrAspAspLeuPheValIleTrpAsnValIleAsnArgGluGluValAsnIle 40
Db 292 AAGCAAAACACAGATGACCTATTGTGTATGAAATGTCGAATCGCGAAGAAAGTAAACATC 351

Oy 41 IleCysCysGluLysValGluGlnAspAlaIleArgGlyIleIleHisMetIleLeuLys 60
Db 352 ATTGCTCGCGAAGGTGAGCAGGATCTGCTAGAGGATCATTCACATGTTTGTAA 411

Oy 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluIleTrpAsnIleProLeu 80
Db 412 AAGGTTTCAGAGTCCTGTAACTCTTCTTAATCCCTTAAGAGGTGAGACTATCCCTTA 471

Oy 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnIleThrSerGluGlyAspLeuAspAsp 100
Db 472 TTTCAGGACTTGAAATGCAAGATCTTTTCATCAGACATCAGAAAGGAGACTTGACGAT 531

Oy 101 LeuAlaGlnAspLeuLysAspLeuIleThrIleHisThrProSerPheLeuAsnPheIleProLeu 120
Db 532 TTGGCTCGAGTTTAAAGACTTGTACCATACCCCATCTTTCTGAACTTTATCCCTT 591

Oy 121 GlyIleAspIleAspIleIlePheAsnLeuLysSerIlePheThrGluProValLeuIleTrp 140
Db 592 GGTGAGATATTGACATATTATTTAACTTGAAGACACCTTCACAGAACTGTCTGTGG 651

Oy 141 ArgIleAspGlnHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla 160
Db 652 AGGAGAGCAACACACACACCGGTGAGCAGCTGACCTGAAATGGCTCTGACAGCT 711

Oy 161 LeuGlnSerProCysIleIleGluGlyLysSerGlyLysSerIleLeuLeuGln 180
Db 712 CTTCAGACCCCTGCATATTGAAGGGAAATCTGGCAAGCAAGCTCCTGCTGAG 771

Oy 181 ArgIleAlaMetLeuIleTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 200
Db 772 CGCATTCGCAATGCTCTGGGGCTCCGGAAGATGCAAGGCTCTGACCAAGTTCAAAATTCGCT 831

Oy 201 PhePheLeuArgLeuSerArgAlaGlnGlyGluLeuPheGlnIleThrLeuCysAspGlnLeu 220
Db 832 TTCTTCCTCCGCTCAGCAGGGCCAGAGGTGACTTTTGAAGCCCTGTGATCACTC 891

Oy 221 LeuAspIleProGlyThrIleArgLysGlnIlePheMetAlaMetLeuLeuLysLeuArg 240
Db 892 CTGGATATACCTGGCAGCAATAGCAGAGACATTCATAGCCATCTGCTGAAGCTGGCG 951

Oy 241 GlnArgValIleuPheLeuLeuAspGlyIleTrpAsnGluPheLysProGlnAsnCysProGlu 260
Db 952 CAGAGGGTCTCTTCTTCCTGATGCTACATGAATTCAGGCCCAAGCTGCCAGAA 1011

Oy 261 IleGluAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValIleThrThr 280
Db 1012 ATCGAAGCCCTGATTAAGGAAACCAAGCTTCAAGAACTGATGCTGACCACTACC 1071

Oy 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300
Db 1072 ACTGAGTCCCTGAGGCACATAGCGCAGTTGTGTCCTGACCTGAGGTGGGATATAG 1131

Oy 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValIleuLysGluLeuAlaGluGly 320
Db 1132 ACAGAAAGACAGGCCCAAGGCTCTCATCCAGAACTGATCAAGAACTGCTGAAAGC 1191

Oy 321 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340
Db 1192 TTGTGCTCCAAATTCACAAATCCAGGTGCTTGAAGAAATCTCATGAACCCCTCTCTT 1251

Oy 341 ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr 360
Db 1252 GTGCTCATCAGCTTGCAATCAGATGAGTGAATGATGATTCACATCCACACCAAAACA 1311

Oy 361 ThrLeuPheHisThrPheIleTrpAspLeuLeuIleGlnLysAsnLysHisLysGly 380
Db 1312 ACGCTGTTCATACCTCTTATGATCTGTGATACAGAAACCAACAAACATTAAGGT 1371

Oy 381 ValAlaIleAspAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGlnGly 400
Db 1372 GTGGCTGCAGAGACTTATTCGAGGCTGAGCCCTGTGGATCTGAGTCTGAGAGGT 1431

Oy 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420
Db 1432 GTGTTCTCCCAACAACTTGATTTGCACTGCAGATGTGTCAGAGGTGAATGAGATGTC 1491

Oy 421 LeuLeuThrThrGlyLeuLeuCysLysIleThrAlaGlnArgPheLysProLysIleLys 440
Db 1492 CTGCTGACAACTGGGCTCTCTGTAATATACAGCTCAAGGTTCAAGCAAGATTAATA 1551

Oy 441 PhePheHisLysSerPheGlnGluIleThrAlaGlyArgLeuSerSerLeuLeuThr 460
Db 1552 TTCTTTCACAAAGTCAATTCAGAGATACACAGCAGACCAAGACCTCAGAGTTTATTTGACG 1611

Oy 461 SerHisGluProGluGlnValIleThrLysGlyAsnGlyIleLeuGlnLysMetValSerIle 480
Db 1612 TCTCATGAGCCAGAGAGAGTGCACAGGGAATGTTACTTGCAAAAATGTTTCCATT 1671

Oy 481 SerAspIleThrSerThrIleSerSerLeuLeuArgIleIleCysGlySerSerValGlu 500
Db 1672 TCGGACATTAATCATTATAGCAGCTGCTCCGCTACACTGGGGTCAATCTGTGAA 1731

Oy 501 AlaThrArgAlaValMetLysHisLeuAlaValIleTrpGlnHisGlyCysLeuLeuGly 520
Db 1732 GCCACCAAGGCTGTTATAGACACTCCAGCAGAGTATCAACACAGGCTGCCCTTCTCGGA 1791

Oy 521 LeuSerIleAlaLysArgProLeuIleTrpArgGlnIleSerLeuGlnSerValLysAsnThr 540
Db 1792 CTTCATATCGCCAGAGGCTCTCTGAGACAGGAATCTTTGCAAAAGTGTAAAAACACC 1851

Oy 541 ThrGluGlnIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560
Db 1852 ACTGAGCAAGAAATCTGAAAGCCATTAACATCAATCTCTTGTGAGAGTGGCATTCAT 1911

QY 561 LeuTYGInGInuSerThrSerLysSerAlaLeuSerGInGInuPheGluAlaPhePheGln 580
 |||||||
 Db 1912 TTATATCAAGAGATACATCAAAATCAGCCCTGAGCAGAAATTTGAAGCTTTCTTCAA 1971
 QY 581 GYLysSerLeuYrIleAsnSerGlyAsnIleProAspYrIleuPheAspPhePheGlu 600
 |||||||
 Db 1972 GGTAAGGCTTATATCAACTCAGGGACATCCCGATTACTTATTTGACTTTTGAA 2031
 QY 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheYrGlyAla 620
 |||||||
 Db 2032 CATTGCCCAATGTGCAAGTGCCTGACTTCACTTAACGGCTTTTATGGGGAGCT 2091
 QY 621 MetAlaSerTrpGluYrAlaAlaGluAspThrGlyIleHisMetGluAlaPro 640
 |||||||
 Db 2092 ATGGCTTCATGGGAAAGGCTGCAGAGACAGGTGGAATCCCATGAGGAAGGCCCA 2151
 QY 641 GluThrYrIleProSerArgAlaValSerLeuPheAsnTrpLysGInuPheArg 660
 |||||||
 Db 2152 GAACCTTACTTCCACCAAGGCTGTATCTTTGTTCTTCAAGTGAAGAGCAAGATTACG 2211
 QY 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGInuAspIleThrYrLeu 680
 |||||||
 Db 2212 ACTGTGAGGTTCACACCTCCGGATTTCAGCAAGTTGAATGAAGATATCAGATATCTG 2271
 QY 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGInuIleLysArgCysAlaGlyVal 700
 |||||||
 Db 2272 GGGAAATATTCAGCTCTGCACACAGCTCAGCTGCATAAAGATGCTGCTGTG 2331
 QY 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleYrSerLeuMetValGlu 720
 |||||||
 Db 2332 GCTGGAAAGCTCAGTTGGTCTCAGCACCCTGTAAGAACATTATTTCTCATGTGTGAA 2391
 QY 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740
 |||||||
 Db 2392 GCCAGTCCCTCACCATAGAAGATGAGAGGACATCATCTGTGAACAACTGAAACCC 2451
 QY 741 LeuSerIleHisAspLeuGInuAsnGInuArgLeuProGlyLeuThrAspSerLeuGly 760
 |||||||
 Db 2452 TTGGTGTTCATGACCTACAGAAATCAACGGCTGCCGGTGTGTGACTGTGACGCTTGG 2511
 QY 761 AsnLeuLysAsnLeuThrIleMetAspAsnIleLysMetAsnGluAlaAspAla 780
 |||||||
 Db 2512 AACTTGAAGAACCCTTAAACCTCATATATGATTAACATTAAGATGAAGAAGATGCT 2571
 QY 781 IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800
 |||||||
 Db 2572 ATAAATCTACTGAAAGCCTGAAACCTGAAACCTGAAAGATGTGTATTTATTCATTGACCAC 2631
 QY 801 LeuSerAspIleGlyGluGlyMetAspYrIleValLysSerLeuSerSerGluProCys 820
 |||||||
 Db 2632 TTGTCTGACATTTGAGAGGAGATGATTAATGATCAAGTCTGTCAAGTGAACCTGT 2691
 QY 821 AspLeuGluGluIleGInuLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840
 |||||||
 Db 2692 GACCTTGAAGAAATTCATTAATAGTCTCTGCTGCTGTGTCTGCAATGCAAGTGAATCTTA 2751
 QY 841 AlaGInuAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnYrLeu 860
 |||||||
 Db 2752 GCTCAGATCTTCAACAATTTGGTCAAACTGAGCATTTCTGTATTAATCAGAAATTAACCTG 2811
 QY 861 GluLysAspGluAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGln 880
 |||||||
 Db 2812 GAAAAAGATGGAATGGAAGCTTTCATGAACTGATGCACAGAGATGAACGTCTGGAACAG 2871
 QY 881 LeuThrAlaLeuMetLeuProTrpGluCysAspValGInuGlySerLeuSerSerLeuLeu 900
 |||||||
 Db 2872 CTACCCCACTGATGCTGCCCTGGGCTGTGACTGCAGAGGACACCTGAGAGAGCTGTG 2931
 QY 901 LysHisLeuGluGluValProGInuLeuValLysLeuGlyLeuLysAsnTrpArgLeuThr 920
 |||||||
 Db 2932 AAACATTTGGAGAGGCCCAACACATCGTCAAGCTTGGGTTGAAAACTGAGAGCTCACA 2991
 QY 921 AspThrIleuIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940

Db 2992 GATACAGAGATGGAATTTAGGCGCATTTTGGAAAGAACCTTGAAAACTTCAG 3051
 QY 941 GluLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyVal 960
 |||||||
 Db 3052 CATTGAAATTTGGCGGAAATTCGTGTGACGATGATGATGCTTCCCTTCATGGGTGA 3111
 QY 961 PheGluAsnLeuLysGInuLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980
 |||||||
 Db 3112 TTGGAGAAATCTTAAGCAATTAATGTTTGTGACTTATGTAATAAGATTTCTAAGTGA 3171
 QY 981 ProAlaLeuValArgLysLeuSerGInuValLeuSerLysLeuThrPheLeuGInuAla 1000
 |||||||
 Db 3172 CCAGCATTTAGTCAGAAACCTTACGCCAGTGTATACCAAGTTAACTTTGCAAGAGCT 3231
 QY 1001 ArgLeuValGlyTrpGInuPheAspAspAspLeuSerValIleThrGlyAlaPheLys 1020
 |||||||
 Db 3232 AGCGTTTGGTGGCGCAATTTGATGATGATGATCTGATTTATACAGGTGCTTTAA 3291
 QY 1021 LeuValThrAla 1024
 |||||||
 Db 3292 CTAGTACTGCT 3303

RESULT 4
 US-10-203-138A-4307
 ; Sequence 4307, Application US/10203138A
 ; GENERAL INFORMATION:
 ; APPLICANT: Molecular Dynamics, Inc.
 ; APPLICANT: Penn, Sharon G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
 ; FILE REFERENCE: PB 0004 WO 8
 ; CURRENT APPLICATION NUMBER: US/10/203,138A
 ; CURRENT FILING DATE: 2002-08-02
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 04 February 2000 (04.02.00)
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 26 May 2000 (26.05.00)
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 03 August 2000 (03.08.00)
 ; PRIOR APPLICATION NUMBER: GB 24263,6
 ; PRIOR FILING DATE: 03 October 2000 (03.10.00)
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 27 September 2000 (27.09.00)
 ; PRIOR APPLICATION NUMBER: US 60/234,687
 ; PRIOR FILING DATE: 21 September 2000 (21.09.00)
 ; PRIOR APPLICATION NUMBER: US 09/608,408
 ; PRIOR FILING DATE: 30 June 2000 (30.06.00)
 ; SOFTWARE: Molecular Dynamics Sequence Listing Engine
 ; SEQ ID NO 4307
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: MAP TO AC011232.3
 ; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5
 ; US-10-203-138A-4307

Alignment Scores:
 Pred. No.: 1,15e-55 Length: 421
 Score: 435.00 Matches: 80
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 7.97% Gaps: 0
 DB: 6
 US-09-697-089-2 (1-1024) x US-10-203-138A-4307 (1-421)

```

QY 928 GJYAlaphbPhgGLyysAnpProleuYsAnpHegInclInleuAnleuAlaGLyAsn 947
      |||||||
Db 181 GGTCGATTTTTTGGAAAGAACCCCTCTGAAAAACCTTCAGACAGTTGAATTTGGCGGAAAT 240
QY 948 ArGvaIsErSerAspGlyTrPleuAlaPheMeGlyValPheGluAsnLeuYsGlu 967
      |||||||
Db 241 CGTGTGAGACGATGATGATGGCTTGCTTCATGTGGTGTATTTCGAATCTTAACCAATTA 300
QY 968 ValPhepHeAspPheSerThrylsGluPheLeuProAspProAlaLeuValArgLysLeu 987
      |||||||
Db 301 GGTGTTTTTGACTTGTAGTACTAAAGAAATTTCTACATGCATGCACATATGTCAGAAAACCTT 360
QY 988 SerGInValLeuSerLySLeuThrPheLeuGInGluAlaArgLeuValIGlyTrPcInPhe 1007
      |||||||
Db 361 ACCCAAGTGTATTCCAAAGTTAACTTTTCGCAAGAGCTAAGCTTGTGGGTGGCAAAATT 420

RESULT 5
US-10-203-138A-9429
US-10-203-138A
/ SEQUENCE 9429, APPLICATION US/10203138A
/ GENERAL INFORMATION:
/ APPLICANT: Molecular Dynamics, Inc.
/ APPLICANT: Penn, Sharon G.
/ APPLICANT: Rank, David R.
/ APPLICANT: Hanzel, David K.
/ APPLICANT: Chen, Wensheng
/ TITLE OF INVENTION: HUMAN GENOME- DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
/ FILE REFERENCE: PB 0004 WO 8
/ CURRENT APPLICATION NUMBER: US/10/203,138A
/ CURRENT FILING DATE: 2002-08-02
/ PRIOR APPLICATION NUMBER: US 60/180,312
/ PRIOR FILING DATE: 04 February 2000 (04.02.00)
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 26 May 2000 (26.05.00)
/ PRIOR APPLICATION NUMBER: US 09/632,366
/ PRIOR FILING DATE: 03 August 2000 (03.08.00)
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 03 October 2000 (03.10.00)
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 27 September 2000 (27.09.00)
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 21 September 2000 (21.09.00)
/ PRIOR APPLICATION NUMBER: US 09/608,408
/ PRIOR FILING DATE: 30 June 2000 (30.06.00)
/ NUMBER OF SEQ ID NOS: 15438
/ SOFTWARE: Molecular Dynamics Sequence Listing Engine
/ SEQ ID NO 9429
/ LENGTH: 220
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: MAP TO AC011232.3
/ FEATURE:
/ OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5
/ FEATURE:
/ OTHER INFORMATION: NT HIT: U75273.1, EVALUE 8.20e+00
/ FEATURE:
/ OTHER INFORMATION: EST_HUMAN HIT: AI263294.1, EVALUE 1.00e-121
/ OTHER INFORMATION: SWISSPROT HIT: P24583, EVALUE 1.60e+00
US-10-203-138A-9429

Alignment Scores:
Pred. No.: 2,37e-49 Length: 220
Score: 391.00 Matches: 73
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.16% Indels: 0
DB: 6 Gaps: 0

QY 944 LeuAlaGlyAsnArgValSerSerAspGlyTrPleuAlaPheMeGlyValPheGluAsn 963
US-09-697-089-2 (1-1024) x US-10-203-138A-9429 (1-220)

```

DB: 1 TTTGGGGGAAATCGTGTGACGATGATGAGGCTGCTTCATGAGGGGTGATTTTGACAAAT 60

QY 964 LeuLysGlnLeuValPhePheAspPheSerThrLysGlnPheLeuProAspPricAlaLeu 983

DB 61 CTTAAGCAATTAGTGTGTTTTTTTGTGACTTATGTAAGTAAGATTTTACCGTGCATCCAGCATTA 120

QY 984 ValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAlaArgLeuVal 1003

DB 121 GTCAAGAAAACCTTAGCCCAAGTGTATCCAAAGTTAACTTTTCGCAAGAACGTAAGCTGTGT 180

QY 1004 GlyTrpGlnPheAspAspAspSerValIleThr 1016

DB 181 GGGTGCATTTGATGATGATGATCTCAGTGTATTACA 219

RESULT 6
US-10-285-408-2
Sequence 2, Application US/10285408
GENERAL INFORMATION:
APPLICANT: IKEDA, Johe
TITLE OF INVENTION: Monoclonal Antibodies Against Human Apoptosis Inhibitory Prote
TITLE OF INVENTION: and Method For Assaying the NMP
FILE REFERENCE: 2002-1440/WMC/00653
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: 09/830,338
PRIOR FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: PCT/JP99/05841
PRIOR FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
LENGTH: 5984
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDC
LOCATION: (292)..(4500)
US-10-285-408-2

Alignment Scores:
Pred. No.: 2.2e-30 Length: 5984
Score: 279.00 Matches: 120
Percent Similarity: 53.80% Conservative: 78
Best Local Similarity: 32.61% Mismatches: 156
Query Match: 5.11% Indels: 15
DB: 6 Gaps: 6

US-09-697-089-2 (1-1024) x US-10-285-408-2 (1-5984)

QY 150 GlnGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGluGly 169

DB 1642 GAACCTCTGGTGCTCTCCGAGGCTCTTTGGCAACTTGAACCTGTGCATGTGTGTGAGGGT 1701

QY 170 GlnSerGlyLysGlyLysSerThrLeuLeuGlnIleArgIleAlaMetLeuTrpGlySerGly 189

DB 1702 GAAGCTGGAAAGGAAAGACGCGCTCCTCGAAGAAATAGCTTTTCTGTGGGCAATCGGA 1761

QY 190 LysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSer-----Arg 207

DB 1762 TGCTCTCCCTCGTGTAAACAGGTCCAGCTGGTTCCTACCTCTCCCTAGTTCCACCGA 1821

QY 208 AlaGlnGlyLysLeuPheGlnThrLeuGlnCysAspGlnLeuLeuAspIleProGlyThrIle 227

DB 1822 CCAGACGAGGGGCTGGCCAGTATCATCTGTGACCACTCTCAGAGAAAGAAAGATCTGTT 1881

QY 228 ArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArgValLeuPheLeuLeu 247

DB 1882 ACTGAATGTGCATGAGCAACATTATCCAGACAGTTAAAGATCAAGGCTTATTCCTTTTA 1941

QY 248 AspGlyTrpAsnGlnPheLysProGlnAsnCysProGlnIleGluAlaLeuIleLysGlu 267

DB 1942 GATGCTACCAAGAAATATGTTCATCCCT--CAAGTCATAGGAAACATGATTCAAAAA 1998

Db 2532 TCCTCCCTCCAGAAATTCCTGGCGGAGTGCATGATGTAACCTCTGATTCAGATG 2591
Qy 463 wProgluInuValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIleSerAsp1 483
Db 2592 GCAGAGACATCAAGATTGGAGCTGTATCATATTGAAACAATCAACTACCCAGATGAC 2651
Qy 483 eThSerThrTyrSerSerLeuLeuArgTyrThrCysGly---SerSerValGluValaTh 502
Db 2652 TGTAAAGCCCTACACAACATTTTGTGAATATGTCTCCAGCCTCCCTTCAACAAAAGCAG 2711
Qy 502 rArgAlaValMetLysHisLeu 509
Db 2712 GCCCAAAATGTGTCTCATTTG 2733
RESULT 8
US-09-949-002-125
; Sequence 125, Application US/09949002
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: C1000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 6133
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-125
Alignment Scores:
Pred. No.: 2,27e-30 Length: 6133
Score: 279.00 Matches: 120
Percent Similarity: 53.80% Conservatave: 78
Best Local Similarity: 32.61% Mismatches: 156
Query Match: 5.11% Indels: 15
Gaps: 6
US-09-697-089-2 (1-1024) x US-09-949-002-125 (1-6133)
Qy 150 GluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGluGly 169
Db 1651 GAACCTCTGTGCTGCCTGAGAGTCTTGGCAACTGTGATGTCATGTGTGAGAGGT 1710
Qy 170 GluSerGlyGlySerThrLeuLeuGlnArgIleAlaMetLeuThrGlySerGly 189
Db 1711 GAACCTGGAAGTGAAGACCGCTCCTCGTAAGAAATAGCTTTTGTGTGGCATCTGGA 1770
Qy 190 LysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSer-----Arg 207
Db 1771 TGCAGTCCCTTAACACAGCTGCTTTCATCTCCTCCCTAGTTCCACACAGA 1830
Qy 208 AlaGlnGlyLeuPheGlnThrLeuGlyAspGlnLeuLeuAspIleProGlyThrIle 227
Db 1831 CCAACAGAGGGCTGGCCAGATATCATCTGTACACAGCTCCCTGAAGAAAGAGATCTGT 1890
Qy 228 ArgLysGlnThrPheMetAlaMetLeuLeuLeuArgGlnArgValLeuPheLeuLeu 247
Db 1891 ACTGAATATGTCATGAGGACATATATCCAGCAGTTAAAGATCAAGGTATTCTCTTTTA 1950
Qy 248 AspGlyTyrAsnGluPheLysProGlnAsnCysProGluIleGluAlaLeuIleLysGlu 267
Db 1951 GATGACCTCAAGAAAGATATGTTCAATCCCT--CAAGTCATAGGAAACGATTCATAAAA 2007
Qy 268 AsnHisArgPheLysAsnMetValIleValThrThrThrGluCysLeuArgHisIle 287
Db 2008 AACCACTATTCCTGCGACCTGCTATGTATGTCTGTCCGTACAAACAGGCGACGACATC 2067

Qy 288 ArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMetThrGluAspSerAlaGlnAla 307
Db 2068 CGCCGATACCTAGACACCATCTTAGAGATCAAGCATTTCCCTTTATATATCTCTGCT 2127
Qy 308 LeuIleArgGluValLeuIleLysGluLeuAla-----GluGlyLeuLeuGlnIle 325
Db 2128 ATATTACGGAAGCTCTTTTACATATATATGACTCTCTGCGAAAGTTATGTTACTT 2187
Qy 326 GlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPheValValIleThrCys 345
Db 2188 GGAAGAAGCAAAAGTTTCAGAGATACAGAAACCTCTCTTTGTGTGGCGGATCTGT 2247
Qy 346 Ala-IleGlnMetGlyGluSerGluPheHisSerHisThrGlnThrLeuPheHisTh 365
Db 2248 GCTCATTTGTTTCACTATTCCTTTTACCCATCTTT-GATGATGAGCTGTTTAAATC 2306
Qy 365 PheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGlyValAlaAlaSerAs 385
Db 2307 CTATATGAGACCGCTTTCCTTAAGSACAAA-----GGCAGACGTGAAT 2351
Qy 385 PheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGlyValPheSerHisLys 405
Db 2352 TCTCAAAACCAACTGTGCTCTCTGTGTGAGCTGTGCTGAAGAGGTTTTTTCATGTTG 2411
Qy 405 sPheAspPheGluLeuGlnAspVal-----SerSerValAsnGluAspValLeuLeuTh 423
Db 2412 CTTTGAGTTTATGATGATGATGATGCTGCGAAGCAGAGGGTTGATGAGATGATTAAC 2471
Qy 423 rThrGlyLeuLeuGlySerLysTyrThrAlaGlnArgPheLysProLysTyrLysPhePhe 443
Db 2472 CATGTGCTTGAATGAGCAAAATTTTACAGCCAGAGCTAAGACATCTACCGGTTTTTAAG 2531
Qy 443 sLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuThrSerHisG1 463
Db 2532 TCCTGCCCTCCAGAAATTCCTGGCGGATGAGCTGTGATGTAACCTCGGATTCAGATG 2591
Qy 463 wProgluInuValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIleSerAsp1 483
Db 2592 GCAGAGACATCAAGATTGGAGCTGTATCATATTGAAACAATCAACTACCCAGATGAC 2651
Qy 483 eThSerThrTyrSerSerLeuLeuArgTyrThrCysGly---SerSerValGluValaTh 502
Db 2652 TGTAAAGCCCTACACAACATTTTGTGAATATGTCTCCAGCCTCCCTTCAACAAAAGCAG 2711
Qy 502 rArgAlaValMetLysHisLeu 509
Db 2712 GCCCAAAATGTGTCTCATTTG 2733
RESULT 9
US-09-949-002-656
; Sequence 656, Application US/09949002
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: C1000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 656
; LENGTH: 60194
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-656
Alignment Scores:
Pred. No.: 4.93e-29 Length: 60194
Score: 279.00 Matches: 120
Percent Similarity: 53.80% Conservatave: 78

Best Local Similarity: 32.61% Mismatches: 156
 Query Match: 5.11% Indels: 15
 Gaps: 6
 US-09-697-089-2 (1-1024) x US-09-949-002-656 (1-60194)

QY 150 GlnGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGlnGly 169
 DB 40978 GAACCTGTGGCTGCTGAGCTGTTGGCAACCTTGACCTGTGCATGTGTGGAGGGT 41037
 QY 170 GlnSerGlyLysGlyLysSerThrLeuLeuGlnArgIleAlaMetLeuPrgLysGly 189
 DB 41038 GAACCTGGAAGTGAAGAGACGGCTCTCTGAAGAAATAGCTTTCTGTGGCATCTGGA 41097
 QY 190 LysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSer-----Arg 207
 DB 41098 TGCTGTCCCTGTTAAACAGAGTTCACAGCTGTTTCTACCTCCCTAGTTCACACAGA 41157
 QY 208 AlaGlnGlyLeuPheGlnThrLeuGlnAspGlnLeuLeuAspIleProGlyThrIle 227
 DB 41158 CCAACAGAGGGGCGCCAGATATCATCTGTACACAGCTCTCAGAGAAAGAGATCTGT 41217
 QY 228 ArgGlyGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArgValLeuPheLeu 247
 DB 41218 ACTGAATGTGCATGAGGAACATTAATCCAGACAGTTAAAGATCAGCTTAATCTTTA 41277
 QY 248 AspGlyLysArgGlnPheLysProGlnAsnCysProGlnIleGlnAlaLeuLysGln 267
 DB 41278 GATGATCAACAAGAAATATGTCAATCCCT---CAAGTCATAGGAAGAAATGATTCAAAA 41334
 QY 268 AsnHisArgPheLysAsnMetValIleValIleThrThrThrGlyCysLeuArgHisIle 287
 DB 41335 AACCACTTATCCCGACCTGCTATGATGCTGCTCCGTCACAAACAGGCGCAGGACATC 41394
 QY 288 ArgGlnPheGlyAlaLeuThrAlaGlnValAlaGlyAspMetThrGlnAspSerAlaGlnAla 307
 DB 41395 CGCGGATACCTAGACACCATTTAGAGATCAAAAGCATTCCTTTTAAATACGTCTGT 41454
 QY 308 LeuIleArgGlnValLeuIleLysGlnLeuAla-----GlnGlyLeuLeuGlnIle 325
 DB 41455 ATATTACGGAAGCTCTTTACATATATATGACTGTGCGAAGTTTAAATGTGTACTTT 41514
 QY 326 GlnLysSerArgCysLeuAlaGlnLeuMetLysThrProLeuPheValIleThrCys 345
 DB 41515 GGAAGAGACCAAACTTGCAGAGATACAGAAACTCTCTCTGTGGCGGCATCTGT 41574
 QY 346 Ala-IleGlnMetLysGlnSerGlnPheHisSerHisThrGlnThrThrLeuPheHisIle 365
 DB 41575 GCTCATTTGGTTTCAGTATCTTTGACCCATCTTT---GATGATGTGGCTGTTTCAAGTC 41633
 QY 365 rPheTyAspLeuLeuIleGlnLysAsnLysHisLysGlnValAlaAlaSerAs 385
 DB 41634 CTATATGGAAGCGCTTTCCTTAAGAACAAA-----GCGAAGCTGAAT 41678
 QY 385 rPheIleArgSerLeuAspHisCysGlnAspLeuAlaLeuGlnIleValAlaPheSerHisLys 405
 DB 41679 TCTCAAGCAACTGTCTGCTCTGCTGTGAGCTGCTTGAAGAGGTTTTCATGTG 41738
 QY 405 sPheAspPheGlnLeuGlnAspVal-----SerSerValAsnGlnAspValLeuLeu 423
 DB 41739 CTTTGAGCTTTATGATGATGATCTCGCAAGAGCAGGGGTGATGAGATGAAGATCTAAC 41798
 QY 423 rThrGlyLeuLeuCysLysTyThrAlaGlnArgPheLysProLysTyThrPhePheHis 443
 DB 41799 CATGTGCTTGAAGCAAAATTTTACAGCCAGACCTAAAGACATTTCAACCGCTTTTAAAG 41858
 QY 443 sLysSerPheGlnIleLysTyThrAlaGlyArgGlnSerSerLeuLeuThrSerHisGln 463
 DB 41859 TCCGCTCTCCAAAGATTTCTTCGCGGAGATGAGCGCTGATGAACCTCGATTCAGATAG 41918
 QY 463 uProGlnGlnValThrLysGlyAsnGlyTyThrLeuGlnLysMetValSerIleSerAspIle 483
 DB 41919 GCAGGAACATCAAGATTTGGAGCTGTATCATTTGAAACAAATCAATCAACCATGATGAC 41978

QY 483 eThrSerThrTySerSerLeuLeuArgTyThrCysGly---SerSerValGlnAlaIle 502
 DB 41979 TGTAAGCGCTACAAACAATTTTGAACATATGATCTCCAGCTCTCTTCAACAAAGACAG 42038
 QY 502 rArgAlaValMetLysHisLeu 509
 DB 42039 GCCCAAAATGTGTCTCATTTG 42060

RESULT 10

US-09-949-002-697
 ; Sequence 697, Application US/09949002
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
 ; TITLE OF INVENTION: AND USES THEREOF
 ; FILE REFERENCE: CL000790
 ; CURRENT APPLICATION NUMBER: US/09/949,002
 ; PRIOR FILING DATE: 2000-01-28
 ; PRIOR APPLICATION NUMBER: 60/231,401
 ; NUMBER OF SEQ. ID NOS: 10823
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ. ID NO 697
 ; LENGTH: 60195
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-002-697

Alignment Scores:
 Pred. No.: 4,93e-29 Length: 60195
 Score: 279.00 Matches: 120
 Percent Similarity: 53.80% Conservative: 78
 Best Local Similarity: 32.61% Mismatches: 156
 Query Match: 5.11% Indels: 15
 Gaps: 6

US-09-697-089-2 (1-1024) x US-09-949-002-697 (1-60195)

QY 150 GlnGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGlnGly 169
 DB 40978 GAACCTGTGGCTGCTGAGCTGTTGGCAACTTGAACCTGTGCATGTGTGGAGGGT 41037
 QY 170 GlnSerGlyLysGlyLysSerThrLeuLeuGlnArgIleAlaMetLeuPrgLysGly 189
 DB 41038 GAACCTGGAAGTGAAGAGACGGCTCTCTGAAGAAATAGCTTTCTGTGGCATCTGGA 41097
 QY 190 LysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSer-----Arg 207
 DB 41098 TGCTGTCCCTGTTAAACAGAGTTCACAGCTGTTTCTACCTCTCCCTAGTTCACACAGA 41157
 QY 208 AlaGlnGlyLeuPheGlnThrLeuGlnAspGlnLeuLeuAspIleProGlyThrIle 227
 DB 41158 CCAACAGAGGGGCGCCAGATATCATCTGTACACAGCTCTCAGAGAAAGAGATCTGT 41217
 QY 228 ArgGlyGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArgValLeuPheLeu 247
 DB 41218 ACTGAATGTGCATGAGGAACATTAATCCAGACAGTTAAAGATCAGCTTAATCTTTA 41277
 QY 248 AspGlyLysArgGlnPheLysProGlnAsnCysProGlnIleGlnAlaLeuLysGln 267
 DB 41278 GATGATCAACAAGAAATATGTCAATCCCT---CAAGTCATAGGAAGAAATGATTCAAAA 41334
 QY 268 AsnHisArgPheLysAsnMetValIleValIleThrThrThrGlyCysLeuArgHisIle 287
 DB 41335 AACCACTTATCCCGACCTGCTATGATGCTGCTCCGTCACAAACAGGCGCAGGACATC 41394
 QY 288 ArgGlnPheGlyAlaLeuThrAlaGlnValAlaGlyAspMetThrGlnAspSerAlaGlnAla 307
 DB 41395 CGCGGATACCTAGACACCATTTAGAGATCAAAAGCATTCCTTTTAAATACGTCTGT 41454
 QY 308 LeuIleArgGlnValLeuIleLysGlnLeuAla-----GlnGlyLeuLeuGlnIle 325

```
Db 41455 ATATTACGAACCTCTTTTACATATATATGACTCGTCTCGGAAGTTTATGCTTACTTT 41514
      :::::::::::
Qy 326 GlnlySerArgCysLeuArgAnleuMetLysThrProleuPheValIleThrCys 345
      :::::::::::
Db 41515 GGAAGAACAAGTTTGCAGAAATACAGAAACCTCTCTTTGTGTGGCGGAGATCTGT 41574
      :::::::::::
Qy 346 Ala-IleGlnMetGlyGluSerGluPheHisSerHisThrGlnThrThrLeuPheHisThr 365
      :::::::::::
Db 41575 GCTCATTTGGTTTCACTATCTCTTTTGAACCCATCTTTT-GATGATGTGGCGGTTTTCAGAC 41633
      :::::::::::
Qy 365 rPheTyraSPheLeuIleGlnLysAnlySHisLysGlyValAlaIleSerAs 385
      :::::::::::
Db 41634 CATATGGAACCCCTTTCTCTTAAGAACAA-----GGCAGCCTGAAT 41678
      :::::::::::
Qy 385 PheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGlnGlyValPheSerHisLys 405
      :::::::::::
Db 41679 TCTCAAGCAACTGTGCTCTCTGTGTGAGCTGGCGCTTGAAGAGGTTTTCATGCTTG 41738
      :::::::::::
Qy 405 sPheAspPheGlnLeuGlnAspVal-----SerSerValAsnGlnAspValLeuLeuThr 423
      :::::::::::
Db 41739 CTTTGAAGTTTAATGATGATGATCGCAGAACAGGGGTTGATGAAGATGAAGATCTAAC 41798
      :::::::::::
Qy 423 rThrGlyLeuLeuCysLysTyThrAlaGlnArgPheLysProLysTyThrPhePheHis 443
      :::::::::::
Db 41799 CATGTGCTTGATGACCAATTTTACAGCCAGACTAAGACCATTTCTACCGGTTTTTAAG 41858
      :::::::::::
Qy 443 sLysSerPheGlnGlnTyThrAlaGlnArgLysSerSerLeuLeuThrSerHisGln 463
      :::::::::::
Db 41859 TCTCTGCTTCCCAAGATTTCTTGGCGGAGTGAAGCTGATTCGAATTCGATTCAGATAG 41918
      :::::::::::
Qy 463 uProGlnGlnValThrLysGlyAsnGlyTyThrLeuGlnLysMetValSerIleSerAspIle 483
      :::::::::::
Db 41919 GCAGGAACATCAAGATTGGGAGCTGATCATTTGAAACAAATCAACTCACCATGATGAC 41978
      :::::::::::
Qy 483 eThrSerThrTySerSerLeuLeuArgTyThrCysGly---SerSerValGlnValaThr 502
      :::::::::::
Db 41979 TCTAAGCGGCTACAAACATTTTGTGAACATATGCTCCAGCCCTTCAACAAAGCAAG 42038
      :::::::::::
Qy 502 rArgAlaValMetLysHisLeu 509
      :::::::::::
Db 42039 GCCCAAAATTTGTCTCATTTTG 42060
      :::::::::::
RESULT 11
US-09-724-676-6819
; Sequence 6819, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6819
; LENGTH: 3210
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-6819

Alignment Scores:
Pred. No.: 2,22e-29 Length: 3210
Score: 270.00 Matches: 116
Percent Similarity: 53.13% Conservative: 79
Best Local Similarity: 31.61% Mismatches: 159
Query Match: 4.95% Indels: 13
DB: 5 Gaps: 9

US-09-697-089-2 (1-1024) x US-09-724-676-6819 (1-3210)
Qy 150 GlnGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGlnGly 169
      :::::::::::
Db 693 GAACCTTGCTGCTGCTGCTGCTGCTTGTGGCACTTGAACCTGTGCATGTGTGTGAGGGT 752
```

```
Qy 170 GluSerGlyLysGlyLysSerThrLeuLeuGlnAlaGlnIleAlaMetLeuThrProLysGly 189
      :::::::::::
Db 753 GAAGCTGGGAAGTGAAGAAAGGCTCCCTGAAGAAATATGCTTTGTGTGGCATCTGGA 812
      :::::::::::
Qy 190 LysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSer-----Arg 207
      :::::::::::
Db 813 TCGTGTCCCTGTTAAACAGGTTCCAGCTGGTGTTCCTTACTCTCTCCCTTACTTCCACCA 872
      :::::::::::
Qy 208 AlaGlnGlyLysLeuPheGlnThrLeuCysAspGlnLeuLeuAspIleProGlyThrIle 227
      :::::::::::
Db 873 CCAGACGAGGGGCTGGCCAGTATCATCTGTGACCGAGCTCTAGAGAAAGAGATCTGTT 932
      :::::::::::
Qy 228 ArgGlnGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnAlaValLeuPheLeuLeu 247
      :::::::::::
Db 933 ACTGAATGCTGCTGAGAACATTTCCAGCAGTATTAACAAAGAGTCTTATCTCTTTTA 992
      :::::::::::
Qy 248 ASPGlyTyraSPheGlnPheLysProGlnAsnGlyProGlnIleGlnAlaLeuIleLysGln 267
      :::::::::::
Db 993 GATGACTACAAAGAAATATGTTCAATCCT---CAAGTCATGGAATACTGATTCATAA 1049
      :::::::::::
Qy 268 AsnHisArgPheLysAsnMetValIleValThrThrThrGluCysLeuArgHisIle 287
      :::::::::::
Db 1050 AACCACTTATCCCGGACCTGCTATGATGCTGTCCGACAAACAGGGCCAGGACATC 1109
      :::::::::::
Qy 288 ArgGlnPheGlyAlaLeuThrAlaGlnValAlaAspMetThrGlnAspSerAlaGlnAla 307
      :::::::::::
Db 1110 CCCCAGTACCTAGAGACCATCTTCAAGATCAAGCATTTCCCTTTATATATCTGTGT 1169
      :::::::::::
Qy 308 LeuIleArgGlnValLeuIleLysGlnLeuAla-----GlnGlyLeuLeuGlnIle 325
      :::::::::::
Db 1170 ATATTACGAACCTCTTTTACATATATATGACTGCTCTCCGAAAGTTATGTTACTTT 1229
      :::::::::::
Qy 326 GlnlySerArgCysLeuArgAnleuMetLysThrProleuPheValIleThrCys 345
      :::::::::::
Db 1230 GGAAGAACAAGTTTGCAGAAATACAGAAACCTCTCTGTGGCGGCGGAGATCTGT 1289
      :::::::::::
Qy 346 AlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThrThrLeuPheHisThr 365
      :::::::::::
Db 1290 GCT---CATTTGTTTCAATATCTTTTGACCATCTCTTTGAAGATGATGCTG-----GCTGCT 1340
      :::::::::::
Qy 366 PheTyraSPheLeuIleGlnLysAnlySHisLysGlyValAlaIleSerAsp 385
      :::::::::::
Db 1341 TTCAGTCCCTATATG---GAAGCCTTTCCTTAAGGAACAAGCCAGACGTAATTT--- 1394
      :::::::::::
Qy 386 PheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGlnGlyValPheSerHisLys 405
      :::::::::::
Db 1395 CTCAAAAGCAACTGTGCTCCCTGCTGTGAGCTGGCTTGAAGGGTTTTTCATGATTC 1454
      :::::::::::
Qy 406 PheAspPheGlnLeuGlnAspVal-----SerSerValAsnGlnAspValLeuLeuThr 423
      :::::::::::
Db 1455 TTTGAGTTTAATGATGATATCTCGCAGAACAGGGGTTGATGAAGATGAAGATCAATCAAC 1514
      :::::::::::
Qy 424 rThrGlyLeuLeuCysLysTyThrAlaGlnArgPheLysProLysTyThrLysPhePheHis 443
      :::::::::::
Db 1515 ATGTGCTTGTATGACAAATTTTACAGCCAGACACATGAACCATTTCTACCGGTTTTTAAGT 1574
      :::::::::::
Qy 444 LysSerPheGlnGlnTyThrAlaGlnArgLysSerSerLeuLeuThrSerHisGln 463
      :::::::::::
Db 1575 CCTGCTTCCAAAGAAATTTCTTCCGGGAGATGAGCTGATGAACCTCGCTGATCAATAGG 1634
      :::::::::::
Qy 464 ProGlnGlnValThrLysGlyAsnGlyTyThrLeuGlnLysMetValSerIleSerAspIle 483
      :::::::::::
Db 1635 CAGGAACATCAAGATTGGGAGCTGATCATTTGAAACAAATCAACTCACCATGATGACT 1694
      :::::::::::
Qy 484 rThrSerThrTySerSerLeuLeuArgTyThrCysGly---SerSerValGlnValaThr 502
      :::::::::::
Db 1695 GTAAGCGCTTACAAACATTTTGTGAACATATGCTCCAGCCTCCCTTCAACAAAGCAGGG 1754
      :::::::::::
Qy 503 ArgAlaValMetLysHisLeu 509
      :::::::::::
Db 1755 CCCAAATTTGTCTCATTTTG 1775
      :::::::::::
```

```

RESULT 12
US-09-724-6819
; Sequence 6819, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6819
; LENGTH: 3210
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-6819

Alignment Scores:
Pred. No.: 2,22e-29 Length: 3210
Score: 270.00 Matches: 116
Percent Similarity: 53.13% Conservative: 79
Best Local Similarity: 31.61% Mismatches: 159
Query Match: 4.95% Indels: 13
DB: Gaps: 9

US-09-697-089-2 (1-1024) x US-09-724-676A-6819 (1-3210)
QY 150 GluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGluGly 169
DB 693 GAACCTCTGGTGTGCTGCTGAGAGTCTTTGGCAACTTGAACCTGTCATGTGTGGAGGCT 752
QY 170 GluSerGlyLysGlyLysSerThrLeuLeuGlnArgIleAlaMetLeuTrpGlySeryl 189
DB 753 GAACCTGGAAATGGAAGACGCTCCTCTGAAAGAAATAGCTTTTCTGTGGCAATCTGGA 812
QY 190 LysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSer-----Arg 207
DB 813 TGCCTGTCCTCCCTGTAAACAGGCTCCAGCTGTTTCTACCTCCCTCCTAGTCCACACGA 872
QY 208 AlaGlnGlyGlyLeuPheGluThrLeuGlnLysAspGlnLeuAspIleProGlyThrIle 227
DB 873 CCAGACGAGGGGCTGGCCAGATATCATCTGTGATCCAGCTCCTAGAGAAAGAGATCTGTT 932
QY 228 ArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArgValLeuPheLeuLeu 247
DB 933 ACTGAATATGTCRTGAGAGACATATATCCAGCATTAAGAAATGAGCTGTATTCCTTTTA 992
QY 248 AspGlyTyrAsnGlnPheLysProGlnAsnGlyProGluIleGluAlaLeuIleLysGlu 267
DB 993 GATGACTACCAAGAAATATGTTCAATCCCT--CAAGTCATAGAGAAACTGATTCATAAAA 1049
QY 268 AsnHisArgPheLysAsnMetValIleValThrThrThrGluLysLeuArgHisIle 287
DB 1050 AACCACTTATCCCGACTGCTATGATGTGCTGCTGCTACAAAGAGGCCAGGACATC 1109
QY 288 ArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMetThrGluAspSerAlaGlnAla 307
DB 1110 CGCGGATACCTAGAGACCATTCATGAGATCAAAAGCATTTCCCTTTTATTAATATGTCGT 1169
QY 308 LeuLeuArgGluValLeuIleLysGluLeuAla-----GluGlyLeuLeuLeuGlnIle 325
DB 1170 ATATTACGGAAGCTCTTTTCACTATATATGACTGCTGCGCAAACTTATGAGTTTACTTT 1229
QY 326 GlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPheValIleThrCys 345
DB 1230 GGAAGAAACCAAGTTTCCAGAGATNACAGAAACTCCTCTGTGTGGCGCATCTGT 1289
QY 346 AlaIleGlnMetGlyLysSerGluPheHisSerHisThrGlnThrThrLeuPheHisThr 365
DB 1290 GCT---CATTTGCTTACATATCTTTTACCCATCTTGTATGATGTC-----GCTGCT 1340
QY 366 PheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGlyValAlaAlaLaserasp 385
DB 1341 TTCAAGTCCATATG---GAAGGCTTTTCTTAAAGAACAAAGGACGTAAGATT-- 1394
QY 386 PheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGlnGlyValPheSerHisLys 405
DB 1395 CTCAAGCAACTGTGTCTCTCTGCTGTGAGTGGCTGCTTGAAGGGTTTTCATGTCTGC 1454
QY 406 PheAspPheGluLeuGlnAspVal-----SerSerValAsnGluAspValLeuLeuThr 423
DB 1455 TTTAGATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1514
QY 424 ThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLysPhePheHis 443
DB 1515 ATGTGCTTGATGAGCAATTTTACAGCCAGCACTTAAGCCTTACCTGCTTTTAACT 1574
QY 444 LysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuThrSerHisGlu 463
DB 1575 CTTGCTTCCAAAGATTTTCTTGGGAGATGAGGCTGATGATGATGATGATGATGATGATG 1634
QY 464 ProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIleSerAspIle 483
DB 1635 CAGAACATCAAGATTTGGAGCTGATCATTTTGAACAAATCACTACCCATGATGACT 1694
QY 484 ThrSerThrTyrSerSerLeuLeuArgTyrThrCysGly---SerSerValGluAlaThr 502
DB 1695 GTAAGCGCTACCAACAAATTTTGAACCTATGTCTCCAGCCTCCCTCAACAAAGAGGG 1754
QY 503 ArgAlaValMetLysHisLeu 509
DB 1755 CCCAAATGTGTCTCATTTG 1775

```

```

RESULT 13
US-09-724-676-6801
; Sequence 6801, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6801
; LENGTH: 3597
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-6801

Alignment Scores:
Pred. No.: 2.59e-29 Length: 3597
Score: 270.00 Matches: 116
Percent Similarity: 53.13% Conservative: 79
Best Local Similarity: 31.61% Mismatches: 159
Query Match: 4.95% Indels: 13
DB: Gaps: 9

US-09-697-089-2 (1-1024) x US-09-724-676-6801 (1-3597)
QY 150 GluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGluGly 169
DB 1080 GAACCTCTGGTGTGCTGCTGAGAGTCTTTGGCAACTTGAACCTGTCATGTGTGGAGGCT 1139
QY 170 GluSerGlyLysGlyLysSerThrLeuLeuGlnArgIleAlaMetLeuTrpGlySeryl 189
DB 1140 GAACCTGGAATGGAAGACGCTCCTCTGAAAGAAATAGCTTTTCTGTGGCATCTGGA 1199
QY 190 LysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSer-----Arg 207
DB 1200 TGCCTGTCCTCCCTGTAAACAGGCTCCAGCTGTTTCTACCTCCCTTATGTTCCACAGA 1259
QY 208 AlaGlnGlyGlyLeuPheGluThrLeuGlnLysAspGlnLeuAspIleProGlyThrIle 227
DB 1260 CCAGACGAGGGGCTGGCCAGATATCATCTGTGATCCAGCTCCTAGAGAAAGAGATCTGTT 1319

```

OY	228	ArglysglnthrPheMetAlaMetLeuLeuLysLeuArgGlnArgValLeuPheLeu	247
Db	1320	ACTGAATAGTCGTCRTAGGAAACATTATTCAGACACTTAAATAACAGGTCTTATTCCTTTTA	1379
OY	248	AspGlyTyrAsnGlnPheLysProGlnAsnCysProGluIleGluValaLeuIleLysGlu	267
Db	1380	GATGACCTACAAAGAAATATGTTCAATCCCT---CAAGTCATAGGAAACTGATTCAAAA	1436
OY	268	AsnHisArgPheLysAsnMetValIleValThrThrThrGluCysLeuArgHisIle	287
Db	1437	AACCACCTTATCCGGACCTCCTATGATGATGCTGTCCTGACAAACAGGCGCAGGACATC	1496
OY	288	ArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMetThrGluAspSerAlaGlna	307
Db	1497	CGCGGAATCCTAGACACCATTTGAGATCAACAAAGCATTTCCCTTTATTAATCTCTGCT	1556
OY	308	LeuIleArgGluValLeuIleLysGluLeuAla-----GluGlyLeuLeuGlnIle	325
Db	1557	ATATTACGGAAAGCTCTTTTACATTAATATGACTCCGTCGGAAGTTATAGGTTTACTTT	1616
OY	326	GlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPheValValIleThrCys	345
Db	1617	GGAAAGAACCAAGTTTGACAGAGATACAGAAATCCTCTGTCGGTGGCGGCGATCTGT	1676
OY	346	AlaIleGlnMetGlyLysSerGluPheHisSerHisThrGlnThrThrLeuPheHisThr	365
Db	1677	GCT---CATTTGGTTTCAGTTCCTTTTGACCCATCTTGATGATGTG----GCTCCT	1727
OY	366	PheTyrAspLeuLeuIleGlnLysAsnLysHisLysGluValAlaAlaIleSer	385
Db	1728	TTTCAAGTCCTTATATG---GAACCCCTTCTCTTAGACACAAAGCCGACAGCTAAAT--	1781
OY	386	PheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGlyValPheSerHisLys	405
Db	1782	CTCAAAACAACTGTCGTCCTCTGTGGTAGACGTGGCCTTGAAGGGTTTTTCATGTTC	1841
OY	406	PheAspPheGluLeuGlnAspVal-----SerSerValAsnGluAspValLeuLeuThr	423
Db	1842	TTTTAGTTTAAATGATGTATCTCCGAGAACAGGGGTTGATGAAGATCAACATCTTAAC	1901
OY	424	ThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLysPheHis	443
Db	1902	ATGTCCTTGATGACCAATTTTACAGCCGACAGACTAAGACCACTTACCGGTTTTTAAGT	1961
OY	444	LysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuThrSerHisGlu	463
Db	1962	CTGCTCTTCCAGAAATTTCTGGGGGAGAGGCTGATTTGAACCTCTGGATTCAATAGG	2021
OY	464	ProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerLieserAspIle	483
Db	2022	CAGGACATCAAGATTTGGGACTGTATCTCAATTTGAACAACATCACTCAACCATCATGACT	2081
OY	484	ThrSerThrTyrSerSerLeuLeuAlaGlyTyrThrCysGly---SerSerValGluAlaThr	502
Db	2082	GTAAGCCCTTACAAACAATTTTGAACATATGCTCCAGCCTCCCTTCAACAAACAGGAGG	2141
OY	503	ArgAlaValMetLysHisLeu 509	
Db	2142	CCCAAAATTGTGTCTCATTTTG 2162	
RESULT 14			
US-09-724-676A-6801			
: Sequence 6801, Application US/09724676A			
: GENERAL INFORMATION:			
: APPLICANT: Comugen LTD			
: TITLE OF INVENTION: Variants of alternative splicing			
: FILE REFERENCE: 129181.4 Comugen			
: CURRENT APPLICATION NUMBER: US/09/724,676A			
: CURRENT FILING DATE: 2000-11-28			
: NUMBER OF SEQ. ID NOS: 97222			
: SOFTWARE: PatentIn version 3.2			
: SEQ ID NO 6801			
: LENGTH: 3597			

	TYPE: DNA	ORGANISM: Homo sapiens	US-09-724-676A-6801
Alignment Scores:			
Pred. No.:	2,596-29	Length:	3597
Score:	270.00	Matches:	116
Percent Similarity:	53.13%	Conservative:	79
Best Local Similarity:	31.61%	Mismatches:	159
Query Match:	4.95%	Indels:	13
DB:	5	Gaps:	9
US-09-697-089-2 (1-1024) x US-09-724-676A-6801 (1-3597)			
QY	150	gluIngluLeuThrLeuAsnGlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGluGly	169
DB	1080	GAACCTCGTGGTGGTCCCTGAGGCTCTTGGCAACTGACATGCTGATCTGTGGAGGGT	1139
QY	170	gluSerGlyIlyGlyIlySerThrLeuGlnAlaIleAlaIleLeuThrIleGlySerGly	189
DB	1140	GAAGCTGGAACTGGAAAAGACGGCTCTCTCAAAAAATAGCTTTCTGCGGCATCTGGA	1199
QY	190	LysCysIlyAlaLeuThrIlyPheIlyPheValPhePheLeuArgPheSer-----Arg	207
DB	1200	TGCTGTCCCTGTTAAACAGGTTCCAGCTGGTTTCTTACCTCTCCCTTAGTCCACCA	1255
QY	208	AlaGlnGlyIlyLeuPheGluThrLeuCysAspGlnLeuLeuAspIleProGlyThrIle	227
DB	1260	CCAGACGAGGGGCGTGGCCAGATGATCTGTGACACCTCTAGAGAAACAGATCTGT	1319
QY	228	ArgIlyGlnThrPheMetAlaMetLeuLeuIlyLeuArgGlnAlaGlyAlaPheLeuLeu	247
DB	1320	ACTGAATGTGCTRGAGAACATTATCCAGCACTTAAACATCAGCTCTTATCTTTTA	1379
QY	248	AspGlyIlyAsnGluPheIlyProGlnAsnGlyProGlnIleGlnAlaLeuIlyGlu	267
DB	1380	GATGACTACAAAGAAATATGTTCAATCCCT--CAAGTATAGAAAACCTGATCAAAA	1436
QY	268	AsnHisArgPheIlyAsnMetValIleValThrThrThrGluCysLeuArgHisIle	287
DB	1437	AACCACTATGCCGGACCTGCTATGATGATGTCGTGCCGATCAAAACAGGCCGAGCAATC	1496
QY	288	ArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMetThrGluAspSerAlaGlnAla	307
DB	1497	CGCGCATGCCATGAGACCATTTAGAGATCAAAAGCATTTCCCTTTATATATCTGTCTGT	1556
QY	308	LeuIleArgGluValLeuIleIlyGluLeuAla-----GluGlyLeuLeuLeuGlnIle	325
DB	1557	ATATTACGGAAGCTCTTTTTCACATAAATATACCTGCTGCGAAAGTTTAAAGGTATCTT	1618
QY	326	GlnIlySerArgCysLeuArgAsnLeuMetIlyThrProLeuPheValIleThrCys	345
DB	1617	GGAAAGAACCAAAATTTGGCAGAAATACAGAAAATCTCTCTGTGGTGGCGGCATCTGT	1676
QY	346	AlaIleGlnMetGlyIlySerGluPheHisSerHisThrGlnThrThrPhePheHisThr	365
DB	1677	GCT---CATGTGTTTCAGTATCTTTTGACCAATCTCTTGATGATGTG-----GCTGCT	1727
QY	366	PheIlyAspLeuLeuIleGlnIlyAsnIlyHisIlyHisIlyGlyIlyAlaAlaIleSerAsp	385
DB	1728	TTTCAAGTCTCTTATG---GAACGCTTTCTTAAAGAACAAAGCGACGATCAAAATT--	1781
QY	386	PheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGlyAlaPheSerHisIly	405
DB	1782	CTCAAGCAACTGTGTCTCTGTGGAGCTGGCTTAAAGGCTTTTTCATGTTGC	1841
QY	406	PheAspPheGluLeuGlnAspVal-----SerSerValAsnGluAspValLeuLeuThr	423
DB	1842	TTTAGCTTATATGATGATGATCTCCGCAAGACAGGGGTGATGAAGATGAAGATCTTAAC	1901
QY	424	ThrIlyLeuLeuCysIlyThrAlaGlnAlaGlyPheIlyProIlyIlyIlyPhePheHis	443
DB	1902	ATGTGCTTTTATGAGCAAAATTTACAGCCAGACACTAAAGCACTTGTATACCGGTTTTAGT	1961

```

QY 444 LysSerPheGlnGluThrAlaGlyArgLeuSerSerLeuLeuThrSerHisGlu 463
    :|||||:|||||:|||||:|||||:|||||:
Db 1962 CCTGCTTCAGAAATTTCTTGGGGGATGAGGCTCATTTGAACTCTCGATTCACTAG 2021
QY 464 ProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIleSerAspIle 483
    :|||||:|||||:|||||:|||||:|||||:
Db 2022 CAGAACATCAAGATTGGGACTGTATCATTTGAAACAATCAATCAACCATCATGATGACT 2081
QY 484 ThrSerThrTyrSerSerLeuLeuArgTyrThrCysGly---SerSerValGluAlaThr 502
    :|||||:|||||:|||||:|||||:|||||:
Db 2082 GTAAAGGCGCTACACAAATTTTGAACATATGCTCCAGCTCCCTTCAACAAAGCAGGG 2141
QY 503 ArgAlaValMetLysHisLeu 509
    :|||||:|||||:
Db 2142 CCCAAATTTGTCTCATTTG 2162

RESULT 15
US-09-724-676-6810
; Sequence 6810, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; NUMBER OF SEQ ID NOS: 2000-11-28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6810
; LENGTH: 4143
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-6810

Alignment Scores:
Pred. No.: 3,136-29 Length: 4143
Score: 270.00 Matches: 116
Percent Similarity: 53.13% Conservative: 79
Best Local Similarity: 31.61% Mismatches: 159
Query Match: 4.95% Indels: 13
DB: 5 Gaps: 9

US-09-697-089-2 (1-1024) x US-09-724-676-6810 (1-4143)
QY 150 GlnGlnLeuThrLeuAsnGlyLeuGlnAlaLeuGlnSerProCysIleIleGlnGly 169
    :|||||:|||||:|||||:|||||:|||||:
Db 1626 GAACCTCTGCTGCTGCTGAGGCTTTGGCACTTGAACCTGCTATGCTGTGGAGGGT 1685
QY 170 GluSerGlyLysGlyLysSerThrLeuLeuGlnArgIleAlaMetLeuTrpGlySerGly 189
    :|||||:|||||:|||||:|||||:|||||:
Db 1686 GAAGCTGAAGTGGAAAGCGGCTCTCTGAAGAAATAGCTTTTCTGTGGCATCTGGA 1745
QY 190 LysCysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSer-----Arg 207
    :|||||:|||||:|||||:|||||:|||||:
Db 1746 TGTCTGCTCCCTGTTAAACAGGTTCCAGCTGCTTTTCTACCTCTCCCTTAGTTCACACAGA 1805
QY 208 AlaGlnGlyLysLeuPheGlnThrLeuCysAspGlnLeuLeuAspIleProGlyThrIle 227
    :|||||:|||||:|||||:|||||:|||||:
Db 1806 CCAGACGAGGGGCTGGCCAGTATCATCTGTGACACAGCTCCTAGAGAAAGAGATCTGTT 1865
QY 228 ArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArgValLeuPheLeuLeu 247
    :|||||:|||||:|||||:|||||:|||||:
Db 1866 ACTGAATGTGCTGAGAACATTTATCCAGAGTTTAAAGATCAGGCTTATTCCTTTTA 1925
QY 248 AspGlyTyrAsnGluPheLysProGlnAsnGlyProGluIleGlnAlaLeuIleLysGlu 267
    :|||||:|||||:|||||:|||||:|||||:
Db 1926 GATGACTACAAAGAAATATGTTCAATCCT---CAAGTCAATGAGAAACTGATTCAAAAA 1982
QY 268 AsnHisArgPheLysAsnMetValIleValThrThrThrThrGluCysLeuArgHisIle 287
    :|||||:|||||:|||||:|||||:|||||:
Db 1983 AACCACTTATCCCGGACGCTGCTATGATTGCTGTCCGTAACAACGAGGCGGACATC 2042
QY 288 ArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMetThrGluAspSerAlaGlnAla 307

```

```

Db 2043 CCGCGATACCTAGAGACATTTCTAGAGATCAAGACATTTCCCTTTATATATCTGCT 2102
    :|||||:|||||:|||||:|||||:|||||:
QY 308 LeuIleArgGluValLeuIleLysGluLeuAla-----GlnGlyLeuLeuLeuGlnIle 325
    :|||||:|||||:|||||:|||||:|||||:
Db 2103 ATATTACGGAACCTCTTTTACATATATATGACTCGTGGAAAGTTATGGTTACTTT 2162
QY 326 GlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPheValIleThrCys 345
    :|||||:|||||:|||||:|||||:|||||:
Db 2163 GGAAGAACCAAGTTTGGAGAGATACGAAATACTCTCTTGTGTGGCGGCGATCTGT 2222
QY 346 AlaIleGlnMetCysGluSerGluPheHisSerHisThrGlnThrThrLeuPheHisThr 365
    :|||||:|||||:|||||:|||||:|||||:
Db 2223 GCT---CATTTGTTTCAGATATCTTTTGACCATTCCTTTGATGANGTG-----GCTGCT 2273
QY 366 PheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGlyValAlaAlaSerAsp 385
    :|||||:|||||:|||||:|||||:|||||:
Db 2274 TTCAGTCTCTATATG---GAAAGCCTTTCTTACAGAACAAAGCAGACATGAAAT--- 2327
QY 386 PheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGlyValPheSerHisLys 405
    :|||||:|||||:|||||:|||||:|||||:
Db 2328 CTCAAAGCAACTGTCTCTCTGTGTGAGCTGGCTTGAAGGTTTTCATGTTCC 2387
QY 406 PheAspPheGlnLeuGlnAspVal-----SerSerValAsnGluAspValLeuLeuThr 423
    :|||||:|||||:|||||:|||||:|||||:
Db 2388 TTTGAGTTTAAATGATGATGATCTCCGCAAGCAGGCGTTGATGAAGATGAATCTAAC 2447
QY 424 ThrGlyLeuLeuCysLysTyrThrThrAlaGlnArgArgLeuSerSerLeuLeuThrSerHisGlu 443
    :|||||:|||||:|||||:|||||:|||||:
Db 2448 ATGTGCTTATGACCAATTTTACAGCCGAGACACTTAAGCACTTCTACCGGTTTTTAAGT 2507
QY 444 LysSerPheGlnGluThrThrAlaGlyArgArgLeuSerSerLeuLeuThrSerHisGlu 463
    :|||||:|||||:|||||:|||||:|||||:
Db 2508 CCTGCTTCAGAAATTTCTTGGGGGATGAGGCTGATTTGAACCTCTCGATTCACTAG 2567
QY 464 ProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIleSerAspIle 483
    :|||||:|||||:|||||:|||||:|||||:
Db 2568 CAGAACATCAAGATTGGGACTGTATCATTTGAAACAATCAACTCAACCATGATGACT 2627
QY 484 ThrSerThrTyrSerSerLeuLeuArgTyrThrCysGly---SerSerValGluAlaThr 502
    :|||||:|||||:|||||:|||||:|||||:
Db 2628 GTAAAGCGCTACAAACATTTTGAACATATGCTCCAGCTCCCTTCAACAAAGCAGGG 2687
QY 503 ArgAlaValMetLysHisLeu 509
    :|||||:|||||:
Db 2688 CCCAAATTTGTCTCATTTG 2708

```

Search completed: January 31, 2003, 11:50:02
 Job time : 402 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OW protein - nucleic search, using frame_plus_p2n model

Run on: January 31, 2003, 11:41:11 ; Search time 1277.45 Seconds
(without alignments)
2004.811 Million cell updates/sec

Title: US-09-697-089-2_COPY_1_88
Perfect score: 461
Sequence: 1 MNFKDNRALIQRMGWTVI.....FLKSLKRWNYPLFQDLNGQS 88

Scoring table: BIOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 segs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=rlh
-Q/cgna2_1/USPIO.spool/US09697089/rnatc_29012003_092753_19716/app-query.fasta.1.981
-DB=GenBdb1 -QPM=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=BIOSUM62 -TRANS=human40.cdi -LIST=45
-DOCLALIGN=200 -THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09697089 @CGN 1.1.3568 @rnatc.29012003.092753.19716 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -RAIT -LONGLOG -DEV.TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FEAPOP=6 -FEAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenBdb1:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_com:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rnd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	461	100.0	578	6 AX318095	AX318095 Sequence
2	461	100.0	578	9 AY027790	AY027790 Homo sapi
3	461	100.0	768	6 AX318097	AX318097 Sequence
4	461	100.0	768	9 AY027789	AY027789 Homo sapi
5	461	100.0	1395	6 AX318093	AX318093 Sequence
6	461	100.0	1395	9 AY027788	AY027788 Homo sapi
7	461	100.0	3133	9 AY032589	AY032589 Homo sapi
8	461	100.0	3219	9 AY035391	AY035391 Homo sapi
9	461	100.0	3355	9 AK095467	AK095467 Homo sapi
10	461	100.0	3360	9 BC031555	BC031555 Homo sapi
11	461	100.0	3396	6 AX318091	AX318091 Sequence
12	461	100.0	3396	9 AY027787	AY027787 Homo sapi
13	461	100.0	3581	9 AF376061	AF376061 Homo sapi
14	457	99.1	261	6 AX318172	AX318172 Sequence
15	457	99.1	138909	9 CNS01053	AL121653 BAC seqe
16	457	99.1	160583	2 AC010968	AC010968 Homo sapi
17	341	74.0	107885	2 AC107111	AC107111 Rattus no
18	311	67.5	185465	2 AC101793	AC101793 Mus muscu
19	123.5	26.8	1233	4 AF135968	AF135968 Felis cat
20	118.5	25.7	1215	4 AF135967	AF135967 Canine inte
21	118.5	25.7	1215	6 E32836	E32836 Canine inte
22	118.5	25.7	1560	6 E32838	E32838 Canine inte
23	113	24.5	146451	2 AC019309	AC019309 Homo sapi
24	113	24.5	161218	2 AC011171	AC011171 Homo sapi
25	113	24.5	185983	9 AP000942	AP000942 Homo sapi
26	113	24.5	214484	9 AP001830	AP001830 Homo sapi
27	109	23.6	110000	2 AC095560_0	AC095560 Rattus no
28	109	23.6	110000	2 AC095560_1	Continuation (2 of
29	108	23.4	2380	9 BC016174	BC016174 Homo sapi
30	108	23.4	2531	9 HUMSCPA	LA9431 Homo saplen
31	108	23.4	2589	6 AR129832	AR129832 Sequence
32	108	23.4	3532	6 AR076334	AR076334 Sequence
33	108	23.4	3532	6 AX410708	AX410708 Sequence
34	108	23.4	3532	9 HSU37547	U37547 Human IAP h
35	108	23.4	3732	6 AR106399	AR106399 Sequence
36	108	23.4	3732	6 AR116701	AR116701 Sequence
37	108	23.4	4089	9 BC028578	BC028578 Homo sapi
38	106	23.0	257047	2 AC090879	AC090879 Mus muscu
39	104.5	22.7	156684	2 AP002787	AP002787 Homo sapi
40	104.5	22.7	172488	9 AP001153	AP001153 Homo sapi
41	104	22.6	1770	10 AF183431	AF183431 Rattus no
42	104	22.6	3290	10 AF190020	AF190020 Rattus no
43	103.5	22.5	1215	4 AB027296	AB027296 Sus scrofa
44	103.5	22.5	1218	4 AF090119	AF090119 Equus cab
45	102.5	22.2	321	6 AX318084	AX318084 Sequence

RESULT 1

ALIGNMENTS

AX318095
LOCUS AX318095 578 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 100 from Patent WO0190156.
ACCESSION AX318095
VERSION AX318095.1 GI:17900824
KEYWORDS
SOURCE
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Reed,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,
Oliveira,V.A., Hayashi,H. and Pawlowski,K.
TITLE Card domain containing polypeptides, encoding nucleic acids, and
methods of use
JOURNAL Patent: WO 0190156-A 100 29-NOV-2001;
The Burnham Institute (US)
FEATURES
source
1. 578
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="unnamed protein product"
/protein_id="CAD19342.1"
/protein_start=1
/db_xref="GI:17900825"
/translation="MNFIRKNSRALIORMGMVYIKOITDLEFVWVNLNREVNIIICE
KYEDARGIHMLIKKSESCNLFKSKENNYPLFQDLNGSLTLTA"
BASE COUNT 172 a 106 c 143 g 157 t
ORIGIN

Alignment Scores:
Pred. No.: 1.4e-51 Length: 578
Score: 461.00 Matches: 88
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-697-089-2_COPY_1_88 (1-88) x AX318095 (1-578)

QY 1 MetAsnPhelIeLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
DB 277 ATGAAATTTCAATAAGGACCAATAGCCGACCTTATTCAAAGAAATGGAAATGACGTATATA 336
QY 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle 40
DB 337 AAGCAATTCACAGATGACCTATTGTTGATGGAATGTTCTGAATCGCGAAGAAAGTAAACATC 396
QY 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
DB 397 ATTGCTGCGAGAGAGTGAGACAGATGCTCTAGAGGATCATTCACATGATTTTGAAA 456
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTrpProLeu 80
DB 457 AAGGTTTCAGAGTCCCTGTAACTCTTCTTAATCCCTTAAGAGATGGAACCTATCTCTTA 516
QY 81 PheGlnAspLeuAsnGlyGlnSer 88
DB 517 TTTCAGGACTTGAAATGACAAAGT 540

RESULT 2
LOCUS AY027790 578 bp mRNA linear PRI 20-JUL-2001
DEFINITION Homo sapiens CLAND (CLAN1) mRNA, complete cds.
ACCESSION AY027790
VERSION AY027790.1 GI:14324118
KEYWORDS
SOURCE Homo sapiens.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 578)

AUTHORS Damiano,J.S., Stehlik,C., Pio,F., Godzik,A. and Reed,J.C.
TITLE Clan, a novel human ced-4-like gene
JOURNAL Genomics 75 (1-3), 77-83 (2001)
MEDLINE 21365712
PUBMED 11472070
REFERENCE 2 (bases 1 to 578)
AUTHORS Stehlik,C., Damiano,J.S., Pio,F., Godzik,A. and Reed,J.C.
TITLE Direct Submission
JOURNAL Submitted (21-FEB-2001) Program on Apoptosis and Cell Death
Research, The Burnham Institute, 10901 North Torrey Pines Road, La
Jolla, CA 92037, USA
FEATURES
source
1. 578
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/map="2p22-P21"
/tissue_type="lung"
1. 578
/gene="CLAN1"
/gene="CLAN1"
/gene="CLAN1"
/note="CARD protein; alternatively spliced"
/product="CLAND"
/protein_id="AAK14779.1"
/db_xref="GI:14324119"
/translation="MNFIRKNSRALIORMGMVYIKOITDLEFVWVNLNREVNIIICE
KYEDARGIHMLIKKSESCNLFKSKENNYPLFQDLNGSLTLTA"
BASE COUNT 172 a 106 c 143 g 157 t
ORIGIN

Alignment Scores:
Pred. No.: 1.4e-51 Length: 578
Score: 461.00 Matches: 88
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-697-089-2_COPY_1_88 (1-88) x AY027790 (1-578)

QY 1 MetAsnPhelIeLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
DB 277 ATGAAATTTCAATAAGGACCAATAGCCGACCTTATTCAAAGAAATGGAAATGACGTATATA 336
QY 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle 40
DB 337 AAGCAATTCACAGATGACCTATTGTTGATGGAATGTTCTGAATCGCGAAGAAAGTAAACATC 396
QY 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
DB 397 ATTGCTGCGAGAGAGTGAGACAGATGCTCTAGAGGATCATTCACATGATTTTGAAA 456
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTrpProLeu 80
DB 457 AAGGTTTCAGAGTCCCTGTAACTCTTCTTAATCCCTTAAGAGATGGAACCTATCTCTTA 516
QY 81 PheGlnAspLeuAsnGlyGlnSer 88
DB 517 TTTCAGGACTTGAAATGACAAAGT 540

RESULT 3
LOCUS AX318097 768 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 102 from Patent WO0190156.
ACCESSION AX318097
VERSION AX318097.1 GI:17900826
KEYWORDS
SOURCE human.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Reed,J.C., Plo,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,
Oliveira,V.A., Hayashi,H. and Pawlowski,K.
TITLE Card domain containing polypeptides, encoding nucleic acids, and
METHODS Methods of use
PATENT Patent: WO 0190156-A 102 29-NOV-2001;
JOURNAL The Burnham Institute (US)
FEATURES location/Qualifiers
source 1..768
/organism="Homo sapiens"
/db_xref="taxon:9606"
CDS 277..747
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD19343.1"
/db_xref="GI:17900827"
/translation="MNFIDKNSRALIORMGMTVIKQITDDLFVNNVLRREVNITICE
KVBDARGLIHMLKKSSECNLFKSLKEMNPLFQDINGSLFQTSBGDLDLA
QDLKDIHTPSFLNFPYPLGEDIIDIFMLKSTFTEPVLMRRDQHHRVEQLTVL"
BASE COUNT 218 a 157 c 180 g 213 t
ORIGIN
Alignment Scores:
Pred. No.: 1.94e-51 Length: 768
Score: 461.00 Matches: 88
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-697-089-2_copy_1_88 (1-88) x AX318097 (1-768)
QY 1 Metasnphelleyaspsasnserrargalaleuileglnargmetglymethrvalille 20
DB 277 ATGATTTTCATTAAGACAAATGAGCCCTTATTCATAAAGATGGAGATGACTGTATA 336
QY 21 LysglnlierhraspaspLeuphevaltrpaspnvalleuasnarggluvalasnlle 40
DB 337 AAGCAAAATCAGATGACCTTTTGTATGGAATGTTCGAATCCGGAAGAATAACATC 396
QY 41 Ilcycscysgluylsvaiglnaspalaalaarglylleilshsmetilleuyls 60
DB 397 ATTGCTGCGAGAGAGTGACAGATGCTCTAGAGGATCATTCATGATTTTGA 456
QY 61 LysglSerGIuSerCysAsnLeupheulysSerleuylsGIuTPAsnTyPProleu 80
DB 457 AAGGTTTCAGAGTCCTCTTAACCTCTTAAATCCCTTAAGAGTGAACATATCCCTCTA 516
QY 81 PheglaspLeuAenglylnSer 88
DB 517 TTTCAGGACTTGAAATGACAAAGT 540
RESULT 4
LOCUS AY027789 768 bp mRNA linear PRI 20-JUL-2001
DEFINITION Homo sapiens CLANC (CLANI) mRNA, complete cds.
ACCESSION AY027789
VERSION AY027789.1 GI:14324116
KEYWORDS
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Damiano,J.S., Stehlik,C., Plo,F., Godzik,A. and Reed,J.C.
TITLE Clan, a novel human ced-4-like gene
JOURNAL Genomics 75 (1-3), 77-83 (2001)
MEDLINE 21365712
PUBMED 11472070
REFERENCE 2 (bases 1 to 768)
AUTHORS Stehlik,C., Damiano,J.S., Plo,F., Godzik,A. and Reed,J.C.
TITLE Direct Submission
JOURNAL Submitted (21-FEB-2001) Program on Apoptosis and Cell Death

FEATURES
source location/Qualifiers
1..768
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/map="2p22-p21"
/tissue_type="lung"
1..768
/gene="CLANI"
CDS 277..747
/note="alternatively spliced; similar to Ced-4"
/codon_start=1
/product="CLANC"
/protein_id="AAK14778.1"
/db_xref="GI:14324117"
/translation="MNFIDKNSRALIORMGMTVIKQITDDLFVNNVLRREVNITICE
KVBDARGLIHMLKKSSECNLFKSLKEMNPLFQDINGSLFQTSBGDLDLA
QDLKDIHTPSFLNFPYPLGEDIIDIFMLKSTFTEPVLMRRDQHHRVEQLTVL"
BASE COUNT 218 a 157 c 180 g 213 t
ORIGIN
Alignment Scores:
Pred. No.: 1.94e-51 Length: 768
Score: 461.00 Matches: 88
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-697-089-2_copy_1_88 (1-88) x AY027789 (1-768)
QY 1 Metasnphelleyaspsasnserrargalaleuileglnargmetglymethrvalille 20
DB 277 ATGATTTTCATTAAGACAAATGAGCCCTTATTCATAAAGATGGAGATGACTGTATA 336
QY 21 LysglnlierhraspaspLeuphevaltrpaspnvalleuasnarggluvalasnlle 40
DB 337 AAGCAAAATCAGATGACCTTTTGTATGGAATGTTCGAATCCGGAAGAATAACATC 396
QY 41 Ilcycscysgluylsvaiglnaspalaalaarglylleilshsmetilleuyls 60
DB 397 ATTGCTGCGAGAGTGACAGATGCTCTAGAGGATCATTCATGATTTTGA 456
QY 61 LysglSerGIuSerCysAsnLeupheulysSerleuylsGIuTPAsnTyPProleu 80
DB 457 AAGGTTTCAGAGTCCTCTTAACCTCTTAAATCCCTTAAGAGTGAACATATCCCTCTA 516
QY 81 PheglaspLeuAenglylnSer 88
DB 517 TTTCAGGACTTGAAATGACAAAGT 540
RESULT 5
LOCUS AX318093 1395 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 98 from Patent WO0190156.
ACCESSION AX318093
VERSION AX318093.1 GI:17900822
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Reed,J.C., Plo,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,
Oliveira,V.A., Hayashi,H. and Pawlowski,K.
TITLE Card domain containing polypeptides, encoding nucleic acids, and
METHODS Methods of use
PATENT Patent: WO 0190156-A 98 29-NOV-2001;
JOURNAL The Burnham Institute (US)
FEATURES location/Qualifiers

FEATURES	source
MEDLINE	21268963
PUBMED	11374873
REFERENCE	2 (bases 1 to 3133)
AUTHORS	Bertin, J.
JOURNAL	Direct Submission
TITLE	Submitted (15-APR-2001) Neurobiology, Millennium Pharmaceuticals Inc., 640 Memorial Drive, Cambridge, MA 02139, USA
FEATURES	Location/Qualifiers
source	1..3133
CDS	<p>/organism="Homo sapiens"</p> <p>/db_xref="taxon:9606"</p> <p>36..3110</p> <p>/note="CARD12; CED4/Apaf-1 family member"</p> <p>/codon_start=1</p> <p>/product="caspase recruitment domain protein 12"</p> <p>/translation="MNFIKNSRALIORMGTMVTKQITDDLFWNVNLNREVNICEE KVQDAAAGIILHMLIKKSGESCNLFSLKEWNPFLPDNLGSLFPHQSGDLDLA ODKDIHYPSPLNFPYPLGIDITIFLKSFPNPEMRDQHHNRVLEQTLNLOD LQSPCTIEGSGSKSTLLQRIAMLMNSGCKALKTRKVPFLRLSAQGEPTFLDQ QLDIPETIRKQTPMALMLKQRYLFLVLEGNFEPQNCPELALIKENHREKNMT VPTTECLRIHROGALFAVGDWTEDSAALIREVLKELAEGLLIQKSRCLRM MKPFLVITICAIOMGSEBFSHSQTQTLFETFYDLIQKNKHKGVAASDFISLSDH CGDLAEGVFSHKFDEFLQDVSSVNEVDYLLTGCTYTORERKPKFPFKSPEEY AGRLSILTSHEPEEYTKNGYLOKKVSLSDITSYVSLIRYCGSSVATRAVMKH LAAYVOHCGILGSLIAKRPLMROESLQVKNYNTQDILKININSPFECIHLYOEST SKALSOEPFAPFQGKSLYINSQITDYLDFEPHRLPNCASALDEIKLDYGGANSM EKAEDTGGIIMEBAPETVTPSRVSLFFPMKQEFRLVETLRDFSLNODITTYLCK IFSSATSLRLQIKRCAGVAGSLVYSTCKNITSIAWEASPLTIEDRHITSVNLT LSIHDLQNRQIKPGLINDSLGNLKNLTILINDNTKMNEDAKIAELGKLNKMLFHL THSLDIEGMADYIVKSLSEPCDEFIOLVYSCSAVAVKILKQNLNLYKSLTIDLS ENLEKNGEALAEHLIDRMVNLPEDLTFLMIPMGDVGSGVSLIKHLEVPOLYKGL KNMRIDTEIRIIGAFGRKNPLNFQOLINAGRVSSDGLAPLAGVRENTKQVYFPDF STPEFLPDAIVLVKLSVLSKLPIFLDARLVGMQFDDDLVITGAFKLYTA"</p>
misc_feature	36..299
misc_feature	/note="CARD; Region: caspase recruitment domain"
misc_feature	522..1406
misc_feature	/note="NBS; Region: nucleotide-binding site"
misc_feature	2001..3107
misc_feature	/note="LRR; Region: leucine-rich repeats"
BASE COUNT	903 a 691 c 729 g 810 t
ORIGIN	
Alignment Scores:	
Prod. No.:	9,7e-51
Score:	461.00
Percent Similarity:	100.00%
Best local Similarity:	100.00%
Query Match:	100.00%
DB:	Gaps: 9
US-09-697-089-2_COPY_1_88 (1-88) x AV032589 (1-3133)	
QY	1 Metnshpellelysasapshsersararqalaleuileeginatgmetglymethvaltllle 20
Db	36 ATGAAATTTCAATAAAGGACAAATAGCCGAGCCCTTATTCATAAAGGAGGAAATACGCTTATA 95
QY	21 Lysglnliethraapapleuphevalttrpansvallleuunsatarglugluvalasnlle 40
Db	96 AAGCAATACACAGATGACCTATTGTATGGAATGTTTGATGCGCGAAGAACTAAACATC 155
QY	41 Illeyscysgslulysvalgluglnasplalalaaargelyllellehsmetlleleulys 60
Db	156 ATTTGCTGCGGGAAGGAGGACAGGATGCTCTGAGAGGACATTCACATATTTTGAAA 215
QY	61 LysglsysergluserCysasnleupheuleuysserleuylsglutrpasnttyProheu 80
Db	216 AAGGATTCAGAGCTCTCTGAACCTCTTTCTTAAATCCCTTAAGAGAGTGGAACTATCCTTA 275
QY	81 Pheglnaspleuansnglylnser 88
Db	276 TTTTCAGACTTGAAATGGCAAAAGT 299

LOCUS	AY035391	3219 bp	mRNA	linear	PRI 24-JUL-2001
DEFINITION	Homo sapiens ICE-protease activating factor mRNA, complete cds.				
ACCESSION	AY035391				
VERSION	AY035391.1	GI:14334214			
KEYWORDS					
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	1 (bases 1 to 3219) Poyet,J.L., Srinivasula,S.M., Tiani,M., Razmara,M., Fernandes-Alnemri,T. and Alnemri,E.S.				
TITLE	Identification of Ipa1, a human caspase-1-activating protein related to Apat-1				
JOURNAL	J. Biol. Chem. 276 (30), 28309-28313 (2001)				
MEDLINE	21359454				
PUBMED	11390368				
REFERENCE	2 (bases 1 to 3219) Poyet,J.-L., Srinivasula,S.M., Fernandes-Alnemri,T. and Alnemri,E.S.				
AUTHORS	Direct Submission				
TITLE	Submitted (16-MAY-2001) Microbiology and Immunology, Thomas Jefferson University, 233 S. 10th Street, Philadelphia, PA 19107, USA				
FEATURES	Location/Qualifiers				
SOURCE	1..3219 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="2" /map="p21-22" 145..3219 /note="IPAF; CED4/Apaf-1 family member; caspase-associated recruitment domain containing protein" /codon.start=1 /product="ICE-protease activating factor" /protein_id="AAK59843.1" /db_xref="GI:14334215" /translation="MNFIKDNSNRLIORMGTVIKOITDDLEFYVNVLNREVINICCEKVDAAGLIIMHILKKSGESCNFLKSLKEMVPLFODLNGSLPHQISEGLDILAQDKLDTLPSPFNFLYGLGIDIDIFLFLKSTFEPYLMKRDGHHNVEQLTLGLDIALOSCELTIEGSGSKASTLQRIALMMSGSGKALTKFKEFVFLFRAQGLPFTLCDQLIDPSTIRKQPMFAMLLKLRQVLELDGVMFQNPONCELALEIKENHRKNMVIYTTTPECLRIHROPGALTAIVCGMTEDSNAALIRVYLKELAGLLDQIOKSCILNLMKRPLEFVITCALIQMGSEFESHRTQTLTFEYDILLQKKHKHKGVAASDFIRSLDHCGDLALGVPFSHKFDEFLQVSSVNEVDVLTTLGLCKYAOQRPKYKFFPKSFOYTAGRRLSILTSHPEEYATKNGVLYLOKVASISDITSTYSSILRYTCSSYEATPAVKHLSAAVYHGICGLGISIAKRPLMROESLOSQVNTKEOELKAIINISFEGGILHYORSTSKALSOEFPAFGQSKLYINSGNIDPYLTDEPHEI.PNCASALNDFIKIDFYGGAASWEKAEDTGGIHMEDEAPERTYIPRSAYSLFFRWKQDEPRTLEVTLLDEPSKLKODIRYLGIFTSAYSLRIQIRKACGVASLSLVSTGCNNTSLWEAVSLTIEDERHTTSVNTLDTLSIHLDDNRLPGGLDLSLGNLNLKRLKINDNTKMEEDAIRKLEGLKMLKWCPLHTLSLDEGMDYIVKSLSSPECDLEETQLVSCISANAVYILQNLNHNIVKLSLDLSENTLEKGNALHEHLDIRNVLEQLTALMPGCDVQSSLSLKLHEVPLVKGLKNMRLPTEIRITIGAFGRKPLKTFQOOLNAGRVSDGWLAFMGVEENLKQVFPDFSTHELEPDPALVRKISQVLSKLTPEIQEARLYVQGFDDDLSTVTGAFKLVTA"				
CDS					
BASE COUNT	934 a	696 c	748 g	841 t	
ORIGIN					
Alignment Scores:					
Pred. No.:	1e-50	Length:	3219		
Score:	461.00	Matches:	88		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	100.00%	Indels:	0		
Gap:	9	Gaps:	0		

```

Db      145 ATGAATTTCTAATAAGCAATAGCCGACCCCTTATTCAAAGAAATGGCAATGACTGTTATA 204
Qy      21  LysGlnIleThrAspAspLeuPheValTPRAsnValLeuAsnArgGluValAsnIle 40
Db      205 AAGCAATATCAGATGACCTATTGTTATGGAATGTTCTGAATGCCAGAAAGTAACATC 264
Qy      41  IleCysCysGluIuValGluGlnAspAlaIleArgGlyIleIleHisMetIleLeuLys 60
Db      265 ATTTGCTGCAGAGAGAGGAGGAGATGCTAGAGAGGATCATTCACATGATTTTGAAA 324
Qy      61  LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTPRAsnTyrProLeu 80
Db      325 AAGGTTTCACAGTCTCTTAACCTCTTCTTAATCCCTTAAGAGAGTGAATACCTCTTA 384
Qy      81  PheGlnAspLeuAsnGlyGlnSer 88
Db      385 TTTCAGGACTTGAATGACAAAGT 408

RESULT 9
AK095467
LOCUS      Homo sapiens cDNA FLJ38148 f1s, clone D90ST2003791, highly similar
DEFINITION to Homo sapiens ICE-protease activating factor mRNA.
ACCESSION AK095467
VERSION    AK095467.1 GI:21754727
KEYWORDS   oligo capping; f1s (full insert sequence).
SOURCE     Homo sapiens CD34+ Cells cDNA to mRNA, clone_11b:D90ST2
           clone:D90ST2003791.
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1
AUTHORS   Nishimura,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T.,
           Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K.,
           Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,
           Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
           Yamamoto,K., Isono,Y., Kawal-Hio,Y., Saito,K., Nishikawa,T.,
           Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
           Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fuji,A.,
           Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
           Nagahara,K., Masuno,Y., Nagai,K. and Isogai,T.
           NEDO human cDNA sequencing project
           Unpublished
           2 (bases 1 to 3355)
REFERENCE  2
AUTHORS   Isogai,T. and Yamamoto,J.
TITLE     Direct Submission
JOURNAL   Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
           Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
           (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
           NEDO human cDNA sequencing project supported by Ministry of
           Economy, Trade and Industry of Japan: cDNA full insert sequencing:
           Research Association for Biotechnology (RAB) (supported by Japan
           Construction: Helix Research Institute (HRI) (supported by Japan
           Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
           HRI, and Biotechnology Center, National Institute of Technology and
           Evaluation; clone selection for full insert sequencing: HRI and
           RAB; annotation: HRI and RAB.
           Location/Qualifiers
           1..3355
           /organism="Homo sapiens"
           /db_xref="taxon:9606"
           /clone="D90ST2003791"
           /cell_type="CD34+ Cells"
           /clone_11b="D90ST2"
           /note="cloning vector: pME18SFL3-mRNA from CD34+ cells
           after 9-days ODF induction.-primary culture, CD34+ cells"

BASE COUNT  986 a 726 c 774 g 869 t
ORIGIN
Alignment Scores: 1.05e-50 length: 3355
Score: 461.00 Matches: 88
Percent Similarity: 100.00% Conservative: 0

```

```

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-697-089-2_copy_1_88 (1-88) x AK095467 (1-3355)

Qy      1  MetAspPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
Db      262 ATGAATTTCTAATAAGCAATATAGCCGACCCCTTATTCAAAGAAATGGCAATGACTGTTATA 321
Qy      21  LysGlnIleThrAspAspLeuPheValTPRAsnValLeuAsnArgGluValAsnIle 40
Db      322 AAGCAATATCAGATGACCTATTGTTATGGAATGTTCTGAATGCCAGAAAGTAACATC 381
Qy      41  IleCysCysGluIuValGluGlnAspAlaIleArgGlyIleIleHisMetIleLeuLys 60
Db      382 ATTTGCTGCAGAGAGAGGAGGAGATGCTAGAGAGGATCATTCACATGATTTTGAAA 441
Qy      61  LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTPRAsnTyrProLeu 80
Db      442 AAGGTTTCACAGTCTCTTAACCTCTTCTTAATCCCTTAAGAGAGTGAATACCTCTTA 501
Qy      81  PheGlnAspLeuAsnGlyGlnSer 88
Db      502 TTTCAGGACTTGAATGACAAAGT 525

RESULT 10
BC031555
LOCUS      Homo sapiens, caspase recruitment domain protein 12, clone
DEFINITION MGC:35330 IMAGE:5179909, mRNA, complete cds.
ACCESSION BC031555
VERSION    BC031555.1 GI:21594975
KEYWORDS   MGC.
SOURCE     human.
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 3360)
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE     Direct Submission
JOURNAL   Submitted (06-JUN-2002) National Institutes of Health, Mammalian
           Gene Collection (MGC), Cancer Genomics Office, National Cancer
           Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2530,
           USA
           NIH-MGC Project URL: http://mgc.nci.nih.gov
           Contact: MGC help desk
           Email: cgaps-remail.nih.gov
           Tissue Procurement: Life Technologies, Inc.
           cDNA Library Preparation: Life Technologies, Inc.
           DNA Sequencing by: Baylor College of Medicine Human Genome
           Sequencing Center
           Center code: BCM-HGSC
           Web site: http://www.hgsc.bcm.tmc.edu/cdna/
           Contact: amg@bcm.tmc.edu
           Gunaratne, P.H., Garcia, A.M., Lu, X., Huylk, S.W., Hale, S.M.,
           Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
           Richards, S., Gibbs, R.A.
           Clone distribution: MGC clone distribution information can be found
           through the I.M.A.G.E. Consortium/BLN at: http://image.llnl.gov
           Series: IRAC Plate: 50 Row: a Column: 10
           This clone was selected for full length sequencing because it
           passed the following selection criteria: Hexamer frequency ORF
           analysis.
           Location/Qualifiers
           1..3360
           /organism="Homo sapiens"
           /db_xref="taxon:9606"
           /db_xref="MGC:35330 IMAGE:5179909"
           /tissue_type="Brain, Lung, Testis, adult, pooled whole"

```

/clone.lib="NTH_MGC_115"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
232. .3306
/codon_start=1
/product="caspase recruitment domain protein 12"
/protein_id="AA31555.1"
/db_xref="GI:21594976"
/translation="MNFIKDNRSLAIQRMGTIVIKQITDDLFVNNVNLREEVINIICE
KVEDDAAGIIHMLIKGSESCNLFSLKEMNPPLQDLNGOSLPHQTSGLDDLLA
QDLKDYHPFPLFPLGEDIDIFNLKSTFEPILMRKQDHHRRVQLNLQIA
LQSPICIEGSGKSTLLQRIAMLGSGCKALTKFEVFLRLSRAOGLFETCD
QDLDPGTRKOTFMAMLIKROVLPFLDGYNEKPNQPCFEIELIKENRFRNMVI
VTTTECLRIHROGALTAEVGDMTESAQLIREVILKELAEGLLIQISRLRL
MKTPLFVYITCAIQMGSESESHSTQTLFHTFYDLLLOKNHKKHKAASDFISLDH
RGDLALBGEVSHKDFELQDVSVNEDVLLTGLCKYTAQRPKPKFEFKSFOEY
AGRLISLITSHBEDEVKNGVYLQKWSISDITSVSLRYCGSSVEATRAVMKH
LAAYOHGCLGLSLIAKRPIMROESLOSVMKTTQELIKAININSFVCGIHYOEST
SKSALSOEFEPFGKSLYINSNIPDYLPDFEPHLPNCASALDPKIDFYGMAWS
EKAEDPGGIIHMEAPETIYIPSAVSLFENMKOEPRLIETLRDPSKLNQDITVYIK
IFSSATSLRIQIRKCAVAGSLVLSSTCKNYSILMEASPLTIEDERHITSVNLKT
LTIHDLQNRPLGGLTDSLGNLKNLTKIMONINMEEDAIKLAEGLNKMKCLFHL
THLSDIGEMDYIVKSLSEPCDEIEIQLVSCISANAVKILAOINLNLVSLTSLDS
ENYLEKDNENALHELIDRMNVLBOETALMLPWGCDVOSLSLKLHLEVPOLVKGL
KNMRLTPEIRIILGAFPGKNPLKNEOOLNAGNVSSDGLAFMGVFNELKQLVFEDF
STKEFLDPALVRRLSOVLSKTLFLOEARLVGMQFDDDDLSVITGARLVYA"

BASE COUNT 1011 a 718 c 768 g 863 t
ORIGIN

Alignment Scores:

Pred. No.: 1.05e-50 Length: 3360
Score: 461.00 Matches: 88
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-697-089-2_copy_1_88 (1-88) x BC031555 (1-3360)

Qy 1 MetasphelieAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
Db 232 ATGATTTTCATTAAGACAAATAGCCGACCCCTTATTCAAGATGGAATGACTGTATA 291
Qy 21 LysGlnIleThrAspAspLeuPheValITrpaSValIleuAsArgGluGlnValAsnIle 40
Db 292 AAGCAAAATCACGATGACCTATTGTATGAAATGTTGAAATCGCGAAGAAATAACATC 351
Qy 41 IleCysCysGluIysValGlnAspAlaIleArgGlyIleIleHisMetIleLeuIys 60
Db 352 ATTTCCTCGAAGAGGTGAGCAGATGCTGTACAGGATCATTCACATGATTTTGA 411
Qy 61 LysGlySerGluSerCysAsnLeuPheLeuIysSerLeuIysGluITrpaSntyrProleu 80
Db 412 AAGGTTTCAGAGTCTCTTAACCTCTTCTTAATCCCTTAAGAGATGGAACATATCTCTA 471
Qy 81 PheGlnAspLeuAsnGlyGlnSer 88
Db 472 TTTCAGACTTGAAATGACAAAGT 495

RESULT 11
AX318091 3396 bp DNA linear PAT 14-DEC-2001
LOCUS Sequence 96 from Patent W00190156.
ACCESSION AX318091
VERSION AX318091.1 GI:17900820
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
1 Reed,J.C., Plo,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,
Oliveira,V.A., Hayashi,H. and Pawlowski,K.

TITLE Card domain containing polypeptides, encoding nucleic acids, and
JOURNAL methods of use
Patent: WO 0190156-A 96 29-NOV-2001;
The Burnham Institute (US)
FEATURES
source Location/Qualifiers
1. .3396
/organism="Homo sapiens"
/db_xref="taxon:9606"
CDS
277. .3351
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD91340.1"
/db_xref="GI:17900821"

BASE COUNT 992 a 737 c 793 g 874 t
ORIGIN

Alignment Scores:
Pred. No.: 1.06e-50 Length: 3396
Score: 461.00 Matches: 88
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-697-089-2_copy_1_88 (1-88) x AX318091 (1-3396)

Qy 1 MetasphelieAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
Db 277 ATGATTTTCATTAAGACAAATAGCCGACCCCTTATTCAAGATGGAATGACTGTATA 336
Qy 21 LysGlnIleThrAspAspLeuPheValITrpaSValIleuAsArgGluGlnValAsnIle 40
Db 337 AAGCAAAATCACGATGACCTATTGTATGAAATGTTGAAATCGCGAAGAAATAACATC 396
Qy 41 IleCysCysGluIysValGlnAspAlaIleArgGlyIleIleHisMetIleLeuIys 60
Db 397 ATTTCCTCGAAGAGGTGAGCAGATGCTGTACAGGATCATTCACATGATTTTGA 456
Qy 61 LysGlySerGluSerCysAsnLeuPheLeuIysSerLeuIysGluITrpaSntyrProleu 80
Db 457 AAGGTTTCAGAGTCTCTTAACCTCTTCTTAATCCCTTAAGAGATGGAACATATCTCTA 516
Qy 81 PheGlnAspLeuAsnGlyGlnSer 88
Db 517 TTTCAGACTTGAAATGACAAAGT 540

RESULT 12
AY027787 3396 bp mRNA linear PRI 20-JUL-2001
LOCUS AY027787
DEFINITION Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.
ACCESSION AY027787
VERSION AY027787.1 GI:14324112
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 3396)
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 AUTHORS Damiano, J.S., Stehlik, C., Plo, F., Godzik, A. and Reed, J.C.
 TITLE Clau, a novel human ced-4-like gene
 JOURNAL Genomics 75 (1-3), 77-83 (2001)
 MEDLINE 21365712
 PUBMED 11472070
 REFERENCE 2 (bases 1 to 3396)
 AUTHORS Stehlik, C., Damiano, J.S., Plo, F., Godzik, A. and Reed, J.C.
 TITLE Direct Submission
 JOURNAL Submitted (21-FEB-2001) Program on Apoptosis and Cell Death
 Research, The Burnham Institute, 10901 North Torrey Pines Road, La
 Jolla, CA 92037, USA

FEATURES
 source
 1. .3396
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="2"
 /map="2p22-p21"
 /tissue_type="lung"
 1. .3396
 /gene="CLAN1"
 277. .3351
 /gene="CLAN1"
 /note="alternatively spliced; similar to Ced-4"
 /codon_start=1
 /product="CLAN1"
 /protein_id="AAK14776.1"
 /db_xref="GI:14324113"

gene
 CDS
 277. .3351
 /gene="CLAN1"
 /note="alternatively spliced; similar to Ced-4"
 /codon_start=1
 /product="CLAN1"
 /protein_id="AAK14776.1"
 /db_xref="GI:14324113"

BASE COUNT 992 a 737 c 793 g 874 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.06e-50 Length: 3396
 Score: 461.00 Matches: 88
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0
 US-09-697-089-2_COPY_1_88 (1-88) x AY027787 (1-3396)
 QY 1 Metasnphelelysaspsnsesrarglaleuileglnargmetcylmetrhyallle 20
 Db 277 ATGAAATTCATAAAGACAAATAGCCGACCTTATTCACAAAGAGGAAATGACTGTATTA 336
 QY 21 Lysglntierpraspapleuphevaltrpsanvalleuasapngugluvalasnlle 40
 Db 337 AAGCAAAATCACAGATGACCTATTTGTATGAAATGTCGGAATCGGAAGATAAACATC 396
 QY 41 Illecyscylulysvalgluglnaspalalaarvgliellelshsmetilleulys 60
 Db 397 ATTTCGCGGAGAAAGGTGACAGATGCTCTAGAGGAGCATTCATCATATTTTGA 456

QY 61 Lysglserglusercysasnleupheleulysertleulysglutrpasnytrprolen 80
 Db 457 AAGGTTCAAGATCTCTTAACCTCTTCTTAATCCCTTAAGGAGTGAACATCTCTA 516
 QY 81 Pheglinspleuansglylinsr 88
 Db 517 TTTCAGGACTTGAAATGACAAAGT 540
 RESULT 13
 AF376061
 LOCUS 3581 bp mRNA linear PRI 15-MAY-2001
 DEFINITION Homo sapiens caspase recruitment domain protein 12 mRNA, complete
 cds
 ACCESSION AF376061
 VERSION AF376061.1 GI:14040074
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 3581)
 AUTHORS Gingras, M.-C., Qiu, J. and Margolin, J.F.
 TITLE Differential expression of the caspase recruitment domain protein
 12 (CARD12) during monocytic differentiation
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 3581)
 AUTHORS Gingras, M.-C., Qiu, J. and Margolin, J.F.
 TITLE Direct Submission
 JOURNAL Submitted (03-MAY-2001) Pediatric/Texas Children's Cancer Center,
 Baylor College of Medicine, 6621 Fannin St. MC3-3320, Houston, TX
 77030, USA

FEATURES
 source
 1. .3581
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="2"
 /map="2p21-22"
 /cell_line="U937"
 /cell_type="peripheral blood-derived CD14 mature monocyte"
 490. .3564
 /note="CARD12"
 /codon_start=1
 /product="caspase recruitment domain protein 12"
 /protein_id="AAK33443.1"
 /db_xref="GI:14040075"

CDS
 /translat="MNFIKDNRSLIORMGTVIKOITDDLFYWNVLNREEVNIICE
 KVEQDARGLIIMHILKSGESCNLFKSLKEMVPLFODLNGSLFHOESGDLIDA
 ODKLDYHPSPLNFYPLGEDIDIFNLKSTFEPYLRKDOHHRVEOLTLGLDIA
 LOSPCIIEGSGSKSTLORIMMGSGCKALTPKRFYFELRLSRAOGLETCLD
 QLDIDGTIRKOTFMALTLRORVLFIDGYNDFPQNPONPRELALIKENHRKNMYI
 VTTTECLRIHQFGALTAEGDMTEDSAGALIREVLIKELAGLLDLOIKSCLRLNL
 MKTPLEFVITCAIOMGSEFHSHTQTLFHTFDLLOKKNHKGVAASDFRSLDH
 CGDLAEGVFSHKFEDELQVSVNEDELITGLTLCKYQKRPKPKFHKSFQET
 AGRRLSLTSHPEEYTKNGYLQKVVSTIDITSTYSLLRYTCCSVATPAVAKH
 LAAYVHGCLLGISIAKRLPMBROESLOSVENTEOTIKALININSPEVCIHLYOEST
 SKALSOEFAPFOGSKLYINSNITDYLFDFEHPNCSALDFTKDPYGGAMASW
 EKAEDDTGIMEEAPETYIPSRVSLTFEWMKOFRTLEVLTDESKLNKDRIYKIG
 IPSSATSLRLQIKRCAGVAGSLVSTCKNITSLMVEASPLTIEDRHITVTYNLTK
 LSHIDLQNRPLPGSLDLSGNLKNLTKLINDNIKMEEDAKLAEGIKNKKKCLFHL
 TSHSDIGEMDYIVKLSSEPCDLEELQVSCLSANAVKTLAQNHLNKLKSLIDS
 ENYLEKGNALHELIDRMNVLEQLTALMPGCDVGSLSLKLHLEVPOLVKLGL
 KNNRLDTEIRITIGAFPGKPNLKNFOOLNAGRVSSDGLAMGVEPNKOLVFFDF
 STKEFLDPALVLRKLSOVLKTLFLEQARLVGNQFDDDDLSVITGAFKLVTA"

misc_feature
 /note="Region: caspase recruitment domain"
 502. .741

BASE COUNT 1033 a 781 c 843 g 924 t
 ORIGIN

Alignment Scores:
 Pred. No.: 1.13e-50 Length: 3581
 Score: 461.00 Matches: 88
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-697-089-2_COPY_1_88 (1-88) x AF376061 (1-3581)
QY 1 MetanphelelllysASPasnSerArgAlaleuileglnarGmetGlymetThrValIle 20
DB 490 ATGAATTTTCATTAAGGACAAATAGCCGACCTTATTTCAAAGATGGGATGACTTTATA 549
QY 21 LysGlnIleThrAspAspLeuPheValITrpAsnValIleuAsnArgGluValAsnIle 40
DB 550 AAGCAAAATCACAGATGACCTATTGTATGAAATGTTCTGAATCCGGAAGAAAGTAAACATC 609
QY 41 IllecysGylulysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
DB 610 ATTTCCTCGAGAAAGCTGAGAGAGATCTGCTAGAGGATCATTCACATGATTTTGAAA 669
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluITrpAsnITyPProleu 80
DB 670 AAGGTTTCAGAGTCTCTGTAACCTTTCTTAATCCCTTAAGAGATGAGACTATCTCTTA 729
QY 81 PheGlnAspLeuAsnGlyGlnSer 88
DB 730 TTTCAGACTTGAATGACAAAGT 753
RESULT 14
AX318172 261 bp DNA linear PAT 14-DEC-2001
LOCUS AX318172
DEFINITION Sequence 177 from Patent WO0190156.
ACCESSION AX318172
VERSION AX318172.1 GI:17900863
KEYWORDS
SOURCE human.
ORGANISM human.
REFERENCE
AUTHORS Reed,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H., Oliveira,V.A., Haysnsl,H. and Pawlowski,K.
TITLE Card domain containing polypeptides, encoding nucleic acids, and methods of use
JOURNAL Patent: WO 0190156-A 177 29-NOV-2001;
The Burnham Institute (US)
FEATURES
SOURCE location/Qualifiers
1..261
/organism="Homo sapiens"
/db_xref="taxon:9606"
1..>261
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD19349.1"
/db_xref="GI:17900864"
/translation="MNFIKDNSRALIQKMGWYIKQITTDLEFWNVINRREVNIIICE
KVEDADARGIITHMLTKGSESCNLFLEKEMWPLFDIINGQ"
BASE COUNT 86 a 44 c 59 g 72 t
ORIGIN
Alignment Scores:
Pred. No.: 1.9e-51 Length: 261
Score: 457.00 Matches: 87
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.13% Indels: 0
Gaps: 0
US-09-697-089-2_COPY_1_88 (1-88) x AX318172 (1-261)
QY 1 MetanphelelllysASPasnSerArgAlaleuileglnarGmetGlymetThrValIle 20
DB 1 ATGAATTTTCATTAAGGACAAATAGCCGACCTTATTTCAAAGATGGGATGACTTTATA 60
QY 21 LysGlnIleThrAspAspLeuPheValITrpAsnValIleuAsnArgGluValAsnIle 40
DB 21 LysGlnIleThrAspAspLeuPheValITrpAsnValIleuAsnArgGluValAsnIle 40

DB 61 AAGCAATACAGATGACCTATTGTATGAAATGTTCTGAATCCGGAAGAAAGTAAACATC 120
QY 41 IllecysGylulysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
DB 121 ATTTCCTCGAGAAAGCTGAGAGAGATCTGCTAAGAGGATCATTCACATGATTTTGAAA 180
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluITrpAsnITyPProleu 80
DB 181 AAGGTTTCAGAGTCTCTGTAACCTTTCTTAATCCCTTAAGAGATGAGACTATCTCTTA 240
QY 81 PheGlnAspLeuAsnGlyGln 87
DB 241 TTTCAGACTTGAATGACAA 261
RESULT 15
CNS01DS3/c 138909 bp DNA linear PRI 18-APR-2002
LOCUS CNS01DS3
DEFINITION BAC sequence from the SPG4 candidate region at 2p21-2p22 BAC 164M19 of library CITB_978_SKB from chromosome 2 of Homo sapiens (Human).
ACCESSION AL121653
VERSION AL121653.2 GI:7159616
KEYWORDS SPG4 genomic DNA interval.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Hazan,J., Fonknechten,N., Mavel,D., Paternotte,C., Samson,D., Artiguenave,F., Davoine,C.S., Cruaud,C., Durr,A., Wincker,P., Brotilier,P., Catolico,L., Barbe,V., Burgunder,J.M., Prud'Homme,J.F., Brice,A., Fontaine,B., Hellis,R. and Weissbach,J.
TITLE Spastin, a novel AAA protein, is altered in the most frequent form of autosomal dominant spastic paraplegia
JOURNAL Nat. Genet. (1999) In press
AUTHORS 2 (bases 1 to 138909)
TITLE Direct Submission
JOURNAL Submitted (18-APR-2002) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
COMMENT On Mar 6, 2000 this sequence version replaced gi:6002386.
FEATURES
SOURCE location/Qualifiers
1..138909
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/clone="164M19"
/clone_lib="CITB_978_SKB"
BASE COUNT 39243 a 28424 c 29121 g 42121 t
ORIGIN
Alignment Scores:
Pred. No.: 2.5e-48 Length: 138909
Score: 457.00 Matches: 87
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 98.86% Mismatches: 0
Query Match: 99.13% Indels: 0
Gaps: 0
US-09-697-089-2_COPY_1_88 (1-88) x CNS01DS3 (1-138909)
QY 1 MetanphelelllysASPasnSerArgAlaleuileglnarGmetGlymetThrValIle 20
DB 7638 GTGAATTTTCATTAAGGACAAATAGCCGACCTTATTTCAAAGATGGGATGACTTTATA 76329
QY 21 LysGlnIleThrAspAspLeuPheValITrpAsnValIleuAsnArgGluValAsnIle 40
DB 76328 AAGCAAAATCACAGATGACCTATTGTATGAAATGTTCTGAATCCGGAAGAAAGTAAACATC 76369
QY 41 IllecysGylulysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
DB 76268 ATTTCCTCGAGAAAGCTGAGAGATCTGCTAAGAGGATCATTCACATGATTTTGAAA 76209

QY 61 LysGlySerGlySerCysAsnLeuPheLeuLysSerLeuLysGluTyrPasnTyrProLeu 80
 |||||||
 Db 76208 AAGGTTCAAGAGTCTCTGTAACCTTTCTTAAATCCCTTAGAGAGTGGAACCTATCTCTA 76149
 |||||||
 QY 81 PheGlnAspLeuAsnGlyGlnSer 88
 |||||||
 Db 76148 TTTCAGGACTTGAAATGGACAAAGT 76125
 |||||||

Search completed: January 31, 2003, 15:14:45
 Job time : 1289.45 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 31, 2003, 10:49:01 ; Search time 104.246 Seconds
(without alignments)
1901.038 Million cell updates/sec

Title: US-09-697-089-2_COPY_1_88

Perfect score: 461

Sequence: 1 MAFKDNKSAALQRMGMVYI.....FLKSLKENVYPIFDLNGDS 88

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delpop 6.0 , Delpext 7.0	

Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

```
-MODEL=frimem-p2n.model -DEV=xlh
-Q=/cgn2.1/USPTO.spool/US09697089/r/unat_29012003_092753_19709/app_query.fasta_1_981
-DB=N-Geneseq_101002 -OPMT=fastap -SUFFIX=p2n.rng -MIMATCH=0.1 -LOOPL=0
-LOOEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsun62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09697089_@CGN_1_1_276_@runat_29012003_092753_19709 -NCPD=6 -ICPD=3
-NO_XLPHY -NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -MAIT -LONGLOG -DEV_TIMEOUT=120
-MARN_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELDP=6 -DELEXT=7
```

Database :

```
N_Geneseq_101002.*
1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	461	100.0	578	24	ABK22733	Human CDNA encodin
2	461	100.0	768	24	ABK22734	Human CDNA encodin
3	461	100.0	1395	24	ABK22732	Human CDNA encodin
4	461	100.0	3133	22	AA503945	Human caspase recr
5	461	100.0	3396	24	ABK22731	Human CDNA encodin
6	461	100.0	3545	22	AAH98254	Murine EST-derived
7	458	99.3	3213	22	AAH78219	Nucleotide sequenc
8	457	99.1	261	24	ABK22765	Human CDNA encodin
9	457	99.1	3615	22	AA503946	Human caspase recr
10	392	85.0	2215	22	AAH78218	Nucleotide sequenc
11	118.5	25.7	1215	20	AAK27725	Canine interleukin
12	118.5	25.7	1215	21	AAA13794	Canine interleukin
13	118.5	25.7	1560	20	AAK27727	Canine interleukin
14	118.5	25.7	1560	21	AAA13796	Canine interleukin
15	108	23.4	1435	17	AAH43709	Human inhibitor of
16	108	23.4	2589	18	AAH61590	Human c-IAP1. Hom
17	108	23.4	3532	18	AAH72711	Human inhibitor of
18	108	23.4	3532	20	AAK22143	Human cellular inh
19	108	23.4	3532	24	ABN96857	Gene #3355 used to
20	108	23.4	3732	19	AAH55040	Human HIRP-2 codin
21	103.5	22.5	429	22	ABH09527	Human secreted pro
22	103.5	22.5	1215	22	AA166509	Pig caspase coding
23	102.5	22.2	321	24	ABK22730	Human CDNA encodin
24	102	22.1	2580	18	AAH70838	Human apoptosis in
25	102	22.1	2580	24	ABK93871	Human CDNA encodin
26	100	21.7	2862	18	AAH61592	Murine c-IAP. Mus
27	100	21.7	3151	19	AAH55043	Murine HIRP-2 codi
28	97	21.0	1183	22	AAH55011	CDNA encoding nove
29	97	21.0	1487	22	AAH02763	Human CARD contain
30	97	21.0	3863	22	AAH34888	CDNA encoding nove
31	97	21.0	4466	22	AAH02765	Human NAC gamma or
32	97	21.0	4556	22	AAH02764	Human NAC beta iso
33	97	21.0	5059	22	AAH83652	Human CARD-8 polyP
34	96.5	20.9	549	24	ABK12898	Human protease pr
35	96.5	20.9	879	23	AAH55669	DNA encoding novel
36	96.5	20.9	1252	24	ABK14805	CDNA encoding human
37	96.5	20.9	2662	22	AAH86924	Human immune/haema
38	96.5	20.9	2662	22	AAH86925	Human immune/haema
39	96.5	20.9	2669	22	AAH86923	Human immune/haema
40	95	20.6	1215	17	AAH03179	Human interleukin-1
41	95	20.6	1215	20	AAH03179	Nucleotide sequenc
42	95	20.6	1215	22	AAH24471	Human pre-interleu
43	95	20.6	1215	24	AAH03964	Human caspase-1 co
44	95	20.6	1216	20	AAH01277	Human ICE coding s
45	95	20.6	1216	22	AAH90184	Human interleukin-

ALIGNMENTS

RESULT 1
ABK22733
ID ABK22733 standard; CDNA; 578 BP.

XX ABK22733:

DT 26-MAR-2002 (first entry)

XX Human cDNA encoding CLAN C.

XX Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
XX abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
KW autoimmune disease; inflammation; keratinocyte hyperplasia;
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
KW balloon angioplasty; restenosis; glioma; carcinoma; melanoma;
KW leukemia; allergy; arthritis; lupus; Schogen's syndrome;
KW Crohn's disease; graft-versus-host disease; stroke;
KW myocardial infarction; heart failure; neurodegenerative disease;

KW Parkinson's disease; Alzheimer's disease; HIV;
KM human immunodeficiency virus infection.
XX
OS Homo sapiens.
XX
PN WO200190156-A2.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-US17158.
XX
PR 24-MAY-2000; 2000US-0579240.
PR 10-OCT-2000; 2000US-0686347.
PR 14-MAR-2001; 2001US-275980P.
PR 23-MAY-2001; 2001US-0864921.
XX
PA (BURN-) BURNHAM INST.
XX
PI Reed JC, Pio FF, Godzik A, Stenlik C, Damiano JS, Lee SH;
PI Oliveira VM, Hayashi H, Pawlowski K;
XX
DR MPI; 2002-083086/11.
DR P-PSDB; AAU80863.
XX
PT New caspase recruitment domain (CARD)-containing polypeptides and
PT encoding nucleic acids, useful for treating abnormal cell proliferation
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
PT arthritis or stroke -
XX
PS Claim 1; Page 177; 216pp; English.
XX
CC The invention relates to an isolated caspase recruitment domain (CARD)
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
CC from it, and the polynucleotides encoding them. Also included are a
CC recombinant vector comprising the polynucleotide, recombinant cells
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
CC and insect cells) and an anti-CARD antibody. The CARD-containing
CC polypeptide and CARD-encoding nucleic acid are useful for treating a
CC pathology characterised by abnormal cell proliferation (e.g. cancer),
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In
CC particular, the polypeptide and nucleic acid are useful for treating
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
CC muscle cell proliferation in arteries following balloon angioplasty
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
CC disease) or immunodeficiency associated disease (e.g. human
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
CC in a variety of diagnostic applications. The present sequence is a
CC cDNA encoding a CARD domain containing protein.
XX
SQ Sequence 578 BP; 172 A; 106 C; 143 G; 157 T; 0 other;
XX
Alignment Scores:
Pied. No.: 1,49e-54 Length: 578
Score: 461.00 Matches: 88
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0
US-09-697-089-2_COPY_1_88 (1-88) x ABK22733 (1-578)
OY 1 MetAspPheIleLysAspAsnSerArgAlaLeuIIleGlnArgMetGlyMetPrralle 20
DB 277 ATGAATTTCATAAGGCAATACCCAGCCCTATTCAAGAAATGGGAATGACTGTATA 336
OY 21 LysGlnIleThrAspAspLeuPheValITrpAsnValIleuAsnArgGluGluValAsnIle 40
DB 337 AAGCAATATCAGACATGACCATTTGTATGGAATGCTCTGATGCCAAGAAGTAACATC 396
OY 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60

DB 397 ATTTGCTGCAGAGAGGTGGAGCATGCTGTAGAGGAGATCATTCATGATTTTGAAA 456
OY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTrpPoleu 80
DB 457 AAGGTCACAGTCCGTGTAACTCTTCTTAATCCCTTAAGAGATGGAACATATCTCTA 516
OY 81 PheGlnAspLeuAsnGlyInsler 88
DB 517 TTTCAGACTTGATGACAAACT 540
RESULT 2
ABK22734
ID ABK22734 standard; cDNA; 768 BP.
XX
XX
AC ABK22734;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human cDNA encoding CLAN D.
XX
KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
KW autoimmune disease; inflammation; Keratinocyte hyperplasia;
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;
KW Crohn's disease; graft-versus-host disease; stroke;
KW myocardial infarction; heart failure; neurodegenerative disease;
KW Parkinson's disease; Alzheimer's disease; HIV;
KW human immunodeficiency virus infection.
XX
XX
OS Homo sapiens.
XX
PN WO200190156-A2.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-US17158.
XX
PR 24-MAY-2000; 2000US-0579240.
PR 10-OCT-2000; 2000US-0686347.
PR 14-MAR-2001; 2001US-275980P.
PR 23-MAY-2001; 2001US-0864921.
XX
PA (BURN-) BURNHAM INST.
XX
PI Reed JC, Pio FF, Godzik A, Stenlik C, Damiano JS, Lee SH;
PI Oliveira VM, Hayashi H, Pawlowski K;
XX
DR MPI; 2002-083086/11.
DR P-PSDB; AAU80864.
XX
PT New caspase recruitment domain (CARD)-containing polypeptides and
PT encoding nucleic acids, useful for treating abnormal cell proliferation
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
PT arthritis or stroke -
XX
PS Claim 1; Page 178-179; 216pp; English.
XX
CC The invention relates to an isolated caspase recruitment domain (CARD)
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
CC from it, and the polynucleotides encoding them. Also included are a
CC recombinant vector comprising the polynucleotide, recombinant cells
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
CC and insect cells) and an anti-CARD antibody. The CARD-containing
CC polypeptide and CARD-encoding nucleic acid are useful for treating a
CC pathology characterised by abnormal cell proliferation (e.g. cancer),
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In
CC particular, the polypeptide and nucleic acid are useful for treating
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
CC muscle cell proliferation in arteries following balloon angioplasty
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,

CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
CC disease) or immunodeficiency associated disease (e.g. human
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
CC in a variety of diagnostic applications. The present sequence is a
CC cDNA encoding a CARD domain containing protein.

XX Sequence 768 BP: 218 A; 157 C; 180 G; 213 T; 0 other;

Alignment Scores:

Pred. No.: 2.19e-54 Length: 768
Score: 461.00 Matches: 88
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0

US-09-697-089-2_COPY_1_88 (1-88) x ABR22734 (1-768)

Qy 1 MetasnphellieysAspAsnSerArgAlaLeuileglnArGmetGlyMetThrValIle 20
Db 277 ATGAATTCATTAAGGACAAATAGCCGACCCCTTATTCATAAGATGGATGACTGTGTATA 336
Qy 21 LysglnlierhrAspAspleuPheValTrpAsnValIleuAsnArGluGluValAsnIle 40
Db 337 AAGCAAAATCACAGATGACCTTATTTGTATGAAATGTTCCGAAAGAAAGTAAACATC 396
Qy 41 IleCysCgsluIysValaGluGlnAspAlaIlaArgGlyIleIleHisMetIleLeuIys 60
Db 397 ATTGCTCGAGAGTCCGAGACAGATGCTGCTAGAGGATCATTCACATGATTTTGAAA 456
Qy 61 LysgIserGluSerCysAsnleuPheleuIysSerleuIysGluTrpAsnTyProleu 80
Db 457 AAGGTTTCAGAGTCTGTACCTCTTCTTAATCCCTTAAGAGTGAATATCTCTTA 516
Qy 81 PheGlnAspleuAsnGlyGlnSer 88
Db 517 TTTCAGAGCTTGATGACAAAGT 540

RESULT 3

ABK22732
ID ABR22732 standard; CDNA: 1395 BP.

XX
AC ABR22732;

XX
DT 26-MAR-2002 (first entry)

XX
DE Human cDNA encoding CLAN B.

XX Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
KW autoimmune disease; inflammation; keratinocyte hyperplasia;
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
KW ballooning angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;
KW Crohn's disease; graft-versus-host disease; stroke;
KW myocardial infarction; heart failure; neurodegenerative disease;
KW Parkinson's disease; Alzheimer's disease; HIV;
KW human immunodeficiency virus infection.

XX Homo sapiens.

XX
PN MO200190156-A2.

XX
PD 29-NOV-2001.

XX
PF 24-MAY-2001; 2001WO-US17158.

XX
PR 24-MAY-2000; 2000US-0579240.

XX
PR 10-OCT-2000; 2000US-0686347.

XX
PR 14-MAR-2001; 2001US-275980P.

XX
PR 23-MAY-2001; 2001US-0864921.

XX
PA (BURN-) BURHAM INST.

XX
PI Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;

XX
PI Oliveira VAM, Hayashi H, Pawlowski K;

XX
DR WPI; 2002-083086/11.

XX
P-PSDB; AAU80862.

PT New caspase recruitment domain (CARD)-containing polypeptides and
PT encoding nucleic acids, useful for treating abnormal cell proliferation
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
arthritis or stroke

XX
PS Claim 1; Page 174-176; 216pp; English.

XX The invention relates to an isolated caspase recruitment domain (CARD)
XX -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
XX from it, and the polynucleotides encoding them. Also included are a
XX recombinant vector comprising the polynucleotide, recombinant cells
XX containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
XX and insect cells) and an anti-CARD antibody. The CARD-containing
XX polypeptide and CARD-encoding nucleic acid are useful for treating a
XX pathology characterised by abnormal cell proliferation (e.g. cancer),
XX abnormal cell death (apoptosis), autoimmune diseases or inflammation. In
XX particular, the polypeptide and nucleic acid are useful for treating
XX keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
XX muscle cell proliferation in arteries following balloon angioplasty
XX (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,
XX allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
XX graft-versus-host disease, stroke, myocardial infarction, heart failure,
XX neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
XX disease) or immunodeficiency associated disease (e.g. human
XX immunodeficiency virus (HIV) infection). The nucleic acids are useful
XX in a variety of diagnostic applications. The present sequence is a
XX cDNA encoding a CARD domain containing protein.

XX
SQ Sequence 1395 BP; 436 A; 248 C; 327 G; 384 T; 0 other;

Alignment Scores:

Pred. No.: 4.92e-54 Length: 1395
Score: 461.00 Matches: 88
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0

US-09-697-089-2_COPY_1_88 (1-88) x ABR22732 (1-1395)

Qy 1 MetasnphellieysAspAsnSerArgAlaLeuileglnArGmetGlyMetThrValIle 20

Db 277 ATGAATTCATTAAGGACAAATAGCCGACCCCTTATTCATAAGATGGATGACTGTGTATA 336

Qy 21 LysglnlierhrAspAspleuPheValTrpAsnValIleuAsnArGluGluValAsnIle 40

Db 337 AAGCAAAATCACAGATGACCTTATTTGTATGAAATGTTCCGAAAGAAAGTAAACATC 396

Qy 41 IleCysCgsluIysValaGluGlnAspAlaIlaArgGlyIleIleHisMetIleLeuIys 60

Db 397 ATTGCTCGAGAGTCCGAGACAGATGCTGCTAGAGGATCATTCACATGATTTTGAAA 456

Qy 61 LysgIserGluSerCysAsnleuPheleuIysSerleuIysGluTrpAsnTyProleu 80

Db 457 AAGGTTTCAGAGTCTGTACCTCTTCTTAATCCCTTAAGAGTGAATATCTCTTA 516

Qy 81 PheGlnAspleuAsnGlyGlnSer 88

Db 517 TTTCAGAGCTTGATGACAAAGT 540

RESULT 4

AA303945
ID AAS03945 standard; CDNA: 3133 BP.

XX

AC AAS03945;
 XX 12-SEP-2001 (first entry)
 XX
 DE Human caspase recruitment domain 12 (CARD-12) cDNA.
 XX
 KW Caspase recruitment domain; CARD-12; apoptosis; stress-related pathway;
 KW cancer; viral infection; poxvirus; adenovirus; autoimmune disorder;
 KW systemic lupus erythematosus; arthritis; neurological disorder; stroke;
 KW Alzheimer's disease; amyotrophic lateral sclerosis; haematologic disease;
 KW aplastic anaemia; myocardial infarction; inflammatory disorder;
 KW Crohn's disease; insulin-dependent diabetes; contact dermatitis;
 KW psoriasis; graft rejection; bacterial infection; lepromatous leprosy;
 KW tuberculosis; ischaemic brain injury; hypoxic brain injury; ss;
 KW kidney ischaemia; reperfusion injury; acute bacterial meningitis;
 KW excitotoxic brain damage; liver disease.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 36..3110
 FT /*tag= a
 FT /product= "Human CARD-12"
 XX
 PN W0200130971-A2.
 XX
 PD 03-MAY-2001.
 XX
 PF 26-OCT-2000; 2000MO-US29643.
 XX
 PR 27-OCT-1999; 99US-0161822.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Berlin J, Robison KE;
 XX WPI; 2001-308628/32.
 DR P-PSDB; AA002880.
 XX
 XX
 PT Isolated caspase recruitment domain-12 polypeptide and nucleic acids
 PT encoding them, useful for treating and diagnosing disorders associated
 PT with abnormal apoptosis such as cancer, arthritis and Alzheimer's
 PT disease -
 XX
 PS Claim 2; Fig 1; 93pp; English.
 XX
 CC The sequence represents a cDNA which encodes the human caspase
 CC recruitment domain 12 (CARD-12) polypeptide. CARD domains are found in a
 CC number of proteins that transmit signals that activate apoptosis and
 CC inflammatory pathways in response to stress and other stimuli. Therefore,
 CC CARD-12 and its corresponding nucleic acid may be used in treatment and
 CC diagnosis of patients suffering from disorders associated with an
 CC abnormal level (an increase or a decrease) of apoptotic cell death or
 CC abnormal activity of stress-related pathways. The disorders include
 CC cancer, viral infections (e.g. caused by poxviruses, adenoviruses),
 CC autoimmune disorders (e.g. systemic lupus erythematosus, arthritis),
 CC neurological disorders (e.g. Alzheimer's disease, amyotrophic lateral
 CC sclerosis), haematologic diseases (e.g. aplastic anaemia, myocardial
 CC infarction, stroke), inflammatory and immune system disorders (e.g.
 CC Crohn's disease, insulin-dependent diabetes, contact dermatitis,
 CC psoriasis, graft rejection), bacterial infections (e.g. tuberculosis,
 CC lepromatous leprosy), ischaemic and hypoxic brain injury, kidney
 CC ischaemia/reperfusion injury, excitotoxic brain damage, acute bacterial
 CC meningitis and liver disease.
 XX
 SQ Sequence 3133 BP; 903 A; 691 C; 729 G; 810 T; 0 other;
 Alignment Scores:
 Pred. No.: 1 48e-53 Length: 3133
 Score: 461.00 Matches: 88
 Percent Similarity: 100.008 Conservative: 0
 Best Local Similarity: 100.008 Mismatches: 0
 Query Match: 100.008 Indels: 0

DB: 22 Gaps: 0
 US-09-697-089-2_COPY_1_88 (1-88) x AAS03945 (1-3133)
 QY 1 MetaspheilleysaspansSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
 DB 36 ATGATTTTCATTAAGGCAATATGCGCCCTTATTCAAAGATGGAAAGACGCTATA 95
 QY 21 LysGlnIleThrAspAPLeuPheValTrpAsnValLeuAsnArgGluValAsnIle 40
 DB 96 AAGCAATTCACAGATGACCTATTGTATGGAATGTTGTGAATGCCGAAGATTAACATC 155
 QY 41 IleCysGluIuysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuys 60
 DB 156 ATTTGCGCGCAGAGAGGTGGAGCAGATGCTGTAAGAGGATTCATTCACATGATTTTGAA 215
 QY 61 LysGlySerGluSerCysAsnLeuPheLeuIleYserLeuysGluTrpAsnTrpProLeu 80
 DB 216 AAGGTTTCAGAGTCTCTTAACCTCTTCTTAATCCCTTAAGAGTGAACATCTCTTA 275
 QY 81 PheGlnAspLeuAsnGlyGlnSer 88
 DB 276 TTTCAGCAGCTTGATGACAAAGT 299
 RESULT 5
 ABRK22731
 ID ABRK22731 standard; cDNA; 3396 BP.
 XX
 AC ABRK22731;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human cDNA encoding CLAN A.
 XX
 KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
 KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
 KW autoimmune disease; inflammation; keratinocyte hyperplasia;
 KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
 KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
 KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;
 KW Crohn's disease; graft-versus-host disease; stroke;
 KW myocardial infarction; heart failure; neurodegenerative disease;
 KW Parkinson's disease; Alzheimer's disease; HIV;
 KW human immunodeficiency virus infection.
 XX
 OS Homo sapiens.
 XX
 PN W0200190156-A2.
 XX
 PD 29-NOV-2001.
 XX
 PF 24-MAY-2001; 2001MO-US17158.
 XX
 PR 24-MAY-2000; 2000US-0579240.
 PR 10-OCT-2000; 2000US-0686347.
 PR 14-MAR-2001; 2001US-275980P.
 PR 23-MAY-2001; 2001US-0864921.
 XX
 PA (BURN-) BURNHAM INST.
 XX
 PI Reed JC, Plo FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
 PI Oliveira VAM, Hayashi H, Pawlowski K;
 XX WPI; 2002-083086/11.
 DR P-PSDB; AA080861.
 XX
 PT New caspase recruitment domain (CARD)-containing polypeptides and
 PT encoding nucleic acids, useful for treating abnormal cell proliferation
 PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
 PT arthritis or stroke -
 XX
 PS Claim 1; Page 166-171; 216pp; English.
 XX

CC The invention relates to an isolated caspase recruitment domain (CARD)
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
CC from it, and the polynucleotides encoding them. Also included are a
CC recombinant vector comprising the polynucleotide, recombinant cells
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
CC and insect cells) and an anti-CARD antibody. The CARD-containing
CC polypeptide and CARD-encoding nucleic acid are useful for treating a
CC pathology characterised by abnormal cell proliferation (e.g. cancer). In
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In
CC particular, the polypeptide and nucleic acid are useful for treating
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
CC muscle cell proliferation in arteries following balloon angioplasty
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
CC disease) or immunodeficiency associated disease (e.g. human
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
CC in a variety of diagnostic applications. The present sequence is a
CC cDNA encoding a CARD domain containing protein.

XX SQ Sequence 3396 BP: 992 A; 737 C; 793 G; 874 T; 0 other;

Alignment Scores:

Pred. No.:	1.65e-53	Length:	3396
Score:	461.00	Matches:	88
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-09-697-089-2_COPY_1_88 (1-88) x ABK22731 (1-3396)

OY 1 Metasnphelilelyspasnserrargalaleuileglnarqmetglymethrvalille 20
DB 277 ATGATTTTCATTAAGACAAATAGCCGAGCCCTTATTCAAGAAATGCAATGACTGTATA 336
OY 21 Lysglnilierhraspaspleuphevalitrrpasnvalleuasnargluciluvalasnille 40
DB 337 AAGCAAAATCAGATGACCTATTGTATGAAATGTTCTGAATCGGAGAAAGTAACAATC 396
OY 41 Ilecyscysglulysvalgluclnaspaalaalaarglyllellehismetlleuuls 60
DB 397 ATTTCCTCGAGAAAGATGAGAGATGCTGCTAGAGGATCATTCACATGATTTTGAA 456
OY 61 Lysglyserglusercysasnleupheuleuylsserleuylsglutrpsantrproleu 80
DB 457 AAGGTTTCAGAGTCTCTTAACCTTTCTTAATCCCTTAAGAGATGGAATATCTCTTA 516
OY 81 Pheglnaspleuasnglylinserr 88
DB 517 TTTCAGACTTGATGACAAAGT 540

RESULT 6

AAH98254
ID AAH98254 standard; cDNA: 3545 BP.

XX AAH98254;

XX 12-OCT-2001 (first entry)

XX Murine EST-derived coding sequence SEQ ID NO: 111.

XX Human: sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;

XX Tomato; monkey; dog; sea urchin; expressed sequence tag; EST;

XX diagnostics; forensic test; gene mapping; genetic disorder;

XX biodiversity; gene therapy; nutrition; ss.

XX Mus musculus.

XX WO200154477-A2.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US02687.
XX 25-JAN-2000; 2000US-0491404.
XX 17-JUL-2000; 2000US-0617746.
XX 03-AUG-2000; 2000US-0631451.
XX 15-SEP-2000; 2000US-0663870.
XX (HXSE-) HXSEQ INC.
XX Tang YF, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
XX Cao Y, Drmanac RA, Zhang J, Werhman T;
XX WPT: 2001-476164/51.
XX P-PSDB; AAM23595.
XX Isolated polypeptide for treatment of diseases, diagnostics, raising
XX antibodies and research use -
XX Claim 1: Page 250-251; 1275pp; English.

XX The present invention provides the protein and coding sequences of novel
XX proteins from a variety of organisms, including human, dog, cat, horse,
XX cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
XX urchin and tomato. These were derived from expressed sequence tags (ESTs)
XX from the organism of interest. They can be used in diagnostics,
XX forensics, gene mapping, identification of mutations, to assess
XX biodiversity and for nutritional purposes. The present sequence is a cDNA
XX of the invention.

SQ Sequence 3545 BP: 1038 A; 755 C; 816 G; 936 T; 0 other;

Alignment Scores:

Pred. No.:	1.75e-53	Length:	3545
Score:	461.00	Matches:	88
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09-697-089-2_COPY_1_88 (1-88) x AAH98254 (1-3545)

OY 1 Metasnphelilelyspasnserrargalaleuileglnarqmetglymethrvalille 20
DB 232 ATGATTTTCATTAAGACAAATAGCCGAGCCCTTATTCAAGAAATGCAATGACTGTATA 291
OY 21 Lysglnilierhraspaspleuphevalitrrpasnvalleuasnargluciluvalasnille 40
DB 292 AAGCAAAATCAGATGACCTATTGTATGAAATGTTCTGAATCGGAGAAAGTAACAATC 351
OY 41 Ilecyscysglulysvalgluclnaspaalaalaarglyllellehismetlleuuls 60
DB 352 ATTTCCTCGAGAAAGATGAGAGATGCTGCTAGAGGATCATTCACATGATTTTGAA 411
OY 61 Lysglyserglusercysasnleupheuleuylsserleuylsglutrpsantrproleu 80
DB 412 AAGGTTTCAGAGTCTCTTAACCTTTCTTAATCCCTTAAGAGATGGAATATCTCTTA 471
OY 81 Pheglnaspleuasnglylinserr 88
DB 472 TTTCAGACTTGATGACAAAGT 495

RESULT 7

AAH78219
ID AAH78219 standard; DNA: 3213 BP.

XX AAH78219;

XX 26-NOV-2001 (first entry)

XX Nucleotide sequence of a human secreted polypeptide.

XX Human; secreted polypeptide; nervous disease; muscular disease; tumour;

KW gastrointestinal ulceration; spinal cord disease; trachea disease;
KW thyroid gland disease; ovary disease; prostate disease; heart disease;
KW renal gland disease; small intestine disease; thymus disease;
KW lymph node disease; muscular system disease; colon disease;
KW lipase deficiency; cystic fibrosis; pancreatitis; clot formation;
KW myocardial infarction; angioplasty; liver disease; coagulation disorder;
KW microbial disease; immune disorder; inflammation; transplant rejection;
KW bone thickness; bone density; ferroxidase loss; apoptosis;
KW vascular smooth cell proliferation; vaccine; ss.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..3213
FT /*tag= a
FT /product= "secreted polypeptide"
XX
PN WO20016690-A2.
XX
PD 13-SEP-2001.
XX
PF 05-MAR-2001; 2001WO-US07143.
XX
XX 06-MAR-2000; 2000US-0187107.
PR 13-MAR-2000; 2000US-0188916.
PR 03-OCT-2000; 2000US-0236874.
PR 03-OCT-2000; 2000US-0237846.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;
XX
DR WPI: 2001-570768/64.
XX
DR P-PSDB: AAG67527.
XX
XX Novel isolated secreted polypeptide useful for treating nervous and
PT muscular diseases, gastrointestinal ulceration, coagulation and immune
PT disorders, microbial diseases, inflammation and transplant rejection -
XX
XX
PS Claim 2; Page 53-54; 102pp; English.
XX
XX The present sequence encodes a human secreted polypeptide. The
CC secreted polypeptides and polynucleotides are useful for treating
CC nervous and muscular diseases, for inhibiting tumour formation and
CC metastasis, for treating gastrointestinal ulceration, for preventing
CC and treating diseases in spinal cord, thyroid gland, ovary, prostate,
CC renal gland, small intestine, heart, trachea, thymus, lymph node,
CC muscular system and colon, for treating lipase deficiency in cystic
CC fibrosis and pancreatitis, for treating undesirable clot formation
CC such as myocardial infarction, during angioplasty and all surgical
CC procedures that require decreased blood clot formation, for treating
CC liver diseases, coagulation disorders and microbial diseases, for
CC treating immune disorders, for treating inflammation and transplant
CC rejection, for enhancing bone thickness and increasing bone density,
CC for reducing the loss of essential ferroxidases, for suppressing
CC apoptosis, and for regulating vascular smooth cell proliferation. They
CC may also be used as vaccines.
XX
SQ Sequence 3213 BP; 916 A; 704 C; 756 G; 837 T; 0 other;

Alignment Scores:

Pred. No.:	3.99e-53	Length:	3213
Score:	458.00	Matches:	87
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	98.86%	Mismatches:	0
Query Match:	99.35%	Indels:	0
DB:	22	Gaps:	0

US-09-697-089-2_COPY_1_88 (1-88) x AAH78219 (1-3213)

OY 1 MetasnhetlelysaapsasSerArgAlaleuileglnaargMetgylmethThValile 20
:::|||||

Db 139 TTGAATTCATTAAGACATATAGCCGACCCCTTATTCAAAGATGGAGATCTGTATA 198
OY 21 LysglnleltherrPaasPleuPheValjrrPaanValleuAnaArggluValaSlle 40
|||||
Db 199 AAGCAATACACATGACCTTATTTGTATGATTCGAAATCCGAAAGATTAACATC 258
OY 41 llecyscysgluylusValgluGlnaSpAlaAlaArggyllelleHlHlSmelleLeuyls 60
Db 259 ATTGCTGCGAGAGAGTGACGACGATGCTGCTAGAGGAGATCATTCATGATTTTGAA 318
OY 61 LysglYsergluSerCysAsnLeuPheleuylsSerleuylsGluTpaanTyProleu 80
Db 319 AAGGGTTCAGAGTCCTGTAACTCTTCTTAATCCCTTAAGAGAGTGGAATCTCTTA 378
OY 81 PheGlnaSpLeuAnaSlglnSer 88
Db 379 TTTCAGGACTTGAAATGACAAAGT 402
RESULT 8
ID ABRK22765 standard; cDNA; 261 BP.
XX
AC ABRK22765;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human cDNA encoding CLAN CARD.
XX
KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
KW autoimmune disease; inflammation; keratinocyte hyperplasia;
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
KW leukemia; allergy; arthritis; lupus; Schögen's syndrome;
KW Crohn's disease; graft-versus-host disease; stroke;
KW myocardial infarction; heart failure; neurodegenerative disease;
KW Parkinson's disease; Alzheimer's disease; HIV;
KW human immunodeficiency virus infection.
XX
OS Homo sapiens.
XX
XX WO200190156-A2.
XX
PN 29-NOV-2001.
XX
PD 24-MAY-2001; 2001WO-US17158.
XX
PF 24-MAY-2001; 2000US-0579240.
PR 10-OCT-2000; 2000US-0686347.
PR 14-MAR-2001; 2001US-275980P.
PR 23-MAY-2001; 2001US-0864921.
XX
PA (BURN-) BURNHAM INSR.
XX
XX Reed JC, Plo FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
PI Oliveira VAM, Hayashi H, Pawlowski K;
PI
XX WPI: 2002-083086/11.
DR P-PSDB: AAU80871.
XX
XX New caspase recruitment domain (CARD)-containing polypeptides and
PT encoding nucleic acids, useful for treating abnormal cell proliferation
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
PT arthritis or stroke
XX
PS Claim 1; Page 199; 216pp; English.
XX
XX The invention relates to an isolated caspase recruitment domain (CARD)
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
CC from it, and the polynucleotides encoding them. Also included are a
CC recombinant vector comprising the polynucleotide, recombinant cells
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
CC and insect cells) and an anti-CARD antibody. The CARD-containing

CC polypeptide and CARD-encoding nucleic acid are useful for treating a
CC pathology characterised by abnormal cell proliferation (e.g. cancer),
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In
CC particular, the polypeptide and nucleic acid are useful for treating
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
CC muscle cell proliferation in arteries following balloon angioplasty
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
CC disease) or immunodeficiency associated disease (e.g. human
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
CC in a variety of diagnostic applications. The present sequence is a
CC cDNA encoding a CARD domain containing protein.
XX
SQ Sequence 261 BP; 86 A; 44 C; 59 G; 72 T; 0 other;

Alignment Scores:
Pred. No.: 1.82e-54 Length: 261
Score: 457.00 Matches: 87
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.13% Indels: 0
DB: Gaps: 0

US-09-697-089-2_COPY_1_88 (1-88) x ABR22765 (1-261)

QY 1 MetanphelelieyAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
DB 1 AAGAAATTCATTAAGCAATAGCCGAGCCCTTATTCAAAGATGGAGATGCTGTATA 60
QY 21 LysGlnIleThrAspAspLeuPheValITrpaSnValIleAsnArgGluValAsnIle 40
DB 61 AAGCAATACAGAGATGACCTATTGTATGAAATGTTCTGAATCGCGAAGAACTAAACATC 120
QY 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
DB 121 ATTTCTCGAGAGAGATGAGATGCTGCTAGAGGATCATTCACATGATTTTGAAA 180
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerIleLysGluITrpaSnArgProLeu 80
DB 181 AAGGTTTCAGAGTCTGTACCTCTTTCTTAATCCCTTAAGAGCTGGAACATATCTCTTA 240
QY 81 PheGlnAspLeuAsnGlyGln 87
DB 241 TTTCAGGACTTGATGACAA 261

RESULT 9
AAS03946
ID AAS03946 standard; DNA; 3615 BP.
AC
XX AAS03946;
XX
DT 12-SEP-2001 (first entry)
XX
DE Human caspase recruitment domain 12 (CARD-12) genomic DNA.
XX
KW Caspase recruitment domain; CARD-12; apoptosis; stress-related pathway;
KW cancer; viral infection; poxvirus; adenovirus; autoimmune disorder;
KW systemic lupus erythematosus; arthritis; neurological disorder; stroke;
KW Alzheimer's disease; amyotrophic lateral sclerosis; haematologic disease;
KW aplastic anaemia; myocardial infarction; inflammatory disorder;
KW Crohn's disease; insulin-dependent diabetes; contact dermatitis;
KW psoriasis; graft rejection; bacterial infection; lepromatous leprosy;
KW tuberculosis; ischaemic brain injury; hypoxic brain injury; ds;
KW kidney ischaemia; reperfusion injury; acute bacterial meningitis;
KW excitotoxic brain damage; liver disease.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 1..3615
FT CDS /*tag= a

FT /product= "Human CARD-12"
XX
XX WO200130971-A2.
XX
XX 03-MAY-2001.
XX
XX 26-OCT-2000; 2000WO-US29643.
XX
XX 27-OCT-1999; 99US-0161822.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Bertin J, Robison KE;
XX
XX WPI: 2001-308628/32.
XX
XX P-PSDB; AAU02881.
XX
XX
XX Isolated caspase recruitment domain-12 polypeptide and nucleic acids
XX encoding them, useful for treating and diagnosing disorders associated
XX with abnormal apoptosis such as cancer, arthritis and Alzheimer's
XX disease -
XX
XX Disclosure: Fig 2; 93pp; English.
XX
XX The sequence represents a genomic DNA which encodes the human caspase
XX recruitment domain 12 (CARD-12) polypeptide. CARD domains are found in a
XX number of proteins that transmit signals that activate apoptosis and
XX inflammatory pathways in response to stress and other stimuli. Therefore,
XX CARD-12 and its corresponding nucleic acid may be used in treatment and
XX diagnosis of patients suffering from disorders associated with an
XX abnormal level (an increase or a decrease) of apoptotic cell death or
XX abnormal activity of stress-related pathways. The disorders include
XX cancer, viral infections (e.g. caused by poxviruses, adenoviruses),
XX autoimmune disorders (e.g. systemic lupus erythematosus, arthritis),
XX neurological disorders (e.g. Alzheimer's disease, amyotrophic lateral
XX sclerosis), haematologic diseases (e.g. aplastic anaemia, myocardial
XX infarction, stroke), inflammatory and immune system disorders (e.g.
XX Crohn's disease, insulin-dependent diabetes, contact dermatitis,
XX psoriasis, graft rejection), bacterial infections (e.g. tuberculosis,
XX lepromatous leprosy), ischaemic and hypoxic brain injury, kidney
XX ischaemia/reperfusion injury, excitotoxic brain damage, acute bacterial
XX meningitis and liver disease.
XX
SQ Sequence 3615 BP; 1041 A; 811 C; 845 G; 918 T; 0 other;

Alignment Scores:
Pred. No.: 6.45e-53 Length: 3615
Score: 457.00 Matches: 87
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 98.86% Mismatches: 0
Query Match: 99.13% Indels: 0
DB: Gaps: 0

US-09-697-089-2_COPY_1_88 (1-88) x AAS03946 (1-3615)

QY 1 MetanphelelieyAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
DB 418 GTGAATTCATTAAGCAATAGCCGAGCCCTTATTCAAAGATGGAGATGCTGTATA 477
QY 21 LysGlnIleThrAspAspLeuPheValITrpaSnValIleAsnArgGluValAsnIle 40
DB 478 AAGCAATACAGAGATGACCTATTGTATGAAATGTTCTGAATCGCGAAGAACTAAACATC 537
QY 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
DB 538 ATTTCTCGAGAGATGAGATGCTGCTAGAGGATCATTCACATGATTTTGAAA 597
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerIleLysGluITrpaSnArgProLeu 80
DB 598 AAGGTTTCAGAGTCTGTACCTCTTTCTTAATCCCTTAAGAGCTGGAACATATCTCTTA 657
QY 81 PheGlnAspLeuAsnGlyGlnSer 88
|||||

Db 658 TTTCAGGACTTGAAATGACAAAGT 681

RESULT 10

AAH78218

ID AAH78218 standard; DNA: 2215 BP.

XX

XX AAH78218;

AC

XX

XX 26-NOV-2001 (first entry)

DE Nucleotide sequence of a human secreted polypeptide.

XX

XX Human; secreted polypeptide; nervous disease; muscular disease; tumour;

KW gastrointestinal ulceration; spinal cord disease; trachea disease;

KW thyroid gland disease; ovary disease; prostate disease; heart disease;

KW renal gland disease; small intestine disease; thymus disease;

KW lymph node disease; muscular system disease; colon disease;

KW lipase deficiency; cystic fibrosis; pancreatitis; clot formation;

KW myocardial infarction; angioplasty; liver disease; coagulation disorder;

KW microbial disease; immune disorder; inflammation; transplant rejection;

KW bone thickness; bone density; ferroxidase loss; apoptosis;

KW vascular smooth cell proliferation; vaccine; ss.

XX

OS Homo sapiens.

XX

XX Key Location/Qualifiers

FT 1..2214

FT CDS /*tag= a

FT /product= "secreted polypeptide"

FT /note= "no termination codon given"

XX

XX WO200166690-A2.

XX

PD 13-SEP-2001.

XX

XX 05-MAR-2001; 2001MO-US07143.

XX

XX 06-MAR-2000; 2000US-0187107.

XX

PR 13-MAR-2000; 2000US-0188916.

PR 03-OCT-2000; 2000US-0236874.

PR 03-OCT-2000; 2000US-0237846.

XX

XX (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX

XX Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;

PI

XX WPI: 2001-570768/64.

DR P-PSDB; AAG67526.

XX

XX Novel isolated secreted polypeptide useful for treating nervous and

PT muscular diseases, gastrointestinal ulceration, coagulation and immune

PT disorders, microbial diseases, inflammation and transplant rejection -

XX

XX Claim 2; Page 52-53; 102pp; English.

XX

XX The present sequence encodes a human secreted polypeptide. The

CC secreted polypeptides and polynucleotides are useful for treating

CC nervous and muscular diseases, for inhibiting tumour formation and

CC metastasis, for treating gastrointestinal ulceration, for preventing

CC and treating diseases in spinal cord, thyroid gland, ovary, prostate,

CC renal gland, small intestine, heart, trachea, thymus, lymph node,

CC muscular system and colon, for treating lipase deficiency in cystic

CC fibrosis and pancreatitis, for treating undesirable clot formation

CC such as myocardial infarction, during angioplasty and all surgical

CC procedures that require decreased blood clot formation, for treating

CC liver diseases, coagulation disorders and microbial diseases, for

CC treating immune disorders, for treating inflammation and transplant

CC rejection, for enhancing bone thickness and increasing bone density,

CC for reducing the loss of essential ferroxidases, for suppressing

CC apoptosis, and for regulating vascular smooth cell proliferation. They

CC may also be used as vaccines.

XX

SQ Sequence 2215 BP, 621 A; 522 C; 519 G; 553 T; 0 other;

Alignment Scores:

Pred. No.: 3.54e-44 Length: 2215

Score: 392.00 Matches: 74

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 85.03% Indels: 0

DB: 22 Gaps: 0

US-09-697-089-2_COPY_1_88 (1-88) x AAH78218 (1-2215)

QY 15 MetGlyMetThrValIleLysGlnIleThrAspAspLeuPheValIrrAsnValLeuAsn 34

Db 1 ATGCGAATGACTGTATTAAGCAAAATCACAGAGACCTATTATGAGATGTTCTGAAT 60

QY 35 ArgGlnGluValAsnIleIleCysGlnLysValGlnGlnAspAlaAArgGlyIle 54

Db 61 CGCGAAGAACTAAACATCATTTGCTGCGAGAGGTGAGCAGAGATGCTGTAAGGGATC 120

QY 55 IleHisMetIleLeuLysLysGlySerGlySerCysAsnLeuPheLeuLysSerLeuLys 74

Db 121 ATTCACTGATTTTGAAGAAAGGGTTGAGAGTCTGTAACCTCTTTTAATCCCTTAAG 180

QY 75 GluTrpAsnTrpProLeuPheGlnAspLeuAsnGlyGlnSer 88

Db 181 GAGTGAACATATCCTCTATTTCAGGACTTGAAATGACAAAGT 222

RESULT 11

AAAX27725

ID AAAX27725 standard; DNA: 1215 BP.

XX

XX AAAX27725;

XX

XX 02-JUN-1999 (first entry)

XX

DE Canine interleukin-1 beta convertase coding sequence.

XX

XX Canine; interleukin 18; d118; interleukin 1 beta convertase; ICF; dog;

KW leukocyte; MHC; tumour cell; lymphocyte; Fas ligand; allergy; cancer;

KW immune disorder; infectious disease; skin inflammation; ss.

XX

XX Canis sp.

OS

XX WO9907851-A1.

XX

XX 18-FEB-1999.

PD

XX 07-AUG-1998; 98WO-JP03524.

XX

XX 07-AUG-1997; 97JP-0213754.

PR

XX (TORA) TORAY IND INC.

PA

XX Okano F;

PI

XX WPI: 1999-167427/14.

DR P-PSDB; AAY01315.

XX

XX Canine interleukin 18 and canine interleukin 1-beta convertase -

PT For treatment of immune disorders of dogs including cancer,

PT allergies and inflammatory diseases.

XX

XX Claim 8; Page 26-29; 44pp; Japanese.

XX

XX The invention relates to a canine interleukin 18 (d118) and a canine

CC interleukin 1 beta convertase (d1CE) which can cleave precursor forms of

CC d118 and interleukin 1 beta to give the active forms. Host cells

CC transformed by vectors comprising the d118 DNA (optionally with DNA

CC coding for d1CE) are used for the recombinant expression of the protein.

CC The canine interleukin 18 is able to act on canine leukocytes to induce

CC a factor potentiating the expression of class II MHC on canine tumour

CC cells; to promote the proliferation of canine lymphocytes; to potentiate

CC the expression of Fas ligand on canine lymphocytes and tumour cells; to
CC damage and kill canine tumour cells; to reduce tumour size in the living
CC dog; and to activate canine leukocytes to inhibit allergies. d118 in
CC combination with d112 can be used for the treatment of immune disorders
CC of dogs, such as cancer, allergies, infectious diseases or skin
CC inflammation. The present sequence represents the coding sequence of
CC d118.

XX
SQ Sequence 1215 BP; 347 A; 290 C; 284 G; 294 T; 0 other;

Alignment Scores:

Pred. No.:	1.53e-06	Length:	1215
Score:	118.50	Matches:	26
Percent Similarity:	52.44%	Conservative:	17
Best Local Similarity:	31.71%	Mismatches:	38
Query Match:	25.70%	Indels:	1
Ds:	20	Gaps:	1

US-09-697-089-2_copy_1_88 (1-88) x AAX27725 (1-1215)

OY 4 IlelysaPasnserrArgAlaleuileglnArgetgMetgylmethThValileyscIntle 23
Db 16 CTGAAGGACAGACAGAGCGCTGTTGTCGCGTCAGTAGACATGGGACCATCAATGCTTGG 75
OY 24 ThrAspAspLeuPheValITrpAsnValleuAsnArGluGluVal---AsnIleleCys 42
Db 76 CTGAGTGAACCTCTTGAGAAAAAGAGTCTGAACACAGAGAGATGAGCGAGTGGCGTGT 135
OY 43 CysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLysLysGly 62
Db 136 GCACACTCTACAGTTATGATGATCAGGCCGAGCTTGATGATGATCGCTCTCGGAAAGG 195
OY 63 SerGluSerCysAsnLeuPheLeuLysSerLeuLysGluITPAsnTyrProleupheGln 82
Db 196 CCAATGCGATGCCAGATTTTATTCTAATATTGCAATGAGACATTACCTGGCACAG 255
OY 83 Aspleu 84
Db 256 ACGCTG 261
RESULT 12
AAX13794
ID AAX13794 standard; cDNA; 1215 BP.
XX
AC AAX13794;
XX
DT 27-JUN-2000 (first entry)
XX
DE Canine interleukin 1beta conversion enzyme encoding cDNA SEQ ID NO:2.
XX
KW Canine; dog; interleukin 18; IL-18; interleukin 1beta conversion enzyme;
KW ICE; immune disease; tumour; ss.
XX
OS Canis sp.
XX
XX Key location/Qualifiers
FT CDS 1..1215
FT /tag= a
FT /product= "interleukin 1beta conversion enzyme"
XX
XX JP2000078975-A.
XX
XX 21-MAR-2000.
XX
XX PD 04-AUG-1998; 98JP-0220074.
XX
XX PF 07-AUG-1997; 97JP-0213754.
XX PR 11-DEC-1997; 97JP-0341741.
XX PR 06-JUL-1998; 98JP-0190594.
XX
XX (TORA) TORAY IND INC.
XX
XX PA
XX
XX DR WPI; 2000-342448/30.

DR P-PSDB; AAY82559.

XX Canine interleukin 18 - useful for treating canine immune diseases

PS Claim 8; Page 11-12; 16pp; Japanese.

CC The present invention describes canine interleukin 18 (IL-18). Canine
CC IL-18 is capable of inducing an antiviral activity factor and a factor
CC reinforcing the expression of class II MHC molecules on canine tumour
CC cells by reacting with canine leukocytes, promoting the growth of
CC canine lymphocytes, reinforcing the expression of Fas ligand on canine
CC lymphocytes and canine tumour cells, obstructing and killing canine
CC tumour cells, reducing the tumour formed in a canine body and preventing
CC canine allergy by activating canine leukocytes. Canine IL-18 is used for
CC the treatment of canine immune diseases. The present invention also
CC describes the canine interleukin 1beta conversion enzyme (ICE), which
CC has the ability of cleaving the precursor proteins of interleukin 1beta
CC and IL-18 to convert them to their active types. The present sequence
CC encodes canine ICE.

XX
SQ Sequence 1215 BP; 347 A; 290 C; 284 G; 294 T; 0 other;

Alignment Scores:			
Pred. No.:	1.53e-06	Length:	1215
Score:	118.50	Matches:	26
Percent Similarity:	52.44%	Conservative:	17
Best Local Similarity:	31.71%	Mismatches:	38
Query Match:	25.70%	Indels:	1
Ds:	21	Gaps:	1

US-09-697-089-2_copy_1_88 (1-88) x AAX13794 (1-1215)

OY 4 IlelysaPasnserrArgAlaleuileglnArgetgMetgylmethThValileyscIntle 23
Db 16 CTGAAGGACAGACAGAGCGCTGTTGTCGCGTCAGTAGACATGGGACCATCAATGCTTGG 75
OY 24 ThrAspAspLeuPheValITrpAsnValleuAsnArGluGluVal---AsnIleleCys 42
Db 76 CTGAGTGAACCTCTTGAGAAAAAGAGTCTGAACACAGAGAGATGAGCGAGTGGCGTGT 135
OY 43 CysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLysLysGly 62
Db 136 GCACACTCTACAGTTATGATGATCAGGCCGAGCTTGATGATGATCGCTCTCGGAAAGG 195
OY 63 SerGluSerCysAsnLeuPheLeuLysSerLeuLysGluITPAsnTyrProleupheGln 82
Db 196 CCAATGCGATGCCAGATTTTATTCTAATATTGCAATGAGACATTACCTGGCACAG 255
OY 83 Aspleu 84
Db 256 ACGCTG 261
RESULT 13
AAX27727
ID AAX27727 standard; DNA; 1560 BP.
XX
AC AAX27727;
XX
DT 02-JUN-1999 (first entry)
XX
XX Canine interleukin-1 beta convertase encoding DNA.
XX
XX DE Canine; interleukin 18; d118; interleukin 1 beta convertase; ICE; dog;
XX KW leukocyte; MHC; tumour cell; lymphocyte; Fas ligand; allergy; cancer;
XX KW immune disorder; infectious disease; skin inflammation; ss.
XX
XX OS Canis sp.
XX
XX PN W09907851-A1.
XX
XX PD 18-FEB-1999.
XX
XX PF 07-AUG-1998; 98WO-JP03524.

```
XX 07-AUG-1997; 97JP-0213754.
PR (TORA ) TORAY IND INC.
XX
XX
XX Okano F;
XX
XX WPI; 1999-167427/14.
DR P-PSDB; AAY01315.
XX
XX Canine Interleukin 18 and canine interleukin 1-beta convertase -
PT Treatment of immune disorders of dogs including cancer,
PT allergies and inflammatory diseases.
XX
XX Claim 10; Page 32-35; 44pp; Japanese.
XX
XX The invention relates to a canine interleukin 18 (dli18) and a canine
XX interleukin 1 beta convertase (dice) which can cleave precursor forms of
XX dli18 and interleukin 1 beta to give the active forms. Host cells
XX transformed by vectors comprising the dli18 DNA (optionally with DNA
XX coding for dice) are used for the recombinant expression of the protein.
XX The canine interleukin 18 is able to act on canine leukocytes to induce
XX a factor potentiating the expression of class II MHC on canine tumour
XX cells; to promote the proliferation of canine lymphocytes; to potentiate
XX the expression of Fas ligand on canine lymphocytes and tumour cells; to
XX damage and kill canine tumour cells; to reduce tumour size in the living
XX dog; and to activate canine leukocytes to inhibit allergies. dli18 in
XX combination with dli12 can be used for the treatment of immune disorders
XX of dogs, such as cancer, allergies, infectious diseases or skin
XX inflammation. The present sequence represents the DNA encoding dice.
XX
SQ Sequence 1560 BP; 468 A; 365 C; 355 G; 372 T; 0 other;

Alignment Scores:
Pred. No.: 2.15e-06 Length: 1560
Score: 118.50 Matches: 26
Percent Similarity: 52.44% Conservative: 17
Best Local Similarity: 31.71% Mismatches: 38
Query Match: 25.70% Indels: 1
DB: Gaps: 1

US-09-697-089-2_COPY_1_88 (1-88) x AAX27727 (1-1560)
QY 4 IlelyspasnserrargAlaleuileglnArgetlymetThrvalilelysglnile 23
DB 217 CTGAAGGCAAGAGAGGCTGTGTCGGTCAGTACAGATGGGACCATCAATGCTTTG 276
QY 24 ThrspaspleuphevalitPrasnValleusnArvglugluVal--AsnillelCys 42
DB 277 CTGATGTAACCTTTGAGAAAAGAGTGTGTAACCAAGAGGAGATGAGCGAGTGGGTGT 336
QY 43 CysgluysValgluglnAspAlaAlaArglylleileHsmetilleLeuylslysgly 62
DB 337 GCACACTCTACAGTTATGATCAGGCCGAGTCTGATGTGATCGCTCTCGAAGAGG 396
QY 63 SergluserCysasnleupheleuylsSerleuylsglutPrasnTyrrProleupheHn 82
DB 397 CCAATGATGCCAGATTTTATTTCTAATATTGCAATGAGACATTCACTCGCACAG 456
QY 83 Aspleu 84
DB 457 ACGCTG 462

RESULT 14
AAA13796
ID AAA13796 standard; cDNA; 1560 BP.
XX
XX AAA13796;
XX
XX 27-JUL-2000 (first entry)
XX
XX Canine Interleukin 1beta conversion enzyme encoding cDNA SEQ ID NO:4.
XX
```

```
KW Canine; dog; interleukin 18; IL-18; interleukin 1beta conversion enzyme;
KW ICE; Immune disease; tumour; ss.
XX
XX Canis sp.
OS
XX
XX Key Location/Qualifiers
FT CDS 202-1416
FT /tag= a
FT /product= "interleukin 1beta conversion enzyme"
XX
XX JP2000078975-A.
XX
XX 21-MAR-2000.
XX
XX 04-AUG-1998; 98JP-0220074.
XX
XX 07-AUG-1997; 97JP-0213754.
PR 11-DEC-1997; 97JP-0341741.
PR 06-JUL-1998; 98JP-0190594.
XX
XX (TORA ) TORAY IND INC.
XX
XX WPI; 2000-342448/30.
DR P-PSDB; AAY82561.
XX
XX Canine interleukin 18 - useful for treating canine immune diseases
XX
XX Claim 10; Page 13-14; 16pp; Japanese.
XX
XX The present invention describes canine interleukin 18 (IL-18). Canine
XX IL-18 is capable of inducing an antiviral activity factor and a factor
XX reinforcing the expression of class II MHC molecules on canine tumour
XX cells by reacting with canine leukocytes, promoting the growth of
XX canine lymphocytes, reinforcing the expression of Fas ligand on canine
XX lymphocytes and canine tumour cells, obstructing and killing canine
XX tumour cells, reducing the tumour formed in a canine body and preventing
XX canine allergy by activating canine leukocytes. Canine IL-18 is used for
XX the treatment of canine immune diseases. The present invention also
XX describes the canine interleukin 1beta conversion enzyme (ICE), which
XX has the ability of cleaving the precursor proteins of interleukin 1beta
XX and IL-18 to convert them to their active types. The present sequence
XX encodes canine ICE.
XX
SQ Sequence 1560 BP; 468 A; 365 C; 355 G; 372 T; 0 other;

Alignment Scores:
Pred. No.: 2.15e-06 Length: 1560
Score: 118.50 Matches: 26
Percent Similarity: 52.44% Conservative: 17
Best Local Similarity: 31.71% Mismatches: 38
Query Match: 25.70% Indels: 1
DB: Gaps: 1

US-09-697-089-2_COPY_1_88 (1-88) x AAA13796 (1-1560)
QY 4 IlelyspasnserrargAlaleuileglnArgetlymetThrvalilelysglnile 23
DB 217 CTGAAGGCAAGAGAGGCTGTGTCGGTCAGTACAGATGGGACCATCAATGCTTTG 276
QY 24 ThrspaspleuphevalitPrasnValleusnArvglugluVal--AsnillelCys 42
DB 277 CTGATGTAACCTTTGAGAAAAGAGTGTGTAACCAAGAGGAGATGAGCGAGTGGGTGT 336
QY 43 CysgluysValgluglnAspAlaAlaArglylleileHsmetilleLeuylslysgly 62
DB 337 GCACACTCTACAGTTATGATCAGGCCGAGTCTGATGTGATCGCTCTCGAAGAGG 396
QY 63 SergluserCysasnleupheleuylsSerleuylsglutPrasnTyrrProleupheHn 82
DB 397 CCAATGATGCCAGATTTTATTTCTAATATTGCAATGAGACATTCACTCGCACAG 456
QY 83 Aspleu 84
DB 457 ACGCTG 462
```

ID	Accession	Standard	CDNA	Length (BP)
DB	457	ACGCTG	462	
RESULT 15				
AAAT43709				
ID	AAAT43709	standard	CDNA: 1435 BP.	
XX				
AC	AAAT43709;			
DT	07-FEB-1997	(first entry)		
XX				
DE	Human inhibitor of apoptosis gene 1 cDNA.			
XX				
KW	Inhibitor of apoptosis 1; hIAP-1; degenerative disease;			
KW	rheumatoid arthritis; septic shock; antiviral; trauma; stroke;			
KW	cell death; oncogenesis; cancer; diagnosis; gene therapy; ss.			
XX				
OS	Homo sapiens.			
XX				
FH	Key	Location/Qualifiers		
FT	CDS	10..1326		
FT		/*tag= a		
FT	primer_bind	complement (10..29)		
FT		/*tag= b		
FT		/note= "5' primer binding site"		
FT	primer_bind	1309..1386		
FT		/*tag= c		
FT		/note= "3' primer binding site"		
XX				
PN	W09635703-A1.			
XX				
PD	14-NOV-1996.			
XX				
PF	11-MAY-1995;	95WO-US05922.		
XX				
PR	11-MAY-1995;	95WO-US05922.		
XX				
PA	(HUMA-) HUMAN GENOME SCI INC.			
XX				
PI	He WW, Hudson PL, Rosen CA;			
XX				
DR	WP1: 1996-518608/51.			
XX				
P-PSDB:	AAW04583.			
XX				
PT	Polynucleotide encoding human inhibitor of apoptosis gene 1 - useful			
XX				
PR	for treating degenerative diseases, as antiviral defence mechanism			
XX				
PT	and preventing cell death during trauma and strokes			
XX				
PS	Claim 7; Page 40; 53pp: English.			
XX				
CC	A cDNA clone (AAAT43709) codes for human inhibitor of apoptosis 1			
CC	(hIAP-1) (AAW04583), a protein useful for treating degenerative			
CC	diseases, as an antiviral defence mechanism and for preventing			
CC	cell death during strokes of trauma. The cDNA can be isolated from			
CC	human Jurkat cell lines or human osteoclastoma stromal cell lines			
CC	and incorporated into bacterial, mammalian or baculovirus expression			
CC	vectors for use in prodn. of recombinant hIAP-1. It can also be			
CC	utilised in the diagnosis or gene therapy of diseases related to			
CC	hIAP-1 under-expression.			
XX				
SO	Sequence 1435 BP; 464 A; 232 C; 317 G; 422 T; 0 other;			
Alignment Scores:				
Pred. NO.:	5.53e-05	Length:	1435	
Score:	108.00	Matches:	29	
Percent Similarity:	58.33%	Conservative:	20	
Best Local Similarity:	34.52%	Mismatch:	33	
Query Match:	23.43%	Indels:	2	
DB:	17	Gaps:	1	
US-09-697-089-2_COPY_1_88 (1-88) x AAAT43709 (1-1435)				

Db	841	TTGCATTAAATGCGAAGAACAGAAATGGCTCTCTTCACAA-----TTGACATGTGTG	894
Oy	21	LyscslIlethraspIeuPheValTTPasValIeuAsnArgGlucIValAsnIle	40
Db	895	CTTCCTCATCTCGGATATCTTTTAAAGGCCAAAGTATTTAAACAGAACATGATATT	954
Oy	41	IleCyscysgluIysValIugIlnaspAlaIaArgGlyIleIleHisIleIeuIys	60
Db	955	ATTAAACAAAANACACGATACCTTTTACAAGCAGAACTGATGTATACCATTTTGGTT	1014
Oy	61	LyscIysSerIuSerCysAsnIeuPheIeuIysSerIeuIuSerIuPasnTyrProIeu	80
Db	1015	AAAGGAATGTGTGGCCCAACATCTTCAAAAACCTGTAAAGAAATGACTCTACATTG	1074
Oy	81	PheGlnAspIeu	84
Db	1075	TATAGAACTTA	1086

Search completed: January 31, 2003, 13:24:16
Job time : 106.246 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 31, 2003, 11:50:07 : Search time 719.086 Seconds

(without alignments)
1981.965 Million cell updates/sec

Title: US-09-697-089-2_COPY_1_88

Perfect score: 461

Sequence: 1 MNRFKDSRALIQMGWTVI.....FLKSLKEMVPLFQDLNGQS 88

Scoring table: BLOSUM62
Xgapop 10.0 , Ygapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+g2n.model -DEV=xlh
-O=/cgn2_1/USPTO.spool/US09697089/runat_29012003_092754_19729/app-query.fasta_1.981
-DB=ST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX-DLsum62 -TRANS-human40.cdi -LIST=45
-DOCALLIGN=200 -THR.SCOR=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09697089_ECGN_1_1885_etunal_29012003_092754_19729 -NCPU=6 -ICPU=3
-NO_XLPPY -NO_MMAR -LARGEOUDRY -NEG_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estln:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_oth:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	461	100.0	748	13 B1908869	B1908869 603066455
2	441	95.7	741	13 B1824482	B1824482 603038854
3	322	69.8	404	17 A0889169	A0889169 HS_2161_B
4	182	39.5	728	9 AL652549	AL652549
5	114.5	24.8	571	12 BF080490	BF080490 231404_MA
6	108	23.4	681	10 B1199526	B1199526
7	108	23.4	757	12 BE744578	BE744578 601577380
8	108	23.4	800	12 BG190354	BG190354 RST9419_A
9	108	23.4	808	12 BG209460	BG209460 RST28980
10	108	23.4	808	12 BG13953	BG13953 RST13094
11	108	23.4	812	12 BG188190	BG188190 RST7203_A
12	108	23.4	963	12 BG287772	BG287772 603384122
13	108	23.4	976	12 BG028431	BG028431 602294338
14	107	23.2	512	14 BQ235318	BQ235318 hds6e06_9
15	106	23.0	665	10 AV682308	AV682308 RST25183
16	106	23.0	791	12 BG212560	BG212560 RST32152
17	104	22.6	741	12 BG205749	BG205749 RST25183
18	104	22.6	835	12 BG139532	BG139532 RST13093
19	103.5	22.5	542	12 BF080489	BF080489 231403_MA
20	101	21.9	613	12 BF213554	BF213554 601845353
21	100	21.7	250	10 AW988325	AW988325 ug05f04_Y
22	100	21.7	467	10 AW988289	AW988289
23	97.5	21.1	663	10 AW958463	AW958463 EST370533
24	97	21.0	588	10 AW372984	AW372984 QVA-BT038
25	97	21.0	809	13 B1830457	B1830457 603073325
26	96	20.8	231	12 BG200554	BG200554 RST19870
27	95.5	20.7	256	9 A1767140	A1767140 w193f12_X
28	95.5	20.7	551	12 BF080849	BF080849 233611_MA
29	95.5	20.7	561	12 BG573534	BG573534 602595339
30	95	20.6	812	12 BG390044	BG390044 602415771
31	93.5	20.3	300	9 A0098419	A0098419
32	93.5	20.3	488	10 AV713637	AV713637 AV113637
33	93.5	20.3	848	9 AL551865	AL551865
34	93.5	20.3	903	13 BM457265	BM457265 AGENCOURT
35	93.5	20.3	1098	12 BG024814	BG024814 602275555
36	93	20.2	583	10 AV654714	AV654714
37	92.5	20.1	635	14 BQ021083	BQ021083 UI-H-DH1-
38	91.5	19.8	490	9 AA070591	AA070591 zms5302_X
39	91.5	19.8	493	10 AV757470	AV757470 AV757470
40	91.5	19.8	795	12 BG547974	BG547974 602576081
41	91.5	19.8	851	13 B1838827	B1838827 603082641
42	91.5	19.8	1062	14 BM920134	BM920134 AGENCOURT
43	89.5	19.4	267	14 BM832207	BM832207 K-EST0106
44	89	19.3	533	10 AW372983	AW372983 QVA-BT038
45	87	18.9	586	13 BM425040	BM425040 Ipsp0104

ALIGNMENTS

RESULT 1
B1908869
LOCUS
DEFINITION B1908869 748 bp mRNA linear EST 16-OCT-2001
603066455P1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:521569 5',
B1908869
ACCESSION
VERSION B1908869
KEYWORDS
SOURCE human
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c9abs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.jnl.gov>
Plate: LAM11541 row: m column: 14
High quality sequence start: 7
High quality sequence stop: 744.
Location/Qualifiers

FEATURES
source

1. 748
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5215659"
/clone_id="NIH_MGC_118"
/tissue_type="leukocyte"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6; Site.1: NotI; Site.2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."
BASE COUNT 236 a 148 c 166 g 198 t
ORIGIN

Alignment Scores:

Pred. No.: 4,06e-54 Length: 748
Score: 461.00 Matches: 88
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-697-089-2_COPY_1_88 (1-88) x B1908869 (1-748)

OY 1 Metasnpheillelysaspsnserrargalaleuileglnarvmetglymethrvalle 20
DB 252 ATGAAATTCATTAAGACAAATAGCCGAGCCCTTATTCAAAGATGGCAATGACTGTATA 311
OY 21 Lysglnlethrasspaspheuphevaltrpaspvalleuasnarvglnuvalasnlle 40
DB 312 AAGCAATCACAGATGACCTATTGTATGATGGAATGTCGATCGGAAGAAATAACATC 371
OY 41 llecycsglulysvalgluGlnaspalaalaarglylleleHismetileleuys 60
DB 372 ATTTGCTGCGAAGAGGTGACAGATGCTCTAGAGGATCATTCATATTTTGA 431
OY 61 LysclysersgluserCysasnleupheleuysserleuysglutrpasntryProleu 80
DB 432 AAGGTTTCAGAGCTCCTGTAACTCTTCTTAATCCCTTAAGAGATGGAACATATCCTTA 491
OY 81 PheGlnaspLeuasnglyGlnSer 88
DB 492 TTTTCAGGACTTGAATGACCAAGT 515

RESULT 2

LOCUS B1824482 741 bp mRNA linear EST 04-OCT-2001
DEFINITION 603038854F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5179909 5',
mRNA sequence.

ACCESSION B1824482
VERSION B1824482.1 GI:15936032
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>,
TITLE 1 (bases 1 to 741)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c9abs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.jnl.gov>
Plate: LAM11448 row: k column: 14
High quality sequence start: 3
High quality sequence stop: 705.
Location/Qualifiers

FEATURES
source

1. 741
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5179909"
/clone_id="NIH_MGC_115"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site.1: NotI; Site.2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
BASE COUNT 233 a 147 c 164 g 197 t
ORIGIN

Alignment Scores:

Pred. No.: 2.58e-51 Length: 741
Score: 441.00 Matches: 88
Percent Similarity: 97.78% Conservative: 0
Best Local Similarity: 97.78% Mismatches: 0
Query Match: 95.66% Indels: 2
DB: 13 Gaps: 0

US-09-697-089-2_COPY_1_88 (1-88) x B1824482 (1-741)

OY 1 Metasnpheillelysaspsnserrarg--Alaleuileglnarvmetglymethrvali 20
DB 228 ATGAAATTCATTAAGACAAATAGCCGAGCCCTTATTCAAAGATGGCAATGACTGTTA 287
OY 20 lelysglnlethrasspaspheuphevaltrpaspvalleuasnarvglnuvalasni 40
DB 288 TAAAGCAATCACAGATGACCTATTGTATGGAATGTCGAAATCGGAAGAAATAACA 347
OY 40 llecycsglulysvalgluGlnaspalaalaarglylleleHismetileleu 60
DB 348 TCATTTGCTGCGAAGAGGTGACAGATGCTCTAGAGGATCATTCACATGATTTGA 407
OY 60 yslsglysergluserCysasnleupheleuysserleuysglutrpasntryPro 80
DB 408 AAAAGGTTTCAGAGCTCCTGTAACTCTTCTTAATCCCTTAAGAGATGGAACATATCCTC 467
OY 80 eupheGlnaspLeuasnglyGlnSer 88
DB 468 TATTTTCAGGACTTGAATGACCAAGT 493

RESULT 3

LOCUS A0889169/c 404 bp DNA linear GSS 10-NOV-1999
DEFINITION HS_2161_B1.A01.T7C CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2161 Col=1 Row=B, DNA sequence.

ACCESSION A0889169
VERSION A0889169.1 GI:6345359
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequencing-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallaceu.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2161 row: B column: 1
Seq primer: F7
Class: BAC ends
High quality sequence stop: 404.
FEATURES
source
1..404
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate-2161 Col-1 Row-B"
/clone_id="C1F Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelOBAC11; BAC clones in E-Coli DH10B"
BASE COUNT 119 a 93 c 70 g 122 t
ORIGIN
Alignment Scores:
Pred. No.: 4,89e-35 Length: 404
Score: 322.00 Matches: 69
Percent Similarity: 88.64% Conservative: 9
Best Local Similarity: 78.41% Mismatches: 10
Query Match: 69.85% Indels: 1
DB: 17 Gaps: 0
US-09-697-089-2_COPY_1_88 (1-88) x A0889169 (1-404)
QY 1 MetasnphelleyAspAsnSerArgAlaLeuileglnArgMetGlyMethrValile 20
Db 351 GTGAATTTCAATAGACGACGATAGCCGAGC-CTTATTCAMAAGATGGGAATGCTGTATA 293
QY 21 LysglnlethrAspAspLeupheValTrpAsnValleuAsnArgGluValAsnile 40
Db 292 GAGCTACTCACAGATGACCTTTTGTATGAATGTATTAATTCAGAAAGATTAACATC 233
QY 41 IleCysCysGluYsValGluGlnAspAlaAlaArgGlyleileHisMetIleleuYs 60
Db 232 ATTTTCTGCGAAGGTGAGACAGATGCTGTAGAGGAGCATTCATCATGATTTTGA 173
QY 61 LysGlySerGluSerCysAsnLeupheleuYsSerleuYsGluTrpAsnTyProleu 80
Db 172 GAGGGTTTCAGAGTCTCTTAACCTTAAGTAAATCCCTTAAGAGTGAACATATCTCTA 113
QY 81 PheGlnAspLeuAsnGlyGlnSer 88
Db 112 TTTCAGGACTTGAAGGACAAAGT 89
RESULT 4
AL652549 728 bp mRNA linear EST 13-DEC-2001
LOCUS AL652549

DEFINITION AL652549 XGC-gastrula Silurana tropicalis cDNA clone Tgas028114 5', mRNA sequence.
ACCESSION AL652549
VERSION AL652549.1 GI:17663115
KEYWORDS EST.
SOURCE western clawed frog.
ORGANISM Silurana tropicalis
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesodactylia; Pipridae; Pipidae; Xenopodinae; Silurana.
AUTHORS Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
TITLE Sanger Xenopus tropicalis EST project 2001 (10_2001)
JOURNAL Unpublished (2001)
COMMENT Contact: Huckle E
Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: Tgas028114.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
FEATURES
source
1..728
/organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="Tgas028114"
/clone_id="XGC-gastrula"
/dev_stage="gastrula (stages 10.5-13 mixed)"
/lab_host="Escherichia coli XL1-blue"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dt primed from 5ug of poly A+ RNA from stages 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."
BASE COUNT 232 a 130 c 168 g 197 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 6,21e-15 Length: 728
Score: 182.00 Matches: 39
Percent Similarity: 65.52% Conservative: 18
Best Local Similarity: 44.83% Mismatches: 30
Query Match: 39.48% Indels: 0
DB: 9 Gaps: 0
US-09-697-089-2_COPY_1_88 (1-88) x AL652549 (1-728)
QY 1 MetasnphelleyAspAsnSerArgAlaLeuileglnArgMetGlyMethrValile 20
Db 122 ATGGAATTAATTAAGAAACTATGACAGCGTTCAGAGATGGAAGACGATTTCT 181
QY 21 LysglnlethrAspAspLeupheValTrpAsnValleuAsnArgGluValAsnile 40
Db 182 GTACAGATTAATAAGACTGTTCCACAGAAATATCTTTCTATGGTGACATGAGCAA 241
QY 41 IleCysCysGluYsValGluGlnAspAlaAlaArgGlyleileHisMetIleleuYs 60
Db 242 ATTCGTCTCTTAAGGTGACCAAGATCTAACACAGAAAGCATTAATGTTATTA 301
QY 61 LysGlySerGluSerCysAsnLeupheleuYsSerleuYsGluTrpAsnTyProleu 80
Db 302 AAAGGACAGAGTCTCTGACCTCGGTACTTCAGTCTCGAATAATCAAGATCTTTTTC 361
QY 81 PheGlnAspLeuAsnGlyGln 87
Db 362 TATGAAGACTTGATTTGACAG 382
RESULT 5
BF080490 571 bp mRNA linear EST 18-OCT-2000
LOCUS BF080490
DEFINITION 231404 MARC 2Pig Sus scrofa cDNA 5', mRNA sequence.

ACCESSION BF080490
 VERSION BF080490.1 GI:10874320
 KEYWORDS EST.
 SOURCE pig.
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 REFERENCE 1 (bases 1 to 571)
 AUTHORS Fahnenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.M., and Keele, J.W.
 TITLE Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine
 JOURNAL Unpublished (2000)
 COMMENT Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt-trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options.
 PCR primers
 FORWARD: AGGAAACACGTATGACCAT
 BACKWARD: GTTTCCTCAGTCACGACG
 Plate: 52 row: B column: 21
 Seq primer: ATTTCAGTCACACTATAG.
 FEATURES
 source
 1..571
 /organism="Sus scrofa"
 /db_xref="taxon:9823"
 /clone_lib="MARC 2Pig"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."
 BASE COUNT 168 a 142 c 138 g 123 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.26e-05 Length: 571
 Score: 114.50 Matches: 22
 Percent Similarity: 56.34% Conservative: 18
 Best Local Similarity: 30.99% Mismatches: 30
 Query Match: 24.84% Indels: 1
 DB: 12 Gaps: 1
 US-09-697-089-2_COPY_1_88 (1-88) x BF080490 (1-571)
 QY 4 11elysaspasnserrgala1aleu11elglnarfmctg1ymcthrval11lelsgln1le 23
 Db 27 CTGAAGGAGAGAGAGAGAGCGCTTTGCTCGTACACTGCGCATGGGAGACATCAATGCGCTC 86
 QY 24 Thraspasp1eupheval1trpaspval1eulsnar1rg1ug1uval1asn1le1le1cys1cys 43
 Db 87 TTGTATGAACATATTACACACACAGAGCTCTGTAACACGAGAGAGAGTGTAGATGATAGATGT 146
 QY 44 Glulysvalglu---gl1nasp1alal1arg1gl1le1le1h1smet1le1leul1s1ys1sly 62
 Db 147 GAACACGCTACAGTATGATAGAGCCCGGAGCTTTGATGTGATGATGATGATGATGATGATGAT 206
 QY 63 Ser1user1cys1asn1leuphe1leul1ys1ser1leu 73
 Db 207 CCCGAGCATGCAAAATTTGCATCAATCATATAT 239
 RESULT 6 681 bp mRNA linear EST 31-AUG-2001
 LOCUS BB199526
 DEFINITION BB199526 RIKEN full-length enriched, 0 day neonate thymus Mus
 ACCESSION BB199526
 musculus cDNA clone A430015K19 3', mRNA sequence.

VERSION BB199526.2 GI:15409668
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 681)
 AUTHORS Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Haru, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Kono, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M., and Hayashizaki, Y.
 TITLE RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
 JOURNAL Unpublished (2001)
 COMMENT On Jun 30, 2000 this sequence version replaced gi:8664479.
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suenho-cho, Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gs.c.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
 wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A., and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
 Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y., and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Yamanaka, T., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T., Ishii, Y., and Hayashizaki, Y.
 Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Func. Genomics 2 pre, 172-186 (2001)
 Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 FEATURES
 source
 Location/Qualifiers
 1..681
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone_lib="A430015K19"
 /clone_lib="RIKEN full-length enriched, 0 day neonate thymus"
 /tissue_type="thymus"
 /dev_stage="0 day neonate"
 /lab_host="DH10B"
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was


```

source
1. .808
/organism="Homo sapiens"
/db_xref="taxon:3606"
/clone_id="Athersys RAGE Library"
/cell_line="HT1080"
/notes="See 'Creation of Genome-wide Protein Expression'
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

BASE COUNT      265 a      111 c      158 g      272 t
ORIGIN

Alignment Scores:
Pred. No.:      0.000185      Length:      808
Score:          108.00      Matches:      29
Percent Similarity: 58.33%      Conservative: 20
Best Local Similarity: 34.52%      Mismatches:  33
Query Match:      23.43%      Indels:      2
DB:               12      Gaps:         1

US-09-697-089-2_COPY_1_88 (1-88) x BG193953 (1-808)
OY      1 MetlaaPhellelyasPasnSerargAlaleuIllegInargMerglyMethrValIle 20
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      2 TTGCTATTATATCGGAAGAACAGAAATGGCTCTCTTCAACAA-----TTGACATGCTGG 55
OY      21 LysGlnIleIleThrasPaspIleuPheValITrPAsnValIleuAsnArgGluValAsnIle 40
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      56 CTTCCTATTCCTGGATTAATCTTTTAAAGGCCAATGTAATTAAACAGACATCATATT 115
OY      41 IlleCysCysGluIuValGluGlnAspAlaIleArgGlyIleIleHisMetIleLeuLys 60
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      116 ATTTAAACAAAAAACACAGATACCTTTACACGCGAGAACATATTGATACCTTTTGCTT 175
OY      61 LysGlySerGluSerCysAsnIleuPheLeuLysSerIleLysGluITrPasnIyrProIleu 80
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      176 AAAGGAATAGCTGGCGCCACATCTTCAAAAACTGCTTAAAGAAATGACTCTACATTG 235
OY      81 PheGlnAspLeu 84
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      236 TATAGAACTTA 247

RESULT 11
LOCUS      BG188190      812 bp      mRNA      linear      EST 21-APR-2001
DEFINITION RST7203 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION  BG188190
VERSION     BG188190.1  GI:13709877
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 812)
AUTHORS    Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
            Lerner,L., Costanzo,D., McElligott,K., Boozar,S., Mays,R., Smith
            ,E., Veloso,N., Kikla,A., Hess,J., Cothren,K., Lo,K., Offenbacher
            ,J., Danzig,J. and Ducar,M.
            Creation of genome-wide protein expression libraries using random
            activation of gene expression
            Nat. Biotechnol. 19 (5), 440-445 (2001)
            21227151
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scaine@atersys.com
            High quality sequence stop: 511.
            Location/Qualifiers
FEATURES

```

FEATURES	source
BASE COUNT	269 a 113 c 156 g 273 t 1 others
ORIGIN	
Alignment Scores:	
Pred. No.:	0.000187
Score:	108.00
Percent Similarity:	58.33%
Best Local Similarity:	34.52%
Query Match:	23.43%
DB:	12
US-09-697-089-2_COPY_1_88 (1-88) x BG188190 (1-812)	
QY	1 MetanpheIIelyAspAsnSerArgAlaLeuIIegInArgMetClymethValIle 20
DB	2 TGTGATTAATTAATCGGAGAGACAAATGGCTCTCTTCAACA-----TTGACATGTGTG 55
QY	21 LysGlnIIethAspAspleuPheValITrPAsnValIleuAsnArgGluGluValAsnIle 40
DB	56 CTTCCTATTCCTGGATTAATCTTTAAAGCCAAATGTAAATTAATAACAGAACATCATATT 115
QY	41 IleCysCysGlnIuValGluGlnAspAlaIleuArgGlyIleIleHisMetIleuLys 60
DB	116 ATTAACAACAAAAACACAGATACCTTTACAGCAGAGAACTGATGATACCATTTTGGTT 175
QY	61 LysGlySerGluSerCysAsnleuPheIleuLysSerIleuLysGluITrPAsnIyrProIeu 80
DB	176 AAGGAAAAAGTCGGCGGCAACATCTTCAAAAACTGTAAAGAAATTGACTCTACATTG 235
QY	81 PheGlnAspLeu 84
DB	236 TATTAAGAACTTA 247
RESULT 12	
LOCUS	BG287772 963 bp mRNA linear EST 21-FEB-2001
DEFINITION	602384122P1 NIH_MGC_93 Homo sapiens CDNA clone IMAGE:4513277 5',
ACCESSION	BG287772
VERSION	BG287772.1 GI:13041938
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE	1 (bases 1 to 963)
JOURNAL	NIH-MGC http://mhc.nci.nih.gov/.
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)
	Unpublished (1999)
	Contact: Robert Strausberg, Ph.D.
	Email: cga@brc-remail.nih.gov
	Tissue Procurement: ATCC
	cDNA Library Preparation: Life Technologies, Inc.
	DNA Sequencing by: Incyte Genomics, Inc.
	Clone distribution: MGC clone distribution information can be
	found through the I.M.A.G.E. Consortium/BLNI at:
	http://image.llnl.gov
	Plate: ILAM10399 row: k column: 06
	High quality sequence stop: 629.
	Location/Qualifiers
	1..963

```
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4513277"
/clone_lib="NIH_MGC_93"
/tissue_type="transitional cell papilloma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: bladder; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

BASE COUNT      325 a      144 c      231 g      262 t      1 others
ORIGIN

Alignment Scores:
Pred. No.:      0.000249      Length:      963
Score:          108.00      Matches:      29
Percent Similarity: 58.33%      Conservative: 20
Best Local Similarity: 34.52%      Mismatches: 33
Query Match:    23.43%      Indels:      2
DB:             12      Gaps:        1

US-09-697-089-2_COPY_1_88 (1-88) x BG287772 (1-963)

QY 1 MetasnpheilleysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
Db 320 TTGTCATTAATTCGGAAGACAGATGCGCTCTTTCACAA-----TTGCATGTGTG 373
QY 21 LysGlnIleThrAspAspLeuPheValITrpAsnValIleAsnArgGluGluValAsnIle 40
Db 374 CTTCCTATCCGCGATAACTTTTAAAGGCCAATGTAATTAATTAACAGAACATGATATT 433
QY 41 IleCysGluIuValGluGlnAspAlaIaArgGlyIleIleHisMetIleLeuIys 60
Db 434 ATTAACAAAAAACAACAGATACCTTTACAGCGAGAGACGATGATGATACATTGGTT 493
QY 61 LysGlySerGluSerCysAsnLeuPheLeuIysSerLeuIysGluITrpAsnTyrProLeu 80
Db 494 AAAGGAATAGCGCGCAACATCTTCAAAACGTGCTAAGAAATGACTCTACATTG 553
QY 81 PheGlnAspLeu 84
Db 554 TATAAGAACTTA 565

RESULT 13
BG028431      976 bp      mRNA      linear      EST 24-JAN-2001
LOCUS      BG028431
DEFINITION      602294338P1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:4389248 5',
ACCESSION      BG028431
VERSION      BG028431.1 GI:12417525
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 976)
AUTHORS      NIH-MGC http://mgc.ncl.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgapds@email.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLM10076 row: k column: 09
High quality sequence stop: 646.
Location/Qualifiers
1..976
```

```
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4389248"
/clone_lib="NIH_MGC_86"
/tissue_type="osteosarcoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: bone; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.53 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

BASE COUNT      368 a      128 c      222 g      258 t
ORIGIN

Alignment Scores:
Pred. No.:      0.000255      Length:      976
Score:          108.00      Matches:      29
Percent Similarity: 58.33%      Conservative: 20
Best Local Similarity: 34.52%      Mismatches: 33
Query Match:    23.43%      Indels:      2
DB:             12      Gaps:        1

US-09-697-089-2_COPY_1_88 (1-88) x BG028431 (1-976)

QY 1 MetasnpheilleysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
Db 146 TTGTCATTAATTCGGAAGACAGATGCGCTCTTTCACAA-----TTGCATGTGTG 199
QY 21 LysGlnIleThrAspAspLeuPheValITrpAsnValIleAsnArgGluGluValAsnIle 40
Db 200 CTTCCTATCCGCGATAACTTTTAAAGGCCAATGTAATTAATTAACAGAACATGATATT 259
QY 41 IleCysGluIuValGluGlnAspAlaIaArgGlyIleIleHisMetIleLeuIys 60
Db 260 ATTAACAAAAAACAACATACCTTTACAGCGAGAGACGATGATGATACATTGGTT 319
QY 61 LysGlySerGluSerCysAsnLeuPheLeuIysSerLeuIysGluITrpAsnTyrProLeu 80
Db 320 AAAGGAATAGCGCGCAACATCTTCAAAACGTGCTAAGAAATGACTCTACATTG 379
QY 81 PheGlnAspLeu 84
Db 380 TATAAGAACTTA 391

RESULT 14
BQ235318      512 bp      mRNA      linear      EST 03-MAY-2002
LOCUS      BQ235318
DEFINITION      hd56e06.g1 Canis Total Brain cDNAs Canis familiaris cDNA clone
ACCESSION      BQ235318
VERSION      BQ235318.1 GI:20431194
KEYWORDS      EST.
SOURCE      dog.
ORGANISM      Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE      1 (bases 1 to 512)
AUTHORS      O'Shaughnessy,A.L., Palmer,L., McCombie,W.R., Baker,J.P., Bahret,A.,
Cunnius,D., Dedhia,N.N., de la Bastide,M., Katzenberger,F., King
,L., Kirchoff,K.A., Miller,B., Muller,S., Nascimento,L.O., Preston
,R.R., Shah,R.S., Spiegel,L.A., Zuttervern,T., Santos,L. and Hannon
,G.J.
Expressed sequence tags from Canis familiaris (dog) (5_2002)
Unpublished (2002)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: hd56 row: e column: 06
Seq primer: -21M130n1vrev
```

High quality sequence stop: 512.

FEATURES

Location/Qualifiers

1. 512

/organism="Canis familiaris"

/db_xref="taxon:9615"

/clone="hd56e06"

/note="Vector: Lambda Zap II: The library was provided by Greg Hannon and Lee Santos (Cold Spring Harbor Laboratory). This library is oligo(dT) primed using stratagene zap cDNA synthesis kit. It was made from dog whole brain cells. Please contact Greg Hannon (hannon@cshl.org) with any library related inquiries."

BASE COUNT

177 a 80 c 121 g 134 t

ORIGIN

Alignment Scores:

Pred. No.: 0.000119 Length: 512
Score: 107.00 Matches: 28
Percent Similarity: 58.33% Conservative: 21
Best Local Similarity: 33.33% Mismatches: 33
Query Match: 23.21% Indels: 2
DB: 14 Gaps: 1

US-09-697-089-2_COPY_1_88 (1-88) x BQ235318 (1-512)

QY 1 MetanphelelySASPAnSerArgAlaLeuileGlnArgMetGlyMetThValIle 20

Db 125 TTGTCATTAAATCGAGAAATGAAATGCTCTTTTCACAG-----TTGACTGTGTG 178

QY 21 LysGlnIleThrAspAspLeuPheValIleTrpAsnValIleuAsnArgGluValAsnIle 40

Db 179 CTTCCTATCCGATATCTTTAAAGCCCAATGTAATTAATAACAGACATGATATC 238

QY 41 IleCysGluIysValGluGlnAspAlaIleArgGlyIleIleHisMetIleLeuIys 60

Db 229 ATTAACAACAAACACATATCTTTCAGACGAGAGAAATGATGATGATCTTACTT 298

QY 61 LysGlySerGluSerCysAsnLeuPheLeuIysSerIleuGluTrpAsnTyProLeu 80

Db 299 AAGGAAACCTGCGCCACATCTTCAAAAGTTGTTAAAGAAATGACACTCTACATTA 358

QY 81 PheGlnAspLeu 84

Db 359 TATAAGACTTA 370

RESULT 15

AV682308 665 bp mRNA linear EST 16-JAN-2002

DEFINITION AV682308 GKB Homo sapiens cDNA clone GKBAC11 5', mRNA sequence.

ACCESSION AV682308

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 665)

AUTHORS

XU,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,

TITLE

Insight into hepatocellular carcinogenesis at transcriptome level

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

MEDLINE

21625106

COMMENT

Contact: Zeguang Han

Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

201203, P. R. China

Tel: 86-21-50801919(ex.45)

Fax: 86-21-50801922

Email: hanzg@chgc.sh.cn

This clone is available at CHGC in Shanghai.

FEATURES

Location/Qualifiers

1. 665

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="GKBAC11"

/note="Vector: Lambda Zap II: The library was provided by Greg Hannon and Lee Santos (Cold Spring Harbor Laboratory). This library is oligo(dT) primed using stratagene zap cDNA synthesis kit. It was made from dog whole brain cells. Please contact Greg Hannon (hannon@cshl.org) with any library related inquiries."

BASE COUNT

223 a 98 c 129 g 213 t 2 others

ORIGIN

Alignment Scores:

Pred. No.: 0.000255 Length: 665
Score: 106.00 Matches: 29
Percent Similarity: 57.83% Conservative: 19
Best Local Similarity: 34.94% Mismatches: 33
Query Match: 22.99% Indels: 2
DB: 10 Gaps: 1

US-09-697-089-2_COPY_1_88 (1-88) x AV682308 (1-665)

QY 2 AsnPhelIeLySASPAnSerArgAlaLeuileGlnArgMetGlyMetThValIleIys 21

Db 1 TCATTAAATTCGAGAAACGAAATGCTCTCTTCAACAA-----TTGACATGTGTGCT 54

QY 22 GlnIleThrAspAspLeuPheValIleTrpAsnValIleuAsnArgGluValAsnIleIle 41

Db 55 CCTATCTCGATATCTTTAAAGCCCAATGTAATTAATAACAGACATGATATTAAT 114

QY 42 CysCysGluIysValGluGlnAspAlaIleArgGlyIleIleHisMetIleLeuIys 61

Db 115 AAGGAAACCTGCGCCACATCTTCAAAAGTTGTTAAAGAAATGACACTCTACATTA 174

QY 62 GlySerGluSerCysAsnLeuPheLeuIysSerIleuGluTrpAsnTyProLeuPhe 81

Db 175 GGAATGCTGCGCCACATCTTCAAAAGTTGTTAAAGAAATGACACTCTACATTA 234

QY 82 GlnAspLeu 84

Db 235 AAGAACTTA 243

Search completed: January 31, 2003, 16:18:48

Job time : 723.086 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 31, 2003, 11:43:51 ; Search time 19.9209 Seconds
(without alignments)
1354.737 Million cell updates/sec

Title: US-09-697-089-2_COPY_1_88

Perfect score: 461
Sequence: 1 MNFIKDSRALIQRMGTVT.....FLSKIKMNPPLFDLDNGQS 88

Scoring table:

BIOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL-frame+ .p2n.model -DEV-xlh
-O=/cgn2_1/USPTO.spool/US09697089/runat_29012003_092754_19735/app-query.fasta_1.981
-DB-issued_patents_NA -QFMT-fastlap -SUFFIX-p2n.rni -MINMATCH=0.1 -LOOPL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST=45 -LOCALIGN=200 -THR SCORE=pcr -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09697089_EGCGN_1_1_37_tunat_29012003_092754_19735 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAP -LARGEQUERY -NES_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued_patents_NA.*
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCFUS.COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	108	23.4	1435	5	PCT-US95-05922A-1
2	108	23.4	2589	4	US-08-569-749-1
3	108	23.4	2589	5	PCT-US96-12860-1
4	108	23.4	3532	2	US-09-205-204-1
5	108	23.4	3732	3	US-09-212-971-7
6	108	23.4	3732	3	US-08-800-929A-7
7	108	23.4	3732	4	US-09-617-053A-7
8	102	22.1	2580	2	US-08-511-485-7
9	100	21.7	2862	4	US-08-569-749-13
10	100	21.7	2862	5	PCT-US96-12860-13
11	100	21.7	3151	3	US-09-212-971-13
12	100	21.7	3151	3	US-08-800-929A-13

13	100	21.7	3151	4	US-09-617-053A-13	Sequence 13, Appl
14	95	20.6	1215	1	US-08-242-663A-1	Sequence 1, Appl
15	95	20.6	1215	3	US-08-954-536-17	Sequence 17, Appl
16	95	20.6	1215	4	US-08-748-547-1	Sequence 1, Appl
17	95	20.6	1215	4	US-09-561-756-4	Sequence 4, Appl
18	95	20.6	1215	4	US-09-227-721-4	Sequence 4, Appl
19	95	20.6	1215	5	PCT-US95-06132-1	Sequence 1, Appl
20	95	20.6	1216	2	US-08-573-880-1	Sequence 1, Appl
21	95	20.6	1216	4	US-09-248-179-1	Sequence 1, Appl
22	95	20.6	1248	2	US-08-391-916A-1	Sequence 1, Appl
23	95	20.6	1373	2	US-08-394-189B-3	Sequence 3, Appl
24	95	20.6	1373	2	PCT-US93-05705-3	Sequence 3, Appl
25	93.5	20.3	1185	2	US-08-391-916A-3	Sequence 3, Appl
26	86	18.7	2601	4	US-08-569-749-3	Sequence 3, Appl
27	86	18.7	2601	5	PCT-US96-12860-3	Sequence 3, Appl
28	86	18.7	2676	2	US-08-511-485-5	Sequence 3, Appl
29	86	18.7	3076	2	US-09-205-144-1	Sequence 5, Appl
30	86	18.7	6669	3	US-09-212-971-5	Sequence 1, Appl
31	86	18.7	6669	3	US-08-800-929A-5	Sequence 5, Appl
32	86	18.7	6669	4	US-09-617-053A-5	Sequence 5, Appl
33	75	16.3	1400	4	US-09-245-281-9	Sequence 40, Appl
34	75	16.3	1400	4	US-09-207-359B-40	Sequence 9, Appl
35	75	16.3	2859	4	US-09-099-041A-9	Sequence 9, Appl
36	75	16.3	2859	4	US-09-245-281-9	Sequence 9, Appl
37	75	16.3	2859	4	US-09-207-359B-9	Sequence 9, Appl
38	75	16.3	3382	4	US-09-099-041A-7	Sequence 7, Appl
39	75	16.3	3382	4	US-09-245-281-7	Sequence 7, Appl
40	75	16.3	3382	4	US-09-207-359B-7	Sequence 7, Appl
41	75	16.3	4302	4	US-09-245-281-38	Sequence 38, Appl
42	75	16.3	4302	4	US-09-207-359B-38	Sequence 38, Appl
43	69	15.0	4141	4	US-09-245-281-42	Sequence 42, Appl
44	69	15.0	4141	4	US-09-207-359B-42	Sequence 42, Appl
45	68.5	14.9	1335	3	US-08-954-536-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
PCT-US95-05922A-1
Sequence 1, Application PC/TUS9505922A
GENERAL INFORMATION:
APPLICANT: HE, ET AL.
TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELIA, BYRNE, BAIN, GILFILLAN,
ADDRESSSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05922A
FILING DATE: 11 MAY 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-292
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

```
;
; LENGTH: 1435 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
; PCT-US95-05922A-1

Alignment Scores:
Pred. No.: 2.81e-06 Length: 1435
Score: 108.00 Matches: 29
Percent Similarity: 58.33% Conservative: 20
Best Local Similarity: 34.52% Mismatches: 33
Query Match: 23.43% Indels: 2
DB: Gaps: 1

US-09-697-089-2_COPY_1_88 (1-88) x PCT-US95-05922A-1 (1-1435)
QY 1 MetasnphelllysaspanserargAlaleuileglnatgmetglymethValile 20
Db 841 TTGTCATTAAATCGGAGAACGAAATGCTCTCTTCACAA-----TTGACATGTGTG 894
QY 21 Lysglnlethrpsapleuphevaltrpsanvalleunarggluvalasnile 40
Db 895 CTTCCTATCTCGATATCTTTAAAGCCCATGTATTAATAACGAAACATGATATT 954
QY 41 llecyscsgluysvalgluglnaspAlaAarglyleilehismetileleuLys 60
Db 955 ATTAACAAAAAACACAGATACCTTTACAAAGCAGAACATGATTAACATTTTGGTT 1014
QY 61 LysgllysergluserCysasnleupheleuLysserleuLysglutrpasnyProleu 80
Db 1015 AAAGGAATGCTGGCCACATCTTCAAAAACGTCTTAAGAAATGACTTACATTG 1074
QY 81 Pheglnaspleu 84
Db 1075 TATAAGAACTTA 1086

RESULT 2
; Sequence 1, Application US/08569749
; Patent No. 6187557
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Goeddel, David V
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/569,749
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DJB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989
; TELEFAX: (415)398-3249
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2589 base pairs
; TYPE: nucleic acid
```

```
;
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-569-749-1

Alignment Scores:
Pred. No.: 6.49e-06 Length: 2589
Score: 108.00 Matches: 29
Percent Similarity: 58.33% Conservative: 20
Best Local Similarity: 34.52% Mismatches: 33
Query Match: 23.43% Indels: 2
DB: Gaps: 1

US-09-697-089-2_COPY_1_88 (1-88) x US-08-569-749-1 (1-2589)
QY 1 MetasnphelllysaspanserargAlaleuileglnatgmetglymethValile 20
Db 1566 TTGTCATTAAATCGGAGAACGAAATGCTCTCTTCACAA-----TTGACATGTGTG 1619
QY 21 Lysglnlethrpsapleuphevaltrpsanvalleunarggluvalasnile 40
Db 1620 CTTCCTATCTCGATATCTTTAAAGCCCATGTATTAATAACGAAACATGATATT 1679
QY 41 llecyscsgluysvalgluglnaspAlaAarglyleilehismetileleuLys 60
Db 1680 ATTAACAAAAAACACAGATACCTTTACAAAGCAGAACATGATTAACATTTTGGTT 1739
QY 61 LysgllysergluserCysasnleupheleuLysserleuLysglutrpasnyProleu 80
Db 1740 AAAGGAATGCTGGCCACATCTTCAAAAACGTCTTAAGAAATGACTTACATTG 1799
QY 81 Pheglnaspleu 84
Db 1800 TATAAGAACTTA 1811

RESULT 3
; PCT-US96-12860-1
; Sequence 1, Application PC/TUS9612860
; GENERAL INFORMATION:
; APPLICANT: TULARIK, INC.
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/12860
; FILING DATE: 06 AUG 1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DJB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989
; TELEFAX: (415)398-3249
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2589 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
```



```

; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PCT-US96-12860-1

Alignment Scores:
Pred. No.: 6.49e-06 Length: 2589
Score: 108.00 Matches: 29
Percent Similarity: 58.33% Conservative: 20
Best Local Similarity: 34.52% Mismatches: 33
Query Match: 23.43% Indels: 2
DB: 5 Gaps: 1

US-09-697-089-2_COPY_1_88 (1-88) x PCT-US96-12860-1 (1-2589)

Oy 1 Metasnpheilelyspaspserserargalaleuileglnargmeglmethrvalille 20
Db 1566 TTGTCATTAAATTCGGAGACAGAAATGGCTCTTTCAACAA-----TTGACATGTGTG 1619

Oy 21 Lysglnlethrspaspleuphevaltrpsanvalleuasnarglgluvalasnlle 40
Db 1620 CTTCCTATCCCGAATACCTTTAAAGGCCAATGTAATTAATAACAGAACATGATATT 1679

Oy 41 llecyscysglulysvalgluclnaspalaalaarglyllelelhemetlleuleuls 60
Db 1680 ATTAAACAAAACACAGATACCTTTACACGACAGAACTGATTGATACCATTTTGGTT 1739

Oy 61 Lysglyserglusercysasnleupheuleuysserleuysglutrpasntyrproleu 80
Db 1740 AAAGGAATGCTGCGGCCACACATCTTCAAAAACGTCTTAAGAAGAAATGACTTCATTTG 1799

Oy 81 pheglnaspleu 84
Db 1800 TATAAGAACTTA 1811

RESULT 4
US-09-205-204-1
; Sequence 1, Application US/09205204
; Patent No. 5958772
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-1 EXPRES
; FILE REFERENCE: PFS-0020
; CURRENT APPLICATION NUMBER: US/09/205, 204
; CURRENT FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 3532
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1160)..(3016)
US-09-205-204-1

Alignment Scores:
Pred. No.: 1.01e-05 Length: 3532
Score: 108.00 Matches: 29
Percent Similarity: 58.33% Conservative: 20
Best Local Similarity: 34.52% Mismatches: 33
Query Match: 23.43% Indels: 2
DB: 2 Gaps: 1

US-09-697-089-2_COPY_1_88 (1-88) x US-09-205-204-1 (1-3532)

Oy 1 Metasnpheilelyspaspserserargalaleuileglnargmeglmethrvalille 20
Db 2531 TTGTCATTAAATTCGGAGACAGAAATGGCTCTTTCAACAA-----TTGACATGTGTG 2584

Oy 21 Lysglnlethrspaspleuphevaltrpsanvalleuasnarglgluvalasnlle 40
Db 2585 CTTCCTATCCCGAATACCTTTAAAGGCCAATGTAATTAATAACAGAACATGATATT 2644
```

```

Oy 41 llecyscysglulysvalgluclnaspalaalaarglyllelelhemetlleuleuls 60
Db 2645 ATTAAACAAAACACAGATACCTTTACAGCAGACAGATGATGATACCATTTTGGTT 2704

Oy 61 Lysglyserglusercysasnleupheuleuysserleuysglutrpasntyrproleu 80
Db 2705 AAAGGAATGCTGCGGCCACACATCTTCAAAAACGTCTTAAGAAGAAATGACTTCATTTG 2764

Oy 81 pheglnaspleu 84
Db 2765 TATAAGAACTTA 2776

RESULT 5
US-09-212-971-7
; Sequence 7, Application US/09212971B
; Patent No. 6107041
; GENERAL INFORMATION:
; APPLICANT: Korneljuk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009002
; CURRENT APPLICATION NUMBER: US/09/212, 971B
; EARLIER FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 60/017, 354
; EARLIER FILING DATE: 1996-04-26
; EARLIER APPLICATION NUMBER: 60/030, 590
; EARLIER FILING DATE: 1996-11-14
; EARLIER APPLICATION NUMBER: 08/800, 929
; EARLIER FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 3732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-212-971-7

Alignment Scores:
Pred. No.: 1.09e-05 Length: 3732
Score: 108.00 Matches: 29
Percent Similarity: 58.33% Conservative: 20
Best Local Similarity: 34.52% Mismatches: 33
Query Match: 23.43% Indels: 2
DB: 3 Gaps: 1

US-09-697-089-2_COPY_1_88 (1-88) x US-09-212-971-7 (1-3732)

Oy 1 Metasnpheilelyspaspserserargalaleuileglnargmeglmethrvalille 20
Db 2751 TTGTCATTAAATTCGGAGACAGATGGCTCTTTCAACAA-----TTGACATGTGTG 2804

Oy 21 Lysglnlethrspaspleuphevaltrpsanvalleuasnarglgluvalasnlle 40
Db 2805 CTTCCTATCCCGAATACCTTTAAAGGCCAATGTAATTAATAACAGAACATGATATT 2864

Oy 41 llecyscysglulysvalgluclnaspalaalaarglyllelelhemetlleuleuls 60
Db 2865 ATTAAACAAAACACAGATACCTTTACACGACAGAACTGATTGATACCATTTTGGTT 2924

Oy 61 Lysglyserglusercysasnleupheuleuysserleuysglutrpasntyrproleu 80
Db 2925 AAAGGAATGCTGCGGCCACACATCTTCAAAAACGTCTTAAGAAGAAATGACTTCATTTG 2984

Oy 81 pheglnaspleu 84
Db 2985 TATAAGAACTTA 2996
```

```
RESULT 6
US-08-800-929A-7
; Sequence 7, Application US/08800929A
; Patent No. 6133437
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF
; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,929A
; FILING DATE: 13-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,590
; FILING DATE: 14-NOV-1996
; APPLICATION NUMBER: 60/017,354
; FILING DATE: 26-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bleker-Brady, Kristina
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 07891/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3732 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-800-929A-7

Alignment Scores:
Pred. No.: 1.09e-05 Length: 3732
Score: 108.00 Matches: 29
Percent Similarity: 58.33% Conservative: 20
Best Local Similarity: 34.52% Mismatches: 33
Query Match: 23.43% Indels: 2
Gaps: 1

US-09-697-089-2_COPY_1_88 (1-88) x US-08-800-800-929A-7 (1-3732)
Oy 1 MetasnpheilelysaspasnserrargAlaleuileglnargmetglymetThValille 20
Db 2751 TTGTCATTAAATTCGGAAGACAGATGCTCTTTCAACA-----TTGACATGTGTG 2804
Oy 21 LysglnilethrAspAspleuPheValITrpAsnValIeuAsnArgGlulGluValAsnIle 40
Db 2805 CTTCCTATCCGGAATATCTTTAAAGCCCAATGTAATTAATAACAGGACATGATATT 2864
Oy 41 IleCysCysgluIysValIgIuGlnAspAlaIaIaarglyIleIleHismetIleuIys 60
Db 2805 CTTCCTATCCGGAATATCTTTAAAGCCCAATGTAATTAATAACAGGACATGATATT 2864
Oy 41 IleCysCysgluIysValIgIuGlnAspAlaIaIaarglyIleIleHismetIleuIys 60
```

```
Db 2865 ATTAACAAAACACAGATACCTTTACAAGCAGAGACATGATGTATACATTGTGTT 2924
Oy 61 LysglYsergluSerCysAsnleuPheIuIysSerIeuIysgluITrpAsnTyProIeu 80
Db 2925 AAAGGAATGCTGGCCACATCTTCAAAAACGTCTAAAGAAATGACTCTACATTG 2984
Oy 81 PheGlnAspleu 84
Db 2985 TATAAGAACTTA 2996

RESULT 7
US-09-617-053A-7
; Sequence 7, Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009003
; CURRENT APPLICATION NUMBER: US/09/617,053A
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 3732
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-617-053A-7

Alignment Scores:
Pred. No.: 1.09e-05 Length: 3732
Score: 108.00 Matches: 29
Percent Similarity: 58.33% Conservative: 20
Best Local Similarity: 34.52% Mismatches: 33
Query Match: 23.43% Indels: 2
Gaps: 1

US-09-697-089-2_COPY_1_88 (1-88) x US-09-617-053A-7 (1-3732)
Oy 1 MetasnpheilelysaspasnserrargAlaleuileglnargmetglymetThValille 20
Db 2751 TTGTCATTAAATTCGGAAGACAGATGCTCTTTCAACA-----TTGACATGTGTG 2804
Oy 21 LysglnilethrAspAspleuPheValITrpAsnValIeuAsnArgGlulGluValAsnIle 40
Db 2805 CTTCCTATCCGGAATATCTTTAAAGCCCAATGTAATTAATAACAGGACATGATATT 2864
Oy 41 IleCysCysgluIysValIgIuGlnAspAlaIaIaarglyIleIleHismetIleuIys 60
Db 2865 ATTAACAAAACACAGATACCTTTACAAGCAGAGACATGATGTATACATTGTGTT 2924
Oy 61 LysglYsergluSerCysAsnleuPheIuIysSerIeuIysgluITrpAsnTyProIeu 80
Db 2925 AAAGGAATGCTGGCCACATCTTCAAAAACGTCTAAAGAAATGACTCTACATTG 2984
Oy 81 PheGlnAspleu 84
Db 2985 TATAAGAACTTA 2996

RESULT 8
US-08-511-485-7
; Sequence 7, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
```

```

:
: APPLICANT: Korneluk, Robert G.
: APPLICANT: Mackenzie, Alexander E.
: APPLICANT: Baird, Stephen
: TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
: NUMBER OF SEQUENCES: 38
: PROBES, AND DETECTION METHODS
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson P.C.
: STREET: 225 Franklin Street
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/511,485
: FILING DATE: 04-AUG-1995
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Clark, Paul T.
: REGISTRATION NUMBER: 30,162
: REFERENCE/DOCKET NUMBER: 07540/002001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617/542-5070
: TELEFAX: 617/542-8906
: TELEX: 200154
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2580 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: both
: MOLECULE TYPE: DNA (genomic)
:
: US-08-511-485-7
:
: Alignment Scores:
: Pred. No.: 4.88e-05 Length: 2580
: Score: 102.00 Matches: 28
: Percent Similarity: 57.14% Conservative: 20
: Best Local Similarity: 33.33% Mismatches: 34
: Query Match: 22.13% Indels: 2
: DB: Gaps: 1
:
: US-09-697-089-2_COPY_1_88 (1-88) x US-08-511-485-7 (1-2580)
:
: QY 1 MetAspHeiLeIySAsPAsnSerArGAlaLeuIleGlnArGMeGlyMeThrValIle 20
:      ::::: ||||| ||||| ||||| :::::
: Db 1609 TTGCTATTAAATCGGAGAACAGATGGCTCTCTTCAACA-----TTGCACATGTGG 1662
:
: QY 21 LysGlnIleThrAspAspLeuPheValTrpAsnValIleuAsnArGluGluValAsnIle 40
:      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: Db 1663 CTCTCATCCCTGGATTAATCTTTAAAGCCCATGTATTAATAACAGAACATATATT 1722
:
: QY 41 IleCysGluValAlaGluGlnAspAlaAlaArGlyIleIleHisMetIleuLys 60
:      ||| ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: Db 1723 ATTAACAACAAAACACAGATACCTTTACAGCGAGAGAACTGATGATTCATTTGGGTT 1782
:
: QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerIleuLysGluTrpAsnTrpLeu 80
:      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: Db 1783 AAGGAAATGCTGCGCCACACATCTTCAAAAACGTCCTTAAAGAAATTGACTCTACATVG 1842
:
: QY 81 PheGlnAspLeu 84
:      ::::: |||||
: Db 1843 TATAGAACTTA 1854
:
: RESULT 9
: US-08-569-749-13
: Sequence 13, Application US/08569749
: Patent No. 6187557
```

```

:
: GENERAL INFORMATION:
: APPLICANT: Rothe, Mike
: APPLICANT: Goettel, David V
: TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
: STREET: 4 Embarcadero Center, Suite 3400
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/569,749
: FILING DATE:
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Brezner, David J.
: REGISTRATION NUMBER: 24,774
: REFERENCE/DOCKET NUMBER: A-62464/DJB
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415)781-1989
: TELEFAX: (415)398-3249
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2862 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
:
: US-08-569-749-13
:
: Alignment Scores:
: Pred. No.: 0.000111 Length: 2862
: Score: 100.00 Matches: 27
: Percent Similarity: 58.33% Conservative: 22
: Best Local Similarity: 32.14% Mismatches: 33
: Query Match: 21.69% Indels: 2
: DB: Gaps: 1
:
: US-09-697-089-2_COPY_1_88 (1-88) x US-08-569-749-13 (1-2862)
:
: QY 1 MetAspHeiLeIySAsPAsnSerArGAlaLeuIleGlnArGMeGlyMeThrValIle 20
:      ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: Db 1836 TTATACGTGATTCGGAGAGATGAGATGGCCCTTTCAACG-----TTGCACATGTGC 1879
:
: QY 21 LysGlnIleThrAspAspLeuPheValTrpAsnValIleuAsnArGluGluValAsnIle 40
:      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: Db 1880 CTCTCATCCCTGGATTAATCTTTGAGGCCAGTGTATTAACAACAGAACATGATATT 1939
:
: QY 41 IleCysGluValAlaGluGlnAspAlaAlaArGlyIleIleHisMetIleuLys 60
:      ||| ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: Db 1940 ATTAGACGAAACACAGATACCTTTACAGCAGACAGACCTTATGACACCTTTAGTC 1999
:
: QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerIleuLysGluTrpAsnTrpLeu 80
:      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: Db 2000 AAGGAAATGCTGCGCCACACATCTTCAAAAACGTCCTGAAAGAAATTGACTCCACGTTA 2059
:
: QY 81 PheGlnAspLeu 84
:      ::::: |||||
: Db 2060 TATGAAACTTA 2071
:
: RESULT 10
: PCT-US96-12860-13
: Sequence 13, Application PC/TUS9612860
: GENERAL INFORMATION:
: APPLICANT: TULARIK, INC.
: TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
```

```

1      NUMBER OF SEQUENCE: 14
2      CORRESPONDENCE ADDRESS:
3      ADDRESSEE: FLEHR, HONBACH, TEST, ALBRITTON & HERBERT
4      STREET: 4 Embarradero Center, Suite 3400
5      CITY: San Francisco
6      STATE: California
7      COUNTRY: USA
8      ZIP: 94111
9      COMPUTER READABLE FORM:
10     MEDIUM TYPE: Floppy disk
11     COMPUTER: IBM PC compatible
12     OPERATING SYSTEM: PC-DOS/MS-DOS
13     SOFTWARE: Patentin Release #1.0, Version #1.30
14     CURRENT APPLICATION DATA:
15     APPLICATION NUMBER: PCT/US96/12860
16     FILING DATE: 06 AUG 1996
17     CLASSIFICATION:
18     PRIOR APPLICATION DATA:
19     APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
20     CLASSIFICATION:
21     ATTORNEY/AGENT INFORMATION:
22     NAME: Brezner, David J.
23     REGISTRATION NUMBER: 24,774
24     REFERENCE/DOCKET NUMBER: A-62464/DJB
25     TELECOMMUNICATION INFORMATION:
26     TELEPHONE: (415)781-1989
27     TELEFAX: (415)398-3249
28     INFORMATION FOR SEO ID NO: 13:
29     SEQUENCE CHARACTERISTICS:
30     LENGTH: 2862 base pairs
31     TYPE: nucleic acid
32     STRANDEDNESS: single
33     TOPOLOGY: linear
34     MOLECULE TYPE: cDNA
35     PCT-US96-12860-13
36
37 Alignment Scores:
38 Pred. No.: 0.000111 length: 2862
39 Score: 100.00 Matches: 27
40 Percent Similarity: 58.3% Conservative: 22
41 Best Local Similarity: 32.14% Mismatches: 33
42 Query Match: 21.69% Indels: 2
43 DB: 5 Gaps: 1
44
45 US-09-697-089-2_COPY_1_88 (1-88) x PCT-US96-12860-13 (1-2862)
46
47 Oy 1 Metcspheilelysaspsasnserrargalaleulleghnargmetclymethrvalle 20
48      :::: ::::: ||| ||||| ||::: :||| :::
49 Db 1826 TTACACTGATGTGGGAAGAAATAAATGCGCCTTTCAACAG-----TTGACACATGTC 1879
50
51 Oy 21 Lysglnliehrspaspaleuphevalittpasvvalleunasnrglgnluvalasnlle 40
52      ||| ||| ||::: ||| ::::: ||| ::::: ||| ::::: |||
53 Db 1880 CTTCCTTCCCTGGATTAATCTCTTGAGGCCAGTGTATTACAAGAAGCACATGATATT 1939
54
55 Oy 41 Ilecyscysglunlysvalnguinaspalaalaaryglyllellhismetlleuleuls 60
56      ||| ::::: ||| ||||| ||::: ||| ::::: ||| ::::: |||
57 Db 1940 ATTAGACAGAAAACACAGATACCCTTACAAGAAGACACTTATTGACACCGTTTTATC 1999
58
59 Oy 61 Lysylserglusercysasnleupheuleulssearleulysglutrpasntyrproleu 80
60      ||||| ::::: ||| ||||| ||| ||||| ||||| ||| ::::: |||
61 Db 2000 AAGGGAATGCTGCAGGCCAACATCTTCAAAAAMACTCTGTGAAGAAATTGACTCCACGTT 2059
62
63 Oy 81 Phcglnaspleu 84
64      ::::: |||
65 Db 2060 TATGAAAACTTA 2071
66
67 RESULT 11
68 US-09-212-971-13
69 ; Sequence 13, Application US/09212971B
70 ; Patent No. 6107041
71 ; GENERAL INFORMATION:
72 ; APPLICANT: Korneiluk, Robert G
73 ; APPLICANT: Mackenzie, Alexander E

```

```

: APPLICANT: Bairston, Peter
: APPLICANT: Baird, Stephen
: APPLICANT: Tsang, Benjamin K
: APPLICANT: Pratt, Christine
: TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
: TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
: TITLE OF INVENTION: DISEASE
: FILE REFERENCE: 07891/009002
: CURRENT APPLICATION NUMBER: US/09/212,971B
: CURRENT FILING DATE: 1998-12-16
: EARLIER APPLICATION NUMBER: 60/017,354
: EARLIER FILING DATE: 1996-04-26
: EARLIER APPLICATION NUMBER: 60/030,590
: EARLIER FILING DATE: 1996-11-14
: EARLIER APPLICATION NUMBER: 08//800,929
: EARLIER FILING DATE: 1997-02-13
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 13
: LENGTH: 3151
: TYPE: DNA
: ORGANISM: Mus musculus
US-09-212-971-13

Alignment Scores:
Pred. No.: 0.000127 Length: 3151
Score: 100.00 Matches: 27
Percent Similarity: 58.33% Conservative: 22
Best Local Similarity: 32.14% Mismatches: 33
Query Match: 21.69% Indels: 2
DB: 3 Gaps: 1

US-09-697-089-2_COPY_1_88 (1-88) x US-09-212-971-13 (1-3151)
OY 1 MetAsnpHeilelYsAsPnsSerArGaLaLeuIleGlnArgMetGlYmetThrValIle 20
Db 2132 TTATACAGCATTCGGAAATAATAGAATGCCTCTTTCAACAG-----TTACACATGTC 2185
OY 21 LysGInIlleThrAsPAsPleuPhueVaITrpAsnValIeUsAnArGglUGluValAsnIle 40
Db 2186 CTTCCTATCCGTGGAAATCTCTTGAAGGCCAGTGTAATTACAAAACAGAACATGATATT 2245
OY 41 IleCysGsgLUlyVsAlGLUgLnAsPaLaIArGgLIlelleHIsMeIleuLyS 60
Db 2246 ATTAACAAGAAAAACAACAATACCCTTACACAGCAGAGCTTATTGACACCGCTTTAATGC 2305
OY 61 LysGlySerGluSerCysAsnLeuPhelEuLySerIeuLySGluTrpAsnTyrrProLeu 80
Db 2306 AAGGGAATAGCTGCAGCACACATCTTCAAATAACTCTGTGAAGGAATGACTCCACGTTA 2365
OY 81 PheGlnAspleu 84
Db 2366 TATGAATAACTTA 2377

RESULT 12
US-08-800-929A-13
: Sequence 13, Application US/08800929A
: Patent No. 6133437
: GENERAL INFORMATION:
: APPLICANT: Korneluk, Robert G
: APPLICANT: Mackenzie, Alexander E
: APPLICANT: Liston, Peter
: APPLICANT: Baird, Stephen
: APPLICANT: Tsang, Benjamin K
: APPLICANT: Pratt, Christine
: TITLE OF INVENTION: DETECTION AND MODULATION OF
: TITLE OF INVENTION: IAPs AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERAT
: TITLE OF INVENTION: DISEASE
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Clark & Elbing LLP
: STREET: 176 Federal Street
: CITY: Boston

```

```
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,929A
FILING DATE: 13-FEB-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 07891/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 3151 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-800-929A-13

Alignment Scores:
Pred. No.: 0.000127 Length: 3151
Score: 100.00 Matches: 27
Percent Similarity: 58.33% Conservative: 22
Best Local Similarity: 32.14% Mismatches: 33
Query Match: 21.69% Indels: 2
Gaps: 1

US-09-697-089-2_COPY_1_88 (1-88) x US-08-800-929A-13 (1-3151)
QY 1 MetasnphellelyspasnserrghlaleuileglnargmetglymetThValille 20
Db 2132 TTATCAGCATTCGGAGAAATGAGATGCGCCCTCTTCACAG-----TTGACACATGTC 2185
QY 21 LysglnlIethraspaspLeupheValItrpansValIleuansarggluGlulValasnlle 40
Db 2186 CTTCCTATCCGATTAATCTTCGAGGCCAGTGAATTACAAACAGGAAACATGATATT 2245
QY 41 IleCysCysgluLyValgluGlnaspAlaIlaargglylelleHlsmetIleleuLy 60
Db 2246 ATTAGACAGAAACACAGATACCTTACACAGACAGAGAGCTTATTGACACCGTTTAACTC 2305
QY 61 LysglYsergluSerCysAsnleupheleuLyserleuLysglultrpansTyProleu 80
Db 2306 AAGGGAATGCTGCAGCCACATCTTCAAAAACCTCTGGAAGAAATTGACTCCACGTTA 2365
QY 81 PheGlnaspLeu 84
Db 2366 TATGAAACTTA 2377

RESULT 13
US-09-617-053A-13
Sequence 13, Application US/09617053A
Patent No. 6300492
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
```

```
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IABs AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
FILE REFERENCE: 07891/009003
CURRENT APPLICATION NUMBER: US/09/617,053A
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 13
LENGTH: 3151
TYPE: DNA
ORGANISM: Mus musculus
US-09-617-053A-13

Alignment Scores:
Pred. No.: 0.000127 Length: 3151
Score: 100.00 Matches: 27
Percent Similarity: 58.33% Conservative: 22
Best Local Similarity: 32.14% Mismatches: 33
Query Match: 21.69% Indels: 2
Gaps: 1

US-09-697-089-2_COPY_1_88 (1-88) x US-09-617-053A-13 (1-3151)
QY 1 MetasnphellelyspasnserrghlaleuileglnargmetglymetThValille 20
Db 2132 TTATCAGCATTCGGAGAAATGAGATGCGCCCTCTTCACAG-----TTGACACATGTC 2185
QY 21 LysglnlIethraspaspLeupheValItrpansValIleuansarggluGlulValasnlle 40
Db 2186 CTTCCTATCCGATTAATCTTCGAGGCCAGTGAATTACAAACAGGAAACATGATATT 2245
QY 41 IleCysCysgluLyValgluGlnaspAlaIlaargglylelleHlsmetIleleuLy 60
Db 2246 ATTAGACAGAAACACAGATACCTTACACAGACAGAGCTTATTGACACCGTTTAACTC 2305
QY 61 LysglYsergluSerCysAsnleupheleuLyserleuLysglultrpansTyProleu 80
Db 2306 AAGGGAATGCTGCAGCCACATCTTCAAAAACCTCTGGAAGAAATTGACTCCACGTTA 2365
QY 81 PheGlnaspLeu 84
Db 2366 TATGAAACTTA 2377

RESULT 14
US-08-242-663A-1
Sequence 1, Application US/08242663A
Patent No. 5492824
GENERAL INFORMATION:
APPLICANT: Talianian, Robert V.
APPLICANT: Dang, Leonard Luan Cao
APPLICANT: Walker, Nigel Pelham Clinton
APPLICANT: Chayur, Taiq
TITLE OF INVENTION: ICE AND ICE-LIKE COMPOSITIONS AND
TITLE OF INVENTION: METHODS OF MAKING SAME
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
```


Mon Feb 3 14:11:41 2003

us-09-697-089-2_copy_1_88.p2n.rni

Page 9

Search completed: January 31, 2003, 15:16:34
Job time : 22.9209 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 31, 2003, 15:16:37 : Search time 24.3692 Seconds
(without alignments)
1622.345 Million cell updates/sec

Title: US-09-697-089-2_COPY_1_88

Perfect score: 461

Sequence: 1 MNFKDNRALIQRMGWTVI.....FLSKREMYNPLPDLDNGS 88

Scoring table:
BLOSUM62
Xgapop 10.0 , Ygapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 396772 seqs, 224632407 residues

Total number of hits satisfying chosen parameters: 793544

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+P2n_model -DEV=xlh
-O=/cgn2_1/USP10.spool/US09697089/r/unat_29012003_092755_19800/app_query.fasta_1.981
-DB=Published.Applications_NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -MATRIX=blsum62
-TRANS=human40.cdi -LIST=45 -DOCCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09697089.ecgn_1_1.48 -r/unat_29012003_092755_19800
-NCPD=6 -ICPD=3 -NO_XLPHY -NO_MMAP -LARGEOUERT -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCRTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	461	100.0	578	US-09-864-921-100
2	461	100.0	768	US-09-864-921-102
3	461	100.0	1395	US-09-864-921-98
4	461	100.0	3072	US-09-841-739-3

5	461	100.0	3133	US-09-841-739-1	Sequence 1, Appl1
6	461	100.0	3396	US-09-864-921-96	Sequence 96, Appl
7	457	99.1	261	US-09-864-921-177	Sequence 177, App
8	457	99.1	3612	US-09-841-739-6	Sequence 6, Appl1
9	457	99.1	3615	US-09-841-739-12	Sequence 12, Appl
10	457	99.1	3615	US-09-841-739-12	Sequence 12, Appl
11	126.5	27.4	1233	US-09-917-265-14	Sequence 14, Appl
12	126.5	27.4	1233	US-09-917-265-14	Sequence 14, Appl
13	123.5	26.8	526	US-09-917-265-17	Sequence 17, Appl
14	123.5	26.8	526	US-09-917-265-19	Sequence 19, Appl
15	123.5	26.8	1230	US-09-917-265-23	Sequence 23, Appl
16	123.5	26.8	1230	US-09-917-265-25	Sequence 25, Appl
17	108	23.4	3532	US-09-880-107-3354	Sequence 3354, Ap
18	108	23.4	3732	US-09-974-592-7	Sequence 7, Appl1
19	102.5	22.2	321	US-09-864-921-69	Sequence 89, Appl
20	102.5	22.2	2580	US-09-201-936-7	Sequence 7, Appl1
21	100	21.7	3151	US-09-974-592-13	Sequence 13, Appl
22	97	21.0	1293	US-09-996-617-6	Sequence 6, Appl1
23	97	21.0	1293	US-09-931-071-6	Sequence 6, Appl1
24	97	21.0	1487	US-09-388-221-7	Sequence 7, Appl1
25	97	21.0	4466	US-09-388-221-11	Sequence 11, Appl
26	97	21.0	4556	US-09-388-221-9	Sequence 9, Appl1
27	97	21.0	5059	US-09-996-617-3	Sequence 3, Appl1
28	97	21.0	5059	US-09-931-071-3	Sequence 3, Appl1
29	95	20.6	1215	US-09-954-697-4	Sequence 4, Appl1
30	95	20.6	1216	US-09-827-708A-1	Sequence 1, Appl1
31	95	20.6	1373	US-09-888-243-3	Sequence 3, Appl1
32	93	20.2	2416	US-09-201-936-41	Sequence 41, Appl
33	91.5	19.8	510	US-09-864-921-85	Sequence 85, Appl1
34	86	18.7	2676	US-09-201-936-5	Sequence 5, Appl1
35	86	18.7	3076	US-09-954-531-16	Sequence 16, Appl
36	86	18.7	3076	US-09-954-531-16	Sequence 16, Appl
37	86	18.7	6669	US-09-974-592-5	Sequence 5, Appl1
38	82.5	17.9	328	US-09-867-701-3	Sequence 3, Appl1
39	77	16.7	460	US-09-960-952-8049	Sequence 8049, Ap
40	75	16.3	1400	US-10-118-984-40	Sequence 40, Appl
41	75	16.3	1400	US-09-728-721-40	Sequence 40, Appl
42	75	16.3	2859	US-10-118-984-9	Sequence 9, Appl1
43	75	16.3	2859	US-09-728-721-9	Sequence 9, Appl1
44	75	16.3	2859	US-10-105-931-9	Sequence 9, Appl1
45	75	16.3	3382	US-10-118-984-7	Sequence 7, Appl1

ALIGNMENTS

RESULT 1
US-09-864-921-100
: Sequence 100, Application US/09864921
: Patent No. US20020176853A1
: GENERAL INFORMATION:
: APPLICANT: Reed, John C.
: APPLICANT: Pio, Frederick F.
: APPLICANT: Godzik, Adam
: APPLICANT: Stehlik, Christian
: APPLICANT: Damiano, Jason S.
: APPLICANT: Lee, Sug-Hyung
: APPLICANT: Oliveira, Vasco A.
: APPLICANT: Pawlowski, Hideki
: APPLICANT: Pawlowski, Krzysztof
: TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
: FILE REFERENCE: P-1J 4757
: CURRENT FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 09/579,240
: PRIOR FILING DATE: 2000-05-24
: PRIOR APPLICATION NUMBER: US 09/686,347
: PRIOR FILING DATE: 2000-10-10
: PRIOR APPLICATION NUMBER: US 60/275,980
: PRIOR FILING DATE: 2001-03-14
: NUMBER OF SEQ ID NOS: 195
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 100

LENGTH: 578
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (277)...(552)
US-09-864-921-100

Alignment Scores:

Pred. No.:	2,3e-59	Length:	578
Score:	461.00	Matches:	88
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-697-089-2_COPY_1_88 (1-88) x US-09-864-921-100 (1-578)

QY 1 MetAsnPhelIeLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
|||||
DB 277 ATGAATTTCAATAAGACAATAGCCGAGCCCTTATTCAAAGAATGGGAATGACTGTATA 336
QY 21 LysGlnIleThrAspAspLeuPheValITrPAsnValLeuAsnArgGluGluValAsnIle 40
|||||
DB 337 AAGCAAAATCACAGATGACCTATTGTATGAAATGTCGATCCGGAAGATTAACATC 396
QY 41 IleCysGlyGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
|||||
DB 397 ATTGCTGCCGAGAGAGTGAGACAGATGCTGCTAGAGGATCATTCATGATTTTGAA 456
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu 80
|||||
DB 457 AAGGTTTCAGAGTCTGTAACTCTTCTTAATAATCCCTTAAGAGATGGAATCATCTCTA 516
QY 81 PheGlnAspLeuAsnGlyGlnSer 88
|||||
DB 517 TTTCAGAGCTTGAATGACAAAGT 540

RESULT 2

US-09-864-921-102
Sequence 102, Application US/09864921
Patent No. US20020176853A1
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Pio, Frederick F.
APPLICANT: Godzik, Adam
APPLICANT: Stehlik, Christian
APPLICANT: Damiano, Jason S.
APPLICANT: Lee, Sung-Hyung
APPLICANT: Oliveira, Vasco A.
APPLICANT: Hayashi, Hideki
APPLICANT: Pawlowski, Krzysztof
TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use
FILE REFERENCE: P-LJ 4752
CURRENT APPLICATION NUMBER: US/09/864, 921
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 09/579, 240
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/686, 347
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 60/275, 980
PRIOR FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 195
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 102
LENGTH: 768
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (277)...(744)
US-09-864-921-102

Alignment Scores:

Pred. No.:	3,47e-59	Length:	768
Score:	461.00	Matches:	88
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-697-089-2_COPY_1_88 (1-88) x US-09-864-921-102 (1-768)

QY 1 MetAsnPhelIeLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
|||||
DB 277 ATGAATTTCAATAAGACAATAGCCGAGCCCTTATTCAAAGAATGGGAATGACTGTATA 336
QY 21 LysGlnIleThrAspAspLeuPheValITrPAsnValLeuAsnArgGluGluValAsnIle 40
|||||
DB 337 AAGCAAAATCACAGATGACCTATTGTATGAAATGTCGATCCGGAAGATTAACATC 396
QY 41 IleCysGlyGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
|||||
DB 397 ATTGCTGCCGAGAGTGAGACAGATGCTGCTAGAGGATCATTCATGATTTTGAA 456
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu 80
|||||
DB 457 AAGGTTTCAGAGTCTGTAACTCTTCTTAATAATCCCTTAAGAGATGGAATCATCTCTA 516
QY 81 PheGlnAspLeuAsnGlyGlnSer 88
|||||
DB 517 TTTCAGAGCTTGAATGACAAAGT 540

RESULT 3

US-09-864-921-98
Sequence 98, Application US/09864921
Patent No. US20020176853A1
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Pio, Frederick F.
APPLICANT: Godzik, Adam
APPLICANT: Stehlik, Christian
APPLICANT: Damiano, Jason S.
APPLICANT: Lee, Sung-Hyung
APPLICANT: Oliveira, Vasco A.
APPLICANT: Hayashi, Hideki
APPLICANT: Pawlowski, Krzysztof
TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use
FILE REFERENCE: P-LJ 4752
CURRENT APPLICATION NUMBER: US/09/864, 921
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 09/579, 240
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/686, 347
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 60/275, 980
PRIOR FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 195
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 98
LENGTH: 1395
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (277)...(1353)
US-09-864-921-98

Alignment Scores:

Pred. No.:	8,27e-59	Length:	1395
Score:	461.00	Matches:	88
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0

```
DB: 9 Gaps: 0
US-09-697-089-2_copy_1_88 (1-88) x US-09-864-921-98 (1-1395)
QY 1 Metanphelellayaspnserrargalaleuileglnaramecilymethrvalille 20
DB 277 ATGAATTTTCATTAAGACAAATAGCCGAGCCCTTATTCAAAGATGGAAATGACTGTATTA 336
QY 21 Lysglnillethrapspleuphevaltrpasnvalleuasargluciluvalasnnile 40
DB 337 AAGCAAAATCAGATGACCTATTGTATGGAATGTTCTGAATCGCGAAGAGTAACATC 396
QY 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
DB 397 ATTTCCTCGAAGAGTGAGCAGCATGCTGCTAGAGGATCATTCACATGATTTTGAAA 456
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu 80
DB 457 AAGGGTTTCAGAGTCCCTGTAACTCTTCTTAATCCCTTAAGAGATGGAATATCCTCTTA 516
QY 81 PheGlnAspLeuAsnGlyInsEr 88
DB 517 TTTCAGGACTTGAAATGACAAAGT 540

RESULT 4
US-09-841-739-3
; Sequence 3, Application US/09841739
; Patent No. US20020034784A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-329001
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3072
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-841-739-3

Alignment Scores:
Pred. No.: 2,6e-58 Length: 3072
Score: 461.00 Matches: 88
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-697-089-2_copy_1_88 (1-88) x US-09-841-739-3 (1-3072)
QY 1 Metanphelellayaspnserrargalaleuileglnaramecilymethrvalille 20
DB 1 ATGAATTTTCATTAAGACAAATAGCCGAGCCCTTATTCAAAGATGGAAATGACTGTATTA 60
QY 21 Lysglnillethrapspleuphevaltrpasnvalleuasargluciluvalasnnile 40
DB 61 AAGCAAAATCAGATGACCTATTGTATGGAATGTTCTGAATCGCGAAGAGTAACATC 120
QY 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
DB 121 ATTTCCTCGAAGAGTGAGCAGCATGCTGCTAGAGGATCATTCACATGATTTTGAAA 180
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu 80
DB 181 AAGGGTTTCAGAGTCCCTGTAACTCTTCTTAATCCCTTAAGAGATGGAATATCCTCTTA 240
QY 81 PheGlnAspLeuAsnGlyInsEr 88
```

```
DB 241 TTTCAGGACTTGAAATGACAAAGT 264

RESULT 5
US-09-841-739-1
; Sequence 1, Application US/09841739
; Patent No. US20020034784A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/09/841,739
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3133
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)...(3107)
US-09-841-739-1

Alignment Scores:
Pred. No.: 2,68e-58 Length: 3133
Score: 461.00 Matches: 88
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-697-089-2_copy_1_88 (1-88) x US-09-841-739-1 (1-3133)
QY 1 Metanphelellayaspnserrargalaleuileglnaramecilymethrvalille 20
DB 36 ATGAATTTTCATTAAGACAAATAGCCGAGCCCTTATTCAAAGATGGAAATGACTGTATTA 95
QY 21 Lysglnillethrapspleuphevaltrpasnvalleuasargluciluvalasnnile 40
DB 96 AAGCAAAATCAGATGACCTATTGTATGGAATGTTCTGAATCGCGAAGAGTAACATC 155
QY 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
DB 156 ATTTCCTCGAAGAGTGAGCAGCATGCTGCTAGAGGATCATTCACATGATTTTGAAA 215
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu 80
DB 216 AAGGGTTTCAGAGTCCCTGTAACTCTTCTTAATCCCTTAAGAGATGGAATATCCTCTTA 275
QY 81 PheGlnAspLeuAsnGlyInsEr 88
DB 276 TTTCAGGACTTGAAATGACAAAGT 299

RESULT 6
US-09-864-921-96
; Sequence 96, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Plo, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
```

;; TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use
;; FILE REFERENCE: P-LJ 4752
;; CURRENT APPLICATION NUMBER: US/09/864,921
;; CURRENT FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 09/579,240
;; PRIOR FILING DATE: 2000-05-24
;; PRIOR APPLICATION NUMBER: US 09/686,347
;; PRIOR FILING DATE: 2000-10-10
;; PRIOR APPLICATION NUMBER: US 60/275,980
;; PRIOR FILING DATE: 2001-03-14
;; NUMBER OF SEQ ID NOS: 195
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 96
;; LENGTH: 3396
;; TYPE: DNA
;; ORGANISM: Homo sapien
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (277)...(3348)
US-09-864-921-96

Alignment Scores:

Pred. No.:	3,01e-58	Length:	3396
Score:	461.00	Matches:	88
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-697-089-2_COPY_1_88 (1-88) x US-09-864-921-96 (1-3396)

OY 1 Metasnphelllelyspaspsnserrargalaleuileglnarqmetglymethrvalille 20
Db 277 ATGATATTTCATAAAGGACAAATAGCCGAGCCCTTATTCAAAAGATGGGAATGACTGTATA 336
OY 21 Lysglnilethrappaspheuphevaltrpansvalileuananarglucglvalasnlle 40
Db 337 AAGCAATACAGATGACCTATTGTATGATGAAATGTCGAATCGGGAAGAAAGTAAACATC 396
OY 41 Ilecygslulysvalgluglnaspalaalaarglyllellehismetilleulys 60
Db 397 ATTGCTCGAGAGAGGTGACAGATGCTGCTAGAGGATCATTCATGATTTTGAA 456
OY 61 Lysglserglusercysasnleupheulysserleulysglutrpasntyrproleu 80
Db 457 AAGGTTTCAGAGTCCCTGTACCTCTTCTTAATCCCTTAAGAGATGGAATATCCTCTA 516
OY 81 Pheglnaspleuasnglyglnser 88
Db 517 TTTCAGACTTGATGACAAAGT 540

RESULT 7

US-09-864-921-177
;; Sequence 177, Application US/09864921
;; Patent No. US20020176853A1
;; GENERAL INFORMATION:
;; APPLICANT: Reed, John C.
;; APPLICANT: Pio, Frederick F.
;; APPLICANT: Godzik, Adam
;; APPLICANT: Stehlik, Christian
;; APPLICANT: Damiano, Jason S.
;; APPLICANT: Lee, Sug-Hyung
;; APPLICANT: Oliveira, Vasco A.
;; APPLICANT: Hayashi, Hideki
;; APPLICANT: Pawlowski, Krzysztof
;; TITLE OF INVENTION: No. US20020176853A1e1 Card Domain Containing
;; FILE REFERENCE: P-LJ 4752
;; CURRENT APPLICATION NUMBER: US/09/864,921
;; CURRENT FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 09/579,240
;; PRIOR FILING DATE: 2000-05-24
;; PRIOR APPLICATION NUMBER: US 09/686,347

;; PRIOR FILING DATE: 2000-10-10
;; PRIOR APPLICATION NUMBER: US 60/275,980
;; PRIOR FILING DATE: 2001-03-14
;; NUMBER OF SEQ ID NOS: 195
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 177
;; LENGTH: 261
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (1)...(261)
US-09-864-921-177

Alignment Scores:

Pred. No.:	2,84e-59	Length:	261
Score:	457.00	Matches:	87
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	99.13%	Indels:	0
DB:	9	Gaps:	0

US-09-697-089-2_COPY_1_88 (1-88) x US-09-864-921-177 (1-261)

OY 1 Metasnphelllelyspaspsnserrargalaleuileglnarqmetglymethrvalille 20
Db 61 AAGCAATACAGATGACCTATTGTATGATGAAATGTCGAATCGGGAAGAAAGTAAACATC 120
OY 41 Ilecygslulysvalgluglnaspalaalaarglyllellehismetilleulys 60
Db 121 ATTGCTCGAGAGGTGACAGATGCTGCTAGAGGATCATTCATGATTTTGAA 180
OY 61 Lysglserglusercysasnleupheulysserleulysglutrpasntyrproleu 80
Db 181 AAGGTTTCAGAGTCCCTGTACCTCTTCTTAATCCCTTAAGAGATGGAATATCCTCTA 240
OY 81 Pheglnaspleuasnglygln 87
Db 241 TTTCAGACTTGATGACAA 261

RESULT 8

US-09-841-739-6
;; Sequence 6, Application US/09841739
;; Patent No. US20020034784A1
;; GENERAL INFORMATION:
;; APPLICANT: Berlin, John
;; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH
;; FILE REFERENCE: 07334-329001
;; CURRENT APPLICATION NUMBER: US/09/841,739
;; CURRENT FILING DATE: 2001-08-29
;; PRIOR APPLICATION NUMBER: US 09/697,089
;; PRIOR FILING DATE: 2000-10-26
;; PRIOR APPLICATION NUMBER: US 60/161,822
;; PRIOR FILING DATE: 1999-10-27
;; NUMBER OF SEQ ID NOS: 16
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 6
;; LENGTH: 3612
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-841-739-6

Alignment Scores:

Pred. No.:	1,29e-57	Length:	3612
Score:	457.00	Matches:	87
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	98.86%	Mismatches:	0
Query Match:	99.13%	Indels:	0
DB:	10	Gaps:	0

```
US-09-697-089-2_COPY_1_88 (1-88) x US-09-841-739-6 (1-3612)

QY 1 Metasnpheilelysaspsnserargalaleuileglnarqmetglymethrvalille 20
Db 418 GTGAATTTCAATAAGACAAATAGCCGACCCCTTATTCAAAAGAAATGGAAATGACGTGTATA 477

QY 21 Lysglnlethrpsaspheuphevaltrpsanvalleunanaagglugluvalasnlle 40
Db 478 AAGCAAAATCACAGATGACATATTGTATGGAATGTTCTGAAATCGCGAAGAACTAAACATC 537

QY 41 IleCysCysgluylsValgluInaspAlaalaarglyleileIleHsmetIleleuyls 60
Db 538 ATTTCGTCGCGAAGAGGTGAGACGATGCTGCTAGAGGATCATTCACATATTTTGAAA 597

QY 61 LysglysergluserCysasnleupheuleuylsSerleuylsglutrpasntyr-Proleu 80
Db 598 AAGGTTTCAGAGTCCTTAACCTCTTCTTAATAATCCCTTAAGAGGTGAAGTAACTATCCTCTA 657

QY 81 PheglnaspleuansglyInser 88
Db 658 TTTCAGGACTTGAAATGGACAAAGT 681

RESULT 9
; Sequence 4, Application US/09841739
; Patent No. US20020034784A1
; GENERAL INFORMATION:
; APPLICANT: Bertlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/09/841,739
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 3615
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3612)
; US-09-841-739-4

Alignment Scores:
Pred. No.: 1,29e-57 Length: 3615
Score: 457.00 Matches: 87
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 98.86% Mismatches: 0
Query Match: 99.13% Indels: 0
Gaps: 0

US-09-697-089-2_COPY_1_88 (1-88) x US-09-841-739-4 (1-3615)

QY 1 Metasnpheilelysaspsnserargalaleuileglnarqmetglymethrvalille 20
Db 418 GTGAATTTCAATAAGACAAATAGCCGACCCCTTATTCAAAAGAAATGGAAATGACGTGTATA 477

QY 21 Lysglnlethrpsaspheuphevaltrpsanvalleunanaagglugluvalasnlle 40
Db 478 AAGCAAAATCACAGATGACATATTGTATGGAATGTTCTGAAATCGCGAAGAACTAAACATC 537

QY 41 IleCysCysgluylsValgluInaspAlaalaarglyleileIleHsmetIleleuyls 60
Db 538 ATTTCGTCGCGAAGAGGTGAGACGATGCTGCTAGAGGATCATTCACATATTTTGAAA 597

QY 61 LysglysergluserCysasnleupheuleuylsSerleuylsglutrpasntyr-Proleu 80
Db 598 AAGGTTTCAGAGTCCTTAACCTCTTCTTAATAATCCCTTAAGAGGTGAAGTAACTATCCTCTA 657
```

```
QY 81 PheglnaspleuansglyInser 88
Db 658 TTTCAGGACTTGAAATGGACAAAGT 681

RESULT 10
; Sequence 12, Application US/09841739
; Patent No. US20020034784A1
; GENERAL INFORMATION:
; APPLICANT: Bertlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/09/841,739
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 3615
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-841-739-12

Alignment Scores:
Pred. No.: 1,29e-57 Length: 3615
Score: 457.00 Matches: 87
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 98.86% Mismatches: 0
Query Match: 99.13% Indels: 0
Gaps: 0

US-09-697-089-2_COPY_1_88 (1-88) x US-09-841-739-12 (1-3615)

QY 1 Metasnpheilelysaspsnserargalaleuileglnarqmetglymethrvalille 20
Db 3198 GTGAATTTCAATAAGACAAATAGCCGACCCCTTATTCAAAAGAAATGGAAATGACGTGTATA 3139

QY 21 Lysglnlethrpsaspheuphevaltrpsanvalleunanaargglugluvalasnlle 40
Db 3138 AAGCAATCACAGATGACCTTTTGTATGGAATGTTCTGAAATCGCGAAGAACTAAACATC 3079

QY 41 IleCysCysgluylsValgluInaspAlaalaarglyleileIleHsmetIleleuyls 60
Db 3078 ATTTCGTCGCGAAGAGGTGAGACGATGCTGCTAGAGGATCATTCACATATTTTGAAA 3019

QY 61 LysglysergluserCysasnleupheuleuylsSerleuylsglutrpasntyr-Proleu 80
Db 3018 AAGGTTTCAGAGTCCTTAACCTCTTCTTAATAATCCCTTAAGAGGTGAAGTAACTATCCTCTA 2959

QY 81 PheglnaspleuansglyInser 88
Db 2958 TTTCAGGACTTGAAATGGACAAAGT 2935

RESULT 11
; Sequence 14, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Borouhns, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREIN
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
```

Db 1218 CTGAAGGAGAGAGAGACAGTTCATCAACTCAGTCGGCATGGGGACCGCTCAACGGCTTG 1159

RESULT 14

RESULT 14

```
US-09-917-265-19/c
; Sequence 19, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Borroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265-19

Alignment Scores:
Pred. No.: 2,27e-09 Length: 526
Score: 123.50 Matches: 27
Percent Similarity: 54.88% Conservative: 18
Best Local Similarity: 32.93% Mismatches: 36
Query Match: 26.79% Indels: 1
DB: 10 Gaps: 1

US-09-697-089-2_COPY_1_88 (1-88) x US-09-917-265-19 (1-526)
QY 4 Ilelyspaspsnserrargalaleuileglargmetglymetthrvalillelysginlle 23
Db 494 CTGAAGGGCAAGAGGAGGAGCTTCATCACTCACTGCGGATGGGAGCGTCAACGGCTTG 435
QY 24 ThrAspAspleuphevalTrpasnvalleuasnarvglucluvalaenilleleCysCys 43
Db 434 CTGATGAACTCTTTGAGAAAACGTCTGACACGAGAGAGATGAGAGATAAATGT 375
QY 44 Glulysvalglu--GlnaspAlaAlaArgGlyllelleHismetilleleulyslysgly 62
Db 374 GAAACGCTACCGTTATGCAAGGCCCGAGCTGTATCGACAGCGCTCGCGGAAAGGG 315
QY 63 SerGluSerCysasnleupheulysserleulysglutrrpasnryrProleuphegln 82
Db 314 CCACGGCGGTCCAGATCTTATCTGTACATCTGTGAGAGAACCCACCTTGACAG 255
QY 83 Aspleu 84
Db 254 ACGCTG 249

RESULT 15
US-09-917-265-23
; Sequence 23, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Borroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 1230
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1230)
; OTHER INFORMATION:
```

```
US-09-917-265-23
Alignment Scores:
Pred. No.: 7.8e-09 Length: 1230
Score: 123.50 Matches: 27
Percent Similarity: 54.88% Conservative: 18
Best Local Similarity: 32.93% Mismatches: 36
Query Match: 26.79% Indels: 1
DB: 10 Gaps: 1

US-09-697-089-2_COPY_1_88 (1-88) x US-09-917-265-23 (1-1230)
QY 4 Ilelyspaspsnserrargalaleuileglargmetglymetthrvalillelysginlle 23
Db 16 CTGAAGGGCAAGAGGAGGAGCTTCATCACTCACTGCGGATGGGAGCGTCAACGGCTTG 75
QY 24 ThrAspAspleuphevalTrpasnvalleuasnarvglucluvalaenilleleCysCys 43
Db 76 CTGATGAACTCTTTGAGAAAACGTCTGACACGAGAGAGATGAGAGATAAATGT 135
QY 44 Glulysvalglu--GlnaspAlaAlaArgGlyllelleHismetilleleulyslysgly 62
Db 136 GAAACGCTACCGTTATGCAAGGCCCGAGCTGTATCGACAGCGCTCGCGGAAAGGG 195
QY 63 SerGluSerCysasnleupheulysserleulysglutrrpasnryrProleuphegln 82
Db 196 CCACGGCGGTCCAGATCTTATCTGTACATCTGTGAGAGAACCCACCTTGACAG 255
QY 83 Aspleu 84
Db 256 ACGCTG 261

Search completed: January 31, 2003, 18:05:09
Job time : 26.3692 secs
```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 31, 2003, 13:16:47 ; Search time 1119.24 Seconds
(without alignments)
1976.816 Million cell updates/sec

Title: US-09-697-089-2_COPY_1_88
Perfect score: 461
Sequence: 1 MNFKDNRRLIQMGMTVL.....FLSKLKMNYPLFDLDNGQS 88

Scoring table:
BLOSUM62
Xgapop 10.0 , Ygapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 24791104 segs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2_1/USPRO.spool/US09697089/unat_29012003_092754_19749/app_query.fasta_1.981
-DB=Pending_Patents_NA_Main -OEMT=fastcap -SUFFIX=p2n.inpm -MINMATCH=0.1
-LOORCL=0 -LOOEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blissum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFRMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09697089@cgn_1_1.3083@unat_29012003_092754_19749
-NCPU=6 -ICPU=3 -NO_XLPHY -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMECUT=120 -WARN_TIMECUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -DELOP=6 -DELEXT=7

Database :

Pending_Patents_NA_Main: *
1: /cgn2_6/ptodata/2/pna/US097A_COMB.seq: *
2: /cgn2_6/ptodata/2/pna/US06_COMB.seq: *
3: /cgn2_6/ptodata/2/pna/US07_COMB.seq: *
4: /cgn2_6/ptodata/2/pna/US08_COMB.seq: *
5: /cgn2_6/ptodata/2/pna/US081_COMB.seq: *
6: /cgn2_6/ptodata/2/pna/US082_COMB.seq: *
7: /cgn2_6/ptodata/2/pna/US083_COMB.seq: *
8: /cgn2_6/ptodata/2/pna/US084_COMB.seq: *
9: /cgn2_6/ptodata/2/pna/US085_COMB.seq: *
10: /cgn2_6/ptodata/2/pna/US086_COMB.seq: *
11: /cgn2_6/ptodata/2/pna/US087_COMB.seq: *
12: /cgn2_6/ptodata/2/pna/US088_COMB.seq: *
13: /cgn2_6/ptodata/2/pna/US089_COMB.seq: *
14: /cgn2_6/ptodata/2/pna/US090_COMB.seq: *
15: /cgn2_6/ptodata/2/pna/US091_COMB.seq: *
16: /cgn2_6/ptodata/2/pna/US092_COMB.seq: *
17: /cgn2_6/ptodata/2/pna/US093_COMB.seq: *
18: /cgn2_6/ptodata/2/pna/US094_COMB.seq: *
19: /cgn2_6/ptodata/2/pna/US095A_COMB.seq: *
20: /cgn2_6/ptodata/2/pna/US095B_COMB.seq: *
21: /cgn2_6/ptodata/2/pna/US095C_COMB.seq: *
22: /cgn2_6/ptodata/2/pna/US095D_COMB.seq: *
23: /cgn2_6/ptodata/2/pna/US096A_COMB.seq: *
24: /cgn2_6/ptodata/2/pna/US096B_COMB.seq: *
25: /cgn2_6/ptodata/2/pna/US096C_COMB.seq: *
26: /cgn2_6/ptodata/2/pna/US096D_COMB.seq: *
27: /cgn2_6/ptodata/2/pna/US096E_COMB.seq: *
28: /cgn2_6/ptodata/2/pna/US097A_COMB.seq: *

29: /cgn2_6/ptodata/2/pna/US097B_COMB.seq: *
30: /cgn2_6/ptodata/2/pna/US097C_COMB.seq: *
31: /cgn2_6/ptodata/2/pna/US098A_COMB.seq: *
32: /cgn2_6/ptodata/2/pna/US098B_COMB.seq: *
33: /cgn2_6/ptodata/2/pna/US098C_COMB.seq: *
34: /cgn2_6/ptodata/2/pna/US099A_COMB.seq: *
35: /cgn2_6/ptodata/2/pna/US099B_COMB.seq: *
36: /cgn2_6/ptodata/2/pna/US099C_COMB.seq: *
37: /cgn2_6/ptodata/2/pna/US099D_COMB.seq: *
38: /cgn2_6/ptodata/2/pna/US100A_COMB.seq: *
39: /cgn2_6/ptodata/2/pna/US100B_COMB.seq: *
40: /cgn2_6/ptodata/2/pna/US101A_COMB.seq: *
41: /cgn2_6/ptodata/2/pna/US101B_COMB.seq: *
42: /cgn2_6/ptodata/2/pna/US102A_COMB.seq: *
43: /cgn2_6/ptodata/2/pna/US102B_COMB.seq: *
44: /cgn2_6/ptodata/2/pna/US6000_COMB.seq: *
45: /cgn2_6/ptodata/2/pna/US6001_COMB.seq: *
46: /cgn2_6/ptodata/2/pna/US6002_COMB.seq: *
47: /cgn2_6/ptodata/2/pna/US6003_COMB.seq: *
48: /cgn2_6/ptodata/2/pna/US6004_COMB.seq: *
49: /cgn2_6/ptodata/2/pna/US6005_COMB.seq: *
50: /cgn2_6/ptodata/2/pna/US6006_COMB.seq: *
51: /cgn2_6/ptodata/2/pna/US6007_COMB.seq: *
52: /cgn2_6/ptodata/2/pna/US6008_COMB.seq: *
53: /cgn2_6/ptodata/2/pna/US6009_COMB.seq: *
54: /cgn2_6/ptodata/2/pna/US6010_COMB.seq: *
55: /cgn2_6/ptodata/2/pna/US6011_COMB.seq: *
56: /cgn2_6/ptodata/2/pna/US6012_COMB.seq: *
57: /cgn2_6/ptodata/2/pna/US6013_COMB.seq: *
58: /cgn2_6/ptodata/2/pna/US6014_COMB.seq: *
59: /cgn2_6/ptodata/2/pna/US6015_COMB.seq: *
60: /cgn2_6/ptodata/2/pna/US6016_COMB.seq: *
61: /cgn2_6/ptodata/2/pna/US6017_COMB.seq: *
62: /cgn2_6/ptodata/2/pna/US6018_COMB.seq: *
63: /cgn2_6/ptodata/2/pna/US6019_COMB.seq: *
64: /cgn2_6/ptodata/2/pna/US6020_COMB.seq: *
65: /cgn2_6/ptodata/2/pna/US6021_COMB.seq: *
66: /cgn2_6/ptodata/2/pna/US6022_COMB.seq: *
67: /cgn2_6/ptodata/2/pna/US6023_COMB.seq: *
68: /cgn2_6/ptodata/2/pna/US6024_COMB.seq: *
69: /cgn2_6/ptodata/2/pna/US6025_COMB.seq: *
70: /cgn2_6/ptodata/2/pna/US6026_COMB.seq: *
71: /cgn2_6/ptodata/2/pna/US6027_COMB.seq: *
72: /cgn2_6/ptodata/2/pna/US6028_COMB.seq: *
73: /cgn2_6/ptodata/2/pna/US6029_COMB.seq: *
74: /cgn2_6/ptodata/2/pna/US6030_COMB.seq: *
75: /cgn2_6/ptodata/2/pna/US6031_COMB.seq: *
76: /cgn2_6/ptodata/2/pna/US6032_COMB.seq: *
77: /cgn2_6/ptodata/2/pna/US6033_COMB.seq: *
78: /cgn2_6/ptodata/2/pna/US6034_COMB.seq: *
79: /cgn2_6/ptodata/2/pna/US6035_COMB.seq: *
80: /cgn2_6/ptodata/2/pna/US6036_COMB.seq: *
81: /cgn2_6/ptodata/2/pna/US6037_COMB.seq: *
82: /cgn2_6/ptodata/2/pna/US6038_COMB.seq: *
83: /cgn2_6/ptodata/2/pna/US6039_COMB.seq: *
84: /cgn2_6/ptodata/2/pna/US6040_COMB.seq: *
85: /cgn2_6/ptodata/2/pna/US6041_COMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Result	Score	Query Match	Length	ID	Description
1	461	100.0	578	33	US-09-864-921-100	Sequence 100, App
2	461	100.0	768	33	US-09-864-921-102	Sequence 102, App
3	461	100.0	1395	33	US-09-864-921-98	Sequence 98, App1
4	461	100.0	3072	1	PCT-US00-29643-3	Sequence 3, App1
5	461	100.0	3072	27	US-09-697-089-3	Sequence 3, App1
6	461	100.0	3072	32	US-09-841-739-3	Sequence 3, App1

7	461	100.0	3075	41	US-10-156-733-1	Sequence 1, Appl1
8	461	100.0	3133	1	PCT-US00-29643-1	Sequence 1, Appl1
9	461	100.0	3133	27	US-09-657-089-1	Sequence 1, Appl1
10	461	100.0	3133	32	US-09-841-739-1	Sequence 1, Appl1
11	461	100.0	3219	41	US-10-156-733-14	Sequence 14, Appl1
12	461	100.0	3396	33	US-09-864-921-96	Sequence 96, Appl1
13	461	100.0	3545	18	US-09-461-404-1319	Sequence 1319, Appl1
14	461	100.0	3545	34	US-09-922-279-1319	Sequence 1319, Appl1
15	461	100.0	3545	34	US-09-922-279A-1319	Sequence 1319, Appl1
16	461	100.0	6012	22	US-09-557-576-911	Sequence 911, Appl1
17	461	100.0	6012	22	US-09-557-576-917	Sequence 917, Appl1
18	461	100.0	6012	38	US-10-042-338-911	Sequence 911, Appl1
19	461	100.0	6012	38	US-10-042-338-917	Sequence 917, Appl1
20	458	99.3	3018	22	US-09-577-408-3077	Sequence 3077, Appl1
21	458	99.3	3213	1	PCT-US01-07143-23	Sequence 23, Appl1
22	458	99.3	3213	42	US-10-221-091-23	Sequence 23, Appl1
23	457	99.1	261	33	US-09-864-921-177	Sequence 177, Appl1
24	457	99.1	2343	22	US-09-578-789-15	Sequence 15, Appl1
25	457	99.1	2343	22	US-09-579-240-15	Sequence 15, Appl1
26	457	99.1	2415	22	US-09-578-789-17	Sequence 17, Appl1
27	457	99.1	2415	22	US-09-579-240-17	Sequence 17, Appl1
28	457	99.1	3260	1	PCT-US01-14826-66	Sequence 66, Appl1
29	457	99.1	3260	26	US-09-667-298-66	Sequence 66, Appl1
30	457	99.1	3612	27	US-09-657-089-6	Sequence 6, Appl1
31	457	99.1	3612	32	US-09-841-739-6	Sequence 6, Appl1
32	457	99.1	3615	1	PCT-US00-29643-4	Sequence 4, Appl1
33	457	99.1	3615	1	PCT-US00-29643-6	Sequence 6, Appl1
34	457	99.1	3615	27	US-09-657-089-4	Sequence 4, Appl1
35	457	99.1	3615	27	US-09-657-089-12	Sequence 12, Appl1
36	457	99.1	3615	32	US-09-841-739-4	Sequence 4, Appl1
37	457	99.1	3615	32	US-09-841-739-12	Sequence 12, Appl1
38	457	99.1	3890	22	US-09-577-088-7078	Sequence 3078, Appl1
39	457	99.1	6800	22	US-09-578-789-73	Sequence 73, Appl1
40	457	99.1	6900	22	US-09-579-240-73	Sequence 73, Appl1
41	457	99.1	6900	27	US-09-666-347-73	Sequence 73, Appl1
42	457	99.1	578	27	US-09-666-347-100	Sequence 100, Appl1
43	445	96.5	768	27	US-09-686-347-98	Sequence 102, Appl1
44	445	96.5	1395	27	US-09-686-347-98	Sequence 98, Appl1
45	445	96.5	3396	27	US-09-686-347-96	Sequence 96, Appl1

ALIGNMENTS

```

RESULT 1
US-09-864-921-100
: Sequence 100, Application US/09864921
: GENERAL INFORMATION:
: APPLICANT: Reed, John C.
: APPLICANT: Pio, Frederick F.
: APPLICANT: Godzik, Adam
: APPLICANT: Stehlik, Christian
: APPLICANT: Damiano, Jason S.
: APPLICANT: Lee, Sug-Hyung
: APPLICANT: Oliveira, Vasco A.
: APPLICANT: Hayashi, Hideki
: APPLICANT: Pawlowski, Krzysztof
: TITLE OF INVENTION: Novel Card Domain Containing
: TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use
: FILE REFERENCE: P-1J 4752
: CURRENT APPLICATION NUMBER: US/09/864,921
: CURRENT FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 09/579,240
: PRIOR FILING DATE: 2000-05-24
: PRIOR APPLICATION NUMBER: US 09/686,347
: PRIOR FILING DATE: 2000-10-10
: PRIOR APPLICATION NUMBER: US 60/275,980
: PRIOR FILING DATE: 2001-03-14
: NUMBER OF SEQ ID NOS: 195
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 100
: LENGTH: 578
: TYPE: DNA
: ORGANISM: Homo sapien

```

```

FEATURE:
: NAME/KEY: CDS
: LOCATION: (277)...(552)
US-09-864-921-100

Alignment Scores:
Pred. No.: 1,298-51
Score: 461.00
Percent Similarity: 100.00%
Best local Similarity: 100.00%
Query Match: 100.00%
DB: 33

US-09-697-089-2-COPY_1-88 (1-88) x US-09-864-921-100 (1-578)
Length: 578
Matches: 88
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

```

Qy	1	MetsnspellielysaspasnserftrpAlaleuileglnnrgmetglymetthValile	20
Db	277	ATGAAATTTTCATAAAGGACAAATAGCCGAGCCCTTATTCATAAAGGAAATGACTGTATA	336
Qy	21	LysglnlierthraspaspLeupheValiTrpAsnValleuAsnArgiugluValAsnile	40
Db	337	AAGCAATCACAGATGACCTTTTGTATGAAATTTCTGATCCGGAAGAAGTAAACATC	396
Qy	41	IleCysCysgsluysValGluInAspAlalaArgIyleIleHsmetIleLeuys	60
Db	397	ATTGCTCTCGAAGAGGTGACAGAGATCTCTGAGGAGATCATTCACATGATTTTGA	456
Qy	61	LysglsyerGiuserCysAsnLeupheLeuIysSerLeuIysgIutrpAsnTyrProleu	80
Db	457	AAGGTTCCAGAGTCTCTGTAACCTCTTTCTTAAATCCCTTAAGAGTAGTGAACACTATCTCTA	516
Qy	81	PheGlnAspLeuAsnGlyGlnSer	88
Db	517	TTTCAGGACTTGAAATGACAAAGT	540

RESULT 2
US-09-864-921-102
; Sequence 102, Application US/09864921

```

RESULT 2
US-09-864-921-102
; Sequence 102, Application US/09864921
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Plo, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: Novel Card Domain Containing
; TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use
; FILE REFERENCE: P-LJ 4732
; CURRENT APPLICATION NUMBER: US/09/864,921
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/666,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 102
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (277)...(744)
US-09-864-921-102

```

Alignment Scores:	
Pred. No.:	1.86e-51
Score:	461.00
Length:	766
Matches:	88

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 33 Gaps: 0

US-09-697-089-2_COPY_1_88 (1-88) x US-09-864-921-102 (1-768)

OY 1 MetasphelelyAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
DB 277 ATGAATTTTCATTAAGACAAATAGCCGAGCCCTTATTCAAGATGGAGATGACTGTATA 336
OY 21 LysGlnIleThrAspAspLeuPheValITrpAsnValIleAsnArgGluGluValAsnIle 40
DB 337 AAGCAATCACAGATGACCTATTGTATGAGATGTTCTGAATCGCGAAGATAAATACATC 396
OY 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
DB 397 ATTTGCTGCGAAGATGGAGCAGATGCTGCTTAAGAGGATCATTCACATGATTTTGA 456
OY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluITrpAsnTyrProLeu 80
DB 457 AAGGTTTCAGACTCCTGTAACTCTTTCTTAATCCCTTAAGAGTGAATATCTCTTA 516
OY 81 PheGlnAspLeuAsnGlyGlnSer 88
DB 517 TTTCAGAGCTTGAATGACAAAGT 540

RESULT 3

US-09-864-921-98
; Sequence 98, Application US/09864921

; GENERAL INFORMATION:

; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sung-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: Novel Card Domain Containing
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 1395
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (277)...(1353)
US-09-864-921-98

Alignment Scores:

Pred. No.: 4.02e-51 Length: 1395
Score: 461.00 Matches: 88
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 33 Gaps: 0

US-09-697-089-2_COPY_1_88 (1-88) x US-09-864-921-98 (1-1395)

OY 1 MetasphelelyAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20

DB 277 ATGAATTTTCATTAAGACAAATAGCCGAGCCCTTATTCAAGATGGAGATGACTGTATA 336
OY 21 LysGlnIleThrAspAspLeuPheValITrpAsnValIleAsnArgGluGluValAsnIle 40
DB 337 AAGCAATCACAGATGACCTATTGTATGAGATGTTCTGAATCGCGAAGATAAATACATC 396
OY 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
DB 397 ATTTGCTGCGAAGATGGAGCAGATGCTGCTTAAGAGGATCATTCACATGATTTTGA 456
OY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluITrpAsnTyrProLeu 80
DB 457 AAGGTTTCAGACTCCTGTAACTCTTTCTTAATCCCTTAAGAGTGAATATCTCTTA 516
OY 81 PheGlnAspLeuAsnGlyGlnSer 88
DB 517 TTTCAGAGCTTGAATGACAAAGT 540

RESULT 4

PCT-US00-29643-3
; Sequence 3, Application PC/TUS0029643

; GENERAL INFORMATION:

; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 0734-136W01
; CURRENT APPLICATION NUMBER: PCT/US00/29643
; CURRENT FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3072
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US00-29643-3

Alignment Scores:

Pred. No.: 1.11e-50 Length: 3072
Score: 461.00 Matches: 88
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-697-089-2_COPY_1_88 (1-88) x PCT-US00-29643-3 (1-3072)

OY 1 MetasphelelyAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
DB 1 ATGAATTTTCATTAAGACAAATAGCCGAGCCCTTATTCAAGATGGAGATGACTGTATA 60
OY 21 LysGlnIleThrAspAspLeuPheValITrpAsnValIleAsnArgGluGluValAsnIle 40
DB 61 AAGCAATCACAGATGACCTATTGTATGAGATGTTCTGAATCGCGAAGATAAATACATC 120
OY 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
DB 121 ATTTGCTGCGAAGATGGAGCAGATGCTGCTTAAGAGGATCATTCACATGATTTTGA 180
OY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluITrpAsnTyrProLeu 80
DB 181 AAGGTTTCAGACTCCTGTAACTCTTTCTTAATCCCTTAAGAGTGAATATCTCTTA 240
OY 81 PheGlnAspLeuAsnGlyGlnSer 88
DB 241 TTTCAGAGCTTGAATGACAAAGT 264

RESULT 5

US-09-697-089-3
; Sequence 3, Application US/09697089

; GENERAL INFORMATION:

APPLICANT: Berlin, John
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
FILE REFERENCE: 07334-136001
CURRENT APPLICATION NUMBER: US/09/697,089
CURRENT FILING DATE: 2000-10-26
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 3072
TYPE: DNA
ORGANISM: Homo sapiens
US-09-697-089-3

Alignment Scores:
Pred. No.: 1,11e-50 Length: 3072
Score: 461.00 Matches: 88
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 27 Gaps: 0

US-09-697-089-2_COPY_1_88 (1-88) x US-09-697-089-3 (1-3072)

QY 1 Metasphelleyaspasnserrargalaleuileglnarqmetglmetthrvalille 20
DB 1 ATGAATTTCAATAAGCAATAGCCGAGCCCTTTTCAATAAGGGAATACCTGTATA 60
QY 21 Lysglnlethrpsaspplleuphevalitrpasnvallleusnarqgluglvalasnlle 40
DB 61 AAGCAATACACAGATGACCTTTTGTATGGAATGTTCTGATCCGGAAGATTAACATC 120
QY 41 Ilcycscysglulysvalgluglnaspalalaargyllellelshmetilleleulys 60
DB 121 ATTGCTGCGAGAGGTGAGACAGATGCTCTAGAGGATCATTCATGATTTTGAAA 180
QY 61 Lysglsyserglusercysasnleupheleulysserleulysglutrpasntyrproleu 80
DB 181 AAGGTTTCAGAGTCTCTTACCTCTTTCTTAAATCCCTTAAGAGTGAATATCCTCTA 240
QY 81 Pheglnaspleuasnglylnser 88
DB 241 TTTCAGGACTTGAAATGACAAAGT 264

RESULT 6
US-09-841-739-3
Sequence 3, Application US/09841739
GENERAL INFORMATION:
APPLICANT: Berlin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
FILE REFERENCE: 07334-3329001
CURRENT APPLICATION NUMBER: US/09/841,739
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 09/697,089
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 3072
TYPE: DNA
ORGANISM: Homo sapiens
US-09-841-739-3

Alignment Scores:
Pred. No.: 1,11e-50 Length: 3072
Score: 461.00 Matches: 88
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
DB: 32 Gaps: 0
US-09-697-089-2_COPY_1_88 (1-88) x US-09-841-739-3 (1-3072)

QY 1 Metasphelleyaspasnserrargalaleuileglnarqmetglmetthrvalille 20
DB 1 ATGAATTTCAATAAGCAATAGCCGAGCCCTTTTCAATAAGGGAATACCTGTATA 60
QY 21 Lysglnlethrpsaspplleuphevalitrpasnvallleusnarqgluglvalasnlle 40
DB 61 AAGCAATACACAGATGACCTTTTGTATGGAATGTTCTGATCCGGAAGATTAACATC 120
QY 41 Ilcycscysglulysvalgluglnaspalalaargyllellelshmetilleleulys 60
DB 121 ATTGCTGCGAGAGGTGAGACAGATGCTCTAGAGGATCATTCATGATTTTGAAA 180
QY 61 Lysglsyserglusercysasnleupheleulysserleulysglutrpasntyrproleu 80
DB 181 AAGGTTTCAGAGTCTCTTACCTCTTTCTTAAATCCCTTAAGAGTGAATATCCTCTA 240
QY 81 Pheglnaspleuasnglylnser 88
DB 241 TTTCAGGACTTGAAATGACAAAGT 264

RESULT 7
US-10-156-733-1
Sequence 1, Application US/10156733
GENERAL INFORMATION:
APPLICANT: Alnemri, Emdad S.
TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING
FILE REFERENCE: 480140.477
CURRENT APPLICATION NUMBER: US/10/156,733
CURRENT FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 3075
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(3075)
US-10-156-733-1

Alignment Scores:
Pred. No.: 1,12e-50 Length: 3075
Score: 461.00 Matches: 88
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 41 Gaps: 0

US-09-697-089-2_COPY_1_88 (1-88) x US-10-156-733-1 (1-3075)
QY 1 Metasphelleyaspasnserrargalaleuileglnarqmetglmetthrvalille 20
DB 1 ATGAATTTCAATAAGCAATAGCCGAGCCCTTTTCAATAAGGGAATACCTGTATA 60
QY 21 Lysglnlethrpsaspplleuphevalitrpasnvallleusnarqgluglvalasnlle 40
DB 61 AAGCAATACACAGATGACCTTTTGTATGGAATGTTCTGATCCGGAAGATTAACATC 120
QY 41 Ilcycscysglulysvalgluglnaspalalaargyllellelshmetilleleulys 60
DB 121 ATTGCTGCGAGAGGTGAGACAGATGCTCTAGAGGATCATTCATGATTTTGAAA 180
QY 61 Lysglsyserglusercysasnleupheleulysserleulysglutrpasntyrproleu 80
DB 181 AAGGTTTCAGAGTCTCTTACCTCTTTCTTAAATCCCTTAAGAGTGAATATCCTCTA 240
QY 81 Pheglnaspleuasnglylnser 88

```
Db      241 TTTCAGACTGATGACAAAGT 264
|||||
RESULT 8
PCT-US00-29643-1
; Sequence 1, Application PC/TUS0029643
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-136W01
; CURRENT APPLICATION NUMBER: PCT/US00/29643
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3133
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)...(3107)
PCT-US00-29643-1

Alignment Scores:
Pred. No.:      1.14e-50      Length:      3133
Score:          461.00        Matches:      88
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%       Indels:      0
DB:             1            Gaps:         0

US-09-697-089-2_COPY_1_88 (1-88) x PCT-US00-29643-1 (1-3133)
Oy      1 MetasphelilelyAspAsnserArgAlaLeuileGlnArgMetGlyMethrValile 20
|||||
Db      36 ATGAATTTCATTAAGGACAAATAGCCGAGCCCTTATTCAAGAGATGGAGTACTCTTTATA 95
|||||
Oy      21 LysGlnIleThrAspAspleuPheValITrPAsnValLeuAsnArgGluGluValAsnIle 40
|||||
Db      96 AAGCAATACACAGATGACTATTGTATGAGATGTCTGAATCGCGAAGAGTAACATC 155
|||||
Oy      41 IleCysCysGluLysValGluGlnAspAlaIaAargGlyIleIleHisMetIleLeuLys 60
|||||
Db      156 ATTTCCTCGAGAAAGGTGAGCAGATGCTCTAGAGGAGTATTCACATGATTTTGGAA 215
|||||
Oy      61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluITrPAsnITrProLeu 80
|||||
Db      216 AAGGTTAGAGTCTCTGTAACCTCTTTCTTTAAATCCCTTAAGAGTGAATCTCTCTA 275
|||||
Oy      81 PheGlnAspleuAsnGlyGlnSer 88
|||||
Db      276 TTTCAGACTGATGACAAAGT 299
|||||

RESULT 9
US-09-697-089-1
; Sequence 1, Application US/09697089
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-136001
; CURRENT APPLICATION NUMBER: US/09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3133
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)...(3107)
US-09-697-089-1

Alignment Scores:
Pred. No.:      1.14e-50      Length:      3133
Score:          461.00        Matches:      88
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%       Indels:      0
DB:             27            Gaps:         0

US-09-697-089-2_COPY_1_88 (1-88) x US-09-697-089-1 (1-3133)
Oy      1 MetasphelilelyAspAsnserArgAlaLeuileGlnArgMetGlyMethrValile 20
|||||
Db      36 ATGAATTTCATTAAGGACAAATAGCCGAGCCCTTATTCAAGAGATGGAGTACTCTTTATA 95
|||||
Oy      21 LysGlnIleThrAspAspleuPheValITrPAsnValLeuAsnArgGluGluValAsnIle 40
|||||
Db      96 AAGCAATACACAGATGACTATTGTATGAGATGTCTGAATCGCGAAGAGTAACATC 155
|||||
Oy      41 IleCysCysGluLysValGluGlnAspAlaIaAargGlyIleIleHisMetIleLeuLys 60
|||||
Db      156 ATTTCCTCGAGAAAGGTGAGCAGATGCTCTAGAGGAGTATTCACATGATTTTGGAA 215
|||||
Oy      61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluITrPAsnITrProLeu 80
|||||
Db      216 AAGGTTAGAGTCTCTGTAACCTCTTTCTTTAAATCCCTTAAGAGTGAATCTCTCTA 275
|||||
Oy      81 PheGlnAspleuAsnGlyGlnSer 88
|||||
Db      276 TTTCAGACTGATGACAAAGT 299
|||||

RESULT 10
US-09-841-739-1
; Sequence 1, Application US/09841739
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH
; FILE REFERENCE: 07334-328001
; CURRENT APPLICATION NUMBER: US/09/841,739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3133
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)...(3107)
US-09-841-739-1

Alignment Scores:
Pred. No.:      1.14e-50      Length:      3133
Score:          461.00        Matches:      88
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%       Indels:      0
DB:             32            Gaps:         0

US-09-697-089-2_COPY_1_88 (1-88) x US-09-841-739-1 (1-3133)
Oy      1 MetasphelilelyAspAsnserArgAlaLeuileGlnArgMetGlyMethrValile 20
|||||
```

```
Db 36 ATGAATTCATTAAGACATATAGCCGACCTTATTCATTAAGATGGAATGACTGTTATA 95
Qy 21 LysglnlethrAspAspLeuPheValTrpAsnValIleuAsnArgGluGluValAsnIle 40
Db 96 AAGCAAAATCAGATGACCTTATTTGTATGAAATGTTGCAATCCGGAAGAAATTAACATC 155
Qy 41 IleCysCysGluYsValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
Db 156 ATTGCTCGAGAGAGTGAGCAGAGATGCTGTAAGAGGATCATTCACATGATTTTGAAA 215
Qy 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerIleuYsGluTrpAsnTyrProleu 80
Db 216 AAGGTTTCAGAGTCTGTGTAACCTCTTTCTTAATCCCTTAAGAGTGAAGTATCTCTTA 275
Qy 81 PheGlnAspLeuAsnGlyGlnSer 88
Db 276 TTTCAGGACTTGAAATGACAAAGT 299

RESULT 11
US-10-156-733-14
; Sequence 14, Application US/10156733
; GENERAL INFORMATION:
; APPLICANT: Alomert, Emad S.
; TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING
; FILE REFERENCE: 480140.477
; CURRENT APPLICATION NUMBER: US/10/156, 733
; CURRENT FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 3219
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-156-733-14

Alignment Scores:
Pred. No.: 1,18e-50 Length: 3219
Score: 461.00 Matches: 88
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 41 Gaps: 0

US-09-697-089-2_COPY_1_88 (1-88) x US-10-156-733-14 (1-3219)
Qy 1 MetAsnPhelIeYsAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
Db 145 ATGAATTTCAATTAAGACAAATAGCCGACCTTATTCATTAAGATGGAATGACTGTTATA 204
Qy 21 LysGlnlethrAspAspLeuPheValTrpAsnValIleuAsnArgGluGluValAsnIle 40
Db 205 AAGCAAAATCAGATGACCTTATTTGTATGAAATGTTGCAATCCGGAAGAAATTAACATC 264
Qy 41 IleCysCysGluYsValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
Db 265 ATTGCTCGAGAGAGTGAGCAGAGATGCTGTAAGAGGATCATTCACATGATTTTGAAA 324
Qy 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerIleuYsGluTrpAsnTyrProleu 80
Db 325 AAGGTTTCAGAGTCTGTGTAACCTCTTTCTTAATCCCTTAAGAGTGAAGTATCTCTTA 384
Qy 81 PheGlnAspLeuAsnGlyGlnSer 88
Db 385 TTTCAGGACTTGAAATGACAAAGT 408

RESULT 12
US-09-864-921-96
; Sequence 96, Application US/09864921
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
```

```
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: Novel Card Domain Containing
; FILE REFERENCE: P-1J 4752
; CURRENT APPLICATION NUMBER: US/09/864, 921
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579, 240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686, 347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275, 980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 3396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (277)...(3348)
US-09-864-921-96

Alignment Scores:
Pred. No.: 1,27e-50 Length: 3396
Score: 461.00 Matches: 88
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 33 Gaps: 0

US-09-697-089-2_COPY_1_88 (1-88) x US-09-864-921-96 (1-3396)
Qy 1 MetAsnPhelIeYsAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
Db 277 ATGAATTTCAATTAAGACAAATAGCCGACCTTATTCATTAAGATGGAATGACTGTTATA 336
Qy 21 LysglnlethrAspAspLeuPheValTrpAsnValIleuAsnArgGluGluValAsnIle 40
Db 337 AAGCAAAATCAGATGACCTTATTTGTATGAAATGTTGCAATCCGGAAGAAATTAACATC 396
Qy 41 IleCysCysGluYsValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
Db 397 ATTGCTCGAGAGAGTGAGCAGAGATGCTGTAAGAGGATCATTCACATGATTTTGAAA 456
Qy 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerIleuYsGluTrpAsnTyrProleu 80
Db 457 AAGGTTTCAGAGTCTGTGTAACCTCTTTCTTAATCCCTTAAGAGTGAAGTATCTCTTA 516
Qy 81 PheGlnAspLeuAsnGlyGlnSer 88
Db 517 TTTCAGGACTTGAAATGACAAAGT 540

RESULT 13
US-09-491-404-1319
; Sequence 1319, Application US/09491404
; GENERAL INFORMATION:
; APPLICANT: Tang, Yuanhua T.
; APPLICANT: Tillinghast, John
; APPLICANT: Slinku, Ankura
; APPLICANT: Liu, Chenghua
; APPLICANT: Dirmanc, Radoje T.
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE REFERENCE: 785
; CURRENT APPLICATION NUMBER: US/09/491, 404
; CURRENT FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 3796
```

```

: SOFTWARE: pl_sp_genes Version 1.0
: SEQ ID NO 1319
: LENGTH: 3545
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: sig_peptide
: LOCATION: (781)...(916)
: OTHER INFORMATION: this location contains the signal peptide sequence,
: OTHER INFORMATION: MLMGSGKCALTKRFVFFRLRSRAOGGLFTLCDLDPETIR, Run with SignalP
: OTHER INFORMATION: MLMGSGKCALTKRFVFFRLRSRAOGGLFTLCDLDPETIR, Run with SignalP
: OTHER INFORMATION: similar to g13688110 in the genepept database release 114,
: OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
US-09-431-404-1319

Alignment Scores:
Pred. No.: 1.34e-50 Length: 3545
Score: 461.00 Matches: 88
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-697-089-2_COPY_1_88 (1-88) x US-09-491-404-1319 (1-3545)

Qy 1 MetanphelelelysaPasnserrgAlaleuileglnatrgmetglymethrvalille 20
Db 232 ATGATTTTCATTAAGACAAATAGCCGACCTTATTCAAGATGGAGATGCTGTATA 291
Qy 21 LysglnlethraspaspLeupheValtrpAsnValleuAsnarGluGluValasnlle 40
Db 292 AAGCAATACACAGATGACCTATTGTATGGAATGTTCTGAATCCGGAAGATAACATC 351
Qy 41 IleCysGluLySValGluGlnAspAlaAlaArgGlylleIleHisMetIleuLyS 60
Db 352 ATTGCTCGAAGAGAGATGAGATGCTGCTAGAGGATCATTCACATGATTTTGA 411
Qy 61 LysGlySerGluSerCysAsnLeupheLeuLySserLeuLySgluTrpAsnLyProleu 80
Db 412 AAGGTTTCAAGAGTCTGTACCTCTTCTTAATCCCTTAAGAGATGGAATATCCTCTA 471
Qy 81 PheGlnAspLeuAsnGlyInser 88
Db 472 TTTCAGGACTTGATGACAAAGT 495

RESULT 14
US-09-922-279-1319
: Sequence 1319, Application US/09922279
: GENERAL INFORMATION:
: APPLICANT: Tang, Yuanhua T.
: APPLICANT: Tillinghast, John
: APPLICANT: Slinku, Ankura
: APPLICANT: Liu, Chenghua
: APPLICANT: Drmanac, Radoje T.
: TITLE OF INVENTION: Novel Contigs Obtained
: TITLE OF INVENTION: From Various Libraries
: FILE REFERENCE: 785
: CURRENT APPLICATION NUMBER: US/09/922.279
: CURRENT FILING DATE: 2001-08-03
: PRIOR APPLICATION NUMBER: 09/491,404
: PRIOR FILING DATE: 2001-01-25
: NUMBER OF SEQ ID NOS: 3796
: SOFTWARE: pl_sp_genes Version 1.0
: SEQ ID NO 1319
: LENGTH: 3545
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: sig_peptide
: LOCATION: (781)...(916)
: OTHER INFORMATION: this location contains the signal peptide sequence,
: OTHER INFORMATION: this location contains the signal peptide sequence,

: OTHER INFORMATION: MLMGSGKCALTKRFVFFRLRSRAOGGLFTLCDLDPETIR, Run with Signal
: OTHER INFORMATION: MLMGSGKCALTKRFVFFRLRSRAOGGLFTLCDLDPETIR, Run with Signal
: OTHER INFORMATION: similar to g13688110 in the genepept database release 114,
: OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
US-09-922-279-1319

Alignment Scores:
Pred. No.: 1.34e-50 Length: 3545
Score: 461.00 Matches: 88
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 34 Gaps: 0

US-09-697-089-2_COPY_1_88 (1-88) x US-09-922-279-1319 (1-3545)

Qy 1 MetanphelelelysaPasnserrgAlaleuileglnatrgmetglymethrvalille 20
Db 232 ATGATTTTCATTAAGACAAATAGCCGACCTTATTCAAGATGGAGATGCTGTATA 291
Qy 21 LysglnlethraspaspLeupheValtrpAsnValleuAsnarGluGluValasnlle 40
Db 292 AAGCAATACACAGATGACCTATTGTATGGAATGTTCTGAATCCGGAAGATAACATC 351
Qy 41 IleCysGluLySValGluGlnAspAlaAlaArgGlylleIleHisMetIleuLyS 60
Db 352 ATTGCTCGAAGAGAGATGAGATGCTGCTAGAGGATCATTCACATGATTTTGA 411
Qy 61 LysGlySerGluSerCysAsnLeupheLeuLySserLeuLySgluTrpAsnLyProleu 80
Db 412 AAGGTTTCAAGAGTCTGTACCTCTTCTTAATCCCTTAAGAGATGGAATATCCTCTA 471
Qy 81 PheGlnAspLeuAsnGlyInser 88
Db 472 TTTCAGGACTTGATGACAAAGT 495

RESULT 15
US-09-922-279A-1319
: Sequence 1319, Application US/09922279A
: GENERAL INFORMATION:
: APPLICANT: Tang, Yuanhua T.
: APPLICANT: Tillinghast, John
: APPLICANT: Slinku, Ankura
: APPLICANT: Liu, Chenghua
: APPLICANT: Drmanac, Radoje T.
: TITLE OF INVENTION: Novel Contigs Obtained
: TITLE OF INVENTION: From Various Libraries
: FILE REFERENCE: 785
: CURRENT APPLICATION NUMBER: US/09/922.279A
: CURRENT FILING DATE: 2001-08-03
: PRIOR APPLICATION NUMBER: 09/491,404
: PRIOR FILING DATE: 2000-01-25
: NUMBER OF SEQ ID NOS: 3796
: SOFTWARE: pl_sp_genes Version 1.0
: SEQ ID NO 1319
: LENGTH: 3545
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: sig_peptide
: LOCATION: (781)...(916)
: OTHER INFORMATION: this location contains the signal peptide sequence,
: OTHER INFORMATION: MLMGSGKCALTKRFVFFRLRSRAOGGLFTLCDLDPETIR, Run with Signal
: OTHER INFORMATION: MLMGSGKCALTKRFVFFRLRSRAOGGLFTLCDLDPETIR, Run with Signal
: OTHER INFORMATION: similar to g13688110 in the genepept database release 114,
: OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
US-09-922-279A-1319

Alignment Scores:
Pred. No.: 1.34e-50 Length: 3545
Score: 461.00 Matches: 88
```

Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 34

Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-09-697-089-2_COPY_1_88 (1-88) x US-09-922-279A-1319 (1-3545)

```
QY 1 MetAsnPhelIeLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 232 ATGAATTTCATAAAGCAATAGCCGAGCCCTTATTCAAAGATGGGATGACTGTATA 291
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle 40
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 292 AAGCAAAATCACAGATGACCTATTGTATGGAATGTCTGAATCGCAAGAGTAACATC 351
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 41 IleCysCysGluLysValGluGlnAspAlaIleArgGlyIleIleHisMetIleLeuLys 60
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 352 ATTTGCTGCGAGAGAGTGAGAGATGCTGCTAGAGGATCATTCACATGATTTTGAA 411
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu 80
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 412 AAGGTTTCAGAGTCTCTGTAACCTTCTTAAATCCCTTAAGAGAGTGGAACATACTCTCTA 471
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 81 PheGlnAspLeuAsnGlyGlnSer 88
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 472 TTTCAGGACTTGATGACAAAGT 495
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

Search completed: January 31, 2003, 17:55:28
Job time : 1122.24 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 31, 2003, 13:24:32 ; Search time 82.778 Seconds
(without alignments)
1295.994 Million cell updates/sec

Title: US-09-697-089-2_COPY_1_88
Perfect score: 461
Sequence: 1 MFNFKDSRALIQHMGMTVL.....FLKSLKEMWYPLFODLNGQS 88

Scoring table:
BIOSUM62
Xgapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2500250 segs, 609544256 residues
Total number of hits satisfying chosen parameters: 5000500

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+P2n.model -DEV=xlh
-O=/cgn2_1/USPFO.spool/US09697089/runat_29012003_092755_19775/app_query.fasta.1.981
-DB=Pending_Patents_NA_New -QFMT=fastap -SUFFIX=P2n.rnpn -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=Dlosum62
-TRANS-human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTPMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09697089.ecgn_1_1_91.etrnat.29012003_092755_19775
-NCPU=6 -ICPU=3 -NO_XLPHY -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONELIG
-DEV.TIMEOUT=130 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	461	100.0	3075 1 PCT-US02-21946A-1	Sequence 1, Appli
2	461	100.0	3219 1 PCT-US02-21946A-14	Sequence 14, Appli
3	461	100.0	3545 6 US-10-276-781-111	Sequence 11, Appl
4	108	23.4	1435 6 US-10-323-643-1	Sequence 1, Appli
5	103.5	22.5	429 6 US-10-276-774-1303	Sequence 1303, Ap
6	97	21.0	5059 1 PCT-US02-04915-82	Sequence 82, Appl
7	96.5	20.9	549 6 US-10-311-035-36	Sequence 36, Appl
8	93	20.2	542 5 US-09-724-676-11471	Sequence 11471, A
9	93	20.2	542 5 US-09-724-676-11471	Sequence 11471, A
10	91.5	19.8	358 5 US-09-724-676-11469	Sequence 11469, A
11	91.5	19.8	358 5 US-09-724-676A-11469	Sequence 11469, A

12	91.5	19.8	362 5	US-09-513-999C-1335	Sequence 1335, Ap
13	91.5	19.8	479 5	US-09-724-676-11470	Sequence 11470, A
14	91.5	19.8	479 5	US-09-724-676A-11470	Sequence 11470, A
15	86	18.7	2563 6	US-10-305-720-1076	Sequence 1076, Ap
16	86	18.7	2916 6	US-09-814-915A-31	Sequence 31, Appl
17	86	18.7	2916 6	US-10-240-425-1436	Sequence 1436, Ap
18	86	18.7	3076 6	US-09-814-915A-11	Sequence 11, Appl
19	75.5	16.4	8201 6	US-10-240-452-27	Sequence 27, Appl
20	75.5	16.4	8201 6	US-10-311-455-279	Sequence 279, App
21	75	16.3	1400 1	PCT-US02-18606-96	Sequence 96, Appl
22	75	16.3	1400 6	US-10-295-981-40	Sequence 40, Appl
23	75	16.3	2859 6	US-10-295-981-9	Sequence 9, Appl1
24	75	16.3	3382 6	US-10-295-981-7	Sequence 7, Appl1
25	75	16.3	4302 1	PCT-US02-38606-95	Sequence 95, Appl
26	75	16.3	4302 6	US-10-295-981-38	Sequence 38, Appl
27	75	16.3	4344 5	US-09-724-676-6860	Sequence 6860, Ap
28	75	16.3	4344 5	US-09-724-676A-6860	Sequence 6860, Ap
29	75	16.3	4373 5	US-09-724-676-6859	Sequence 6859, Ap
30	75	16.3	4373 5	US-09-724-676A-6859	Sequence 6859, Ap
31	75	16.3	4384 5	US-09-949-002-238	Sequence 238, App
32	75	16.3	4390 5	PCT-US02-38606-3	Sequence 3, Appl1
33	75	16.3	4390 5	US-09-949-002-101	Sequence 101, App
34	75	16.3	4570 5	US-09-598-075-169	Sequence 169, App
35	75	16.3	4610 1	PCT-US02-38606-11	Sequence 11, Appl
36	69.5	15.1	1320 6	US-10-123-529-5	Sequence 5, Appl1
37	69.5	15.1	1320 6	US-10-123-529-3	Sequence 3, Appl1
38	69.5	15.1	75033 6	US-10-319-915-18	GENERAL INFORMATION
39	69	15.0	4141 6	US-10-295-981-42	Sequence 42, Appl
40	66	14.3	276 5	US-09-531-113-14339	Sequence 14339, A
41	66	14.3	585 5	US-09-531-113-4197	Sequence 4197, Ap
42	65.5	14.2	473 6	US-10-203-138A-2564	Sequence 2564, Ap
43	65.5	14.2	1209 6	US-10-152-319A-1537	Sequence 1537, Ap
44	65	14.1	1470 6	US-10-295-981-27	Sequence 27, Appl
45	65	14.1	3080 1	PCT-US02-38606-94	Sequence 94, Appl

ALIGNMENTS

RESULT 1
PCT-US02-21946A-1
Sequence 1, Application PC/TUS0221946A
GENERAL INFORMATION:
APPLICANT: Thomas Jefferson University
APPLICANT: Altemari, Emdad S.
TITLE OF INVENTION: IRAF, AN ICE-PROTEASE ACTIVATING
FILE REFERENCE: 480140.477PC
CURRENT APPLICATION NUMBER: PCT/US02/21946A
CURRENT FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 3075
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(3075)
PCT-US02-21946A-1

Alignment Scores:

Pred. No.: 3.72e-54
Score: 461.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 1
Matches: 3075
Conservative: 88
Mismatches: 0
Indels: 0
Gaps: 0

US-09-697-089-2_COPY_1_88 (1-88) x PCT-US02-21946A-1 (1-3075)

QY 1 MetasphenelyletyleAspansSerArgalaletuicleginargmetcl1MetlthValile 20
DB 1 ATGATTTTCATTAAGACATATGCCAGCCCTTATTCAAGATGGATGACTGTATA 60

```

Oy      21  LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle  40
Db      61  AAGCAATACACAGATGACCTTTTGTATGAAATTTTGTGAATCCGCAAGAACTTAACATC  120
Oy      41  IleCysGsgIuLysValGluGlnAspAlaAlaArgGlyIleIleIleHsMetIleLeuLys  60
Db      121  ATTTCCTCCGAGAAAGGTGACGACGATGCTCTAGAGGATCATTCATGATGATTTTGAAA  180
Oy      61  LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu  80
Db      181  AAGGCTTCAGAGTCCCTGTAACCTCTTTCTTAAACCCCTTAAGAGAGTGGAACCTATCTCTA  240
Oy      81  PheGlnAspLeuAsnGlyGlnSer  88
Db      241  TTTGAGGACTTGAAATGGACAAAGT  264

RESULT 2
PCT-US02-21946A-14
; Sequence 14, Application PC/TUS0221946A
; GENERAL INFORMATION:
; APPLICANT: Thomas Jefferson University
; APPLICANT: Ahmedti, Emad S.
; TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING
; TITLE OF INVENTION: FACTOR
; FILE REFERENCE: 480140.477PC
; CURRENT APPLICATION NUMBER: PCT/US02/21946A
; CURRENT FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 3219
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-21946A-14

Alignment Scores:
Pred. NO.:      3,95e-54      Length:      3219
Score:          461.00      Matches:      88
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:              1      Gaps:      0

US-09-697-089-2_COPY_1_88 (1-88) x PCT-US02-21946A-14 (1-3219)

Oy      1  MetAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle  20
Db      145  ATGAATTTCATTAAGAGCAATAATGCGACCCCTTATTCAAAGAAAGGGAATGACTGTATA  204
Oy      21  LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle  40
Db      205  AAGCAATACACAGATGACCTATTGTGTATGGAATGTTGTGAATCCGCAAGAACTTAACATC  264
Oy      41  IleCysGsgIuLysValGluGlnAspAlaAlaArgGlyIleIleIleHsMetIleLeuLys  60
Db      265  ATTTCCTCCGAGAAAGGTGACGACGATGCTCTAGAGGATCATTCATGATGATTTTGAAA  324
Oy      61  LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu  80
Db      325  AAGGCTTCAGAGTCTCTGTAACCTCTTTCTTAAACCCCTTAAGAGAGTGGAACCTATCTCTA  384
Oy      81  PheGlnAspLeuAsnGlyGlnSer  88
Db      385  TTTGAGGACTTGAAATGGACAAAGT  408

RESULT 3
US-10-276-781-111
; Sequence 111, Application US/10276781
; GENERAL INFORMATION:
; APPLICANT: Hysed, Inc.
; APPLICANT: Tang et al.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides

```

```

: FILE REFERENCE: 21272-018 (785 contig)
: CURRENT APPLICATION NUMBER: US/10/276,781
: CURRENT FILING DATE: 2002-11-18
: PRIOR APPLICATION NUMBER: 09/491,404
: PRIOR FILING DATE: 2000-01-25
: NUMBER OF SEQ ID NOS: 2018
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 111
: LENGTH: 3545
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-276-781-111

Alignment Scores:
Pred. NO.:
Score: 4.47e-54 Length: 3545
Percent Similarity: 461.00 Matches: 88
Best Local Similarity: 100.00% Conservative: 0
Query Match: 100.00% Mismatches: 0
DB: Indels: 0
Gaps: 0

US-09-697-089-2_COPY_1_88 (1-88) x US-10-276-781-111 (1-3545)

Oy 1 MetanpellellyrsaspsnsrArqhlaleullelgnArqmetGlymetThrValile 20
Db 232 ATGATTTTCATTAAGGACCAATATGCGACCCCTTTTCATCAAAATAGGATATACGTATATA 293
Oy 21 LysglnlerrhAspAspLeuPheValITrpAsnValleuAsnArqgluGluValAsnIle 40
Db 292 AAGCAAAATCACAGATGACCTTATGTAATGTAATGTCGTGATCCGAAAGTAAATCATC 351
Oy 41 IleCysCysGluValysValGluGlnAspAlaIlaArqgylIleIleHsmetIleLeuLys 60
Db 332 ATTTCCTCGAGAAAGGTGACAGAGATCTCTAGAGGATCATTCACATGATTTGAAA 411
Oy 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu 80
Db 412 AAGGTCCTCAGAGCTCTGTAACTCTTCTTAAATCCCTTAAGAGTGAGTGAACACTATCTCTA 473
Oy 81 PheGlnAspLeuAsnGlyGlnSer 88
Db 472 TTTCAGGACTTGAAATGGACAAAGT 495

RESULT 4
US-10-323-643-1
: Sequence 1, Application US/10323643
: GENERAL INFORMATION:
: APPLICANT: He, et al.
: TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1
: FILE REFERENCE: PFI65PIDI
: CURRENT APPLICATION NUMBER: US/10/323,643
: CURRENT FILING DATE: 2002-12-20
: PRIOR APPLICATION NUMBER: 08/464,588
: PRIOR FILING DATE: 1995-06-05
: PRIOR APPLICATION NUMBER: PCT/US95/05922
: PRIOR FILING DATE: 1995-05-11
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 1
: LENGTH: 1435
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (10)..(1326)
: OTHER INFORMATION:
US-10-323-643-1

Alignment Scores:
Pred. NO.: 4.19e-05 Length: 1435
Score: 108.00 Matches: 29
Percent Similarity: 58.33% Conservative: 20
Best Local Similarity: 34.52% Mismatches: 33

```

```

Query Match:      23.43%      Indels:      2
DB:               6           Gaps:         1

US-09-697-089-2_COPY_1_88 (1-88) x US-10-323-643-1 (1-1435)

QY 1 Metaspheilelyaspasnserrargalaleuileglnargmetglymethrvalille 20
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 841 TTGTCATTAATTCGGAAGACAGATGCGTCTCTTCAACAA-----TTGACATGTGTG 894
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 21 Lysglnilethrraspaspleuphevaltrpaspnvalileuasnaraglgluvalasnlle 40
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 895 CTTCCTATCCGATTAACCTTTTAAAGCCCAATGTAATTAATAACAGACATGATAT 954
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 41 Illecysgsluylsvalgluglnaspalaalargglyllelelshmetlleleuyls 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 955 ATTAACAAACAAACACACATACCTTTACACGAGAGACATGATGATACCATTTTGGTT 1014
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 LysglserrglusercysasnleupheleuylsSerleuylsGluTrpAsnTrpProleu 80
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1015 AAAGAAATGCTGGGCGCAACATCTTCAAAAACGTCTTAAAGAAATTGACTCTACATTG 1074
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 81 Pheglinspleu 84
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1075 TATAAGAACTTA 1086
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
US-10-276-774-1303
; Sequence 1303, Application US/10276774
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 1303
; LENGTH: 429
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-774-1303

Alignment Scores:
Pred. No.:      3,78e-05      Length:      429
Score:          103.50      Matches:      21
Percent Similarity: 59.02%      Conservative: 15
Best Local Similarity: 34.43%      Mismatches: 24
Query Match:    22.45%      Indels:      1
DB:             6           Gaps:         1

US-09-697-089-2_COPY_1_88 (1-88) x US-10-276-774-1303 (1-1429)

QY 9 Argalaleuileglnargmetglymethrvalillelysglnilethraspspleu 28
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 230 CGGCTGCTTATCAATTCATTGCGTGAAGTACAATAATGCTTACTGAGATGATATTG 289
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 29 Valtrpaspnvalileuasnaraglgluvalasnllelellecyscysgluylvalglu 48
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 290 GAGACAAATGCTGAGCGCAGAACACAGATAGTAATAATGGAATAATGACACTT 349
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 49 ---Aspalaalargglyllelelshmetlleleuylslysglserrglusercysasn 67
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 350 ATCATTAAGCGCCGAGATTGCTGTGACTCTGTATTTCGAAAGGGCGACGGGCAATGTA 409
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 68 Leu 68
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 410 ATT 412

```

```

RESULT 6
PCT-US02-04915-82
; Sequence 82, Application PC/TUS0204915
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynn, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
; FILE REFERENCE: 018501-006200PC
; CURRENT APPLICATION NUMBER: PCT/US02/04915
; CURRENT FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 09/784,356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/791,390
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/285,475
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/310,025
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/334,244
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 5059
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-04915-82

Alignment Scores:
Pred. No.:      0.00738      Length:      5059
Score:          97.00      Matches:      24
Percent Similarity: 52.05%      Conservative: 14
Best Local Similarity: 32.88%      Mismatches: 33
Query Match:    21.04%      Indels:      2
DB:             1           Gaps:         1

US-09-697-089-2_COPY_1_88 (1-88) x PCT-US02-04915-82 (1-5059)

QY 3 Pheilelyaspasnserrargalaleuileglnargmetglymethrvalillelysgln 22
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1352 TTTGTGAAGAGAAACACCGCACTCCAAAGCCAGATGGG-----GACCTGAAGAG 1405
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 23 Iletrraspaspleuphevaltrpaspnvalileuasnaraglgluvalasnllelellecys 42
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1406 GTGCTGATGATCTCCAGACATGAGGTCTTACTGAGAAATGAGAGAGAGCTGTGGAG 1465
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 43 Cysgluylsvalgluglnaspalaalargglyllelelshmetlleleuylslysgly 62
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1466 CAGAAAAGACACGCGCAGACAGAAATGAGCGCTTGTGAGCATGTGGAAGAAAGGG 1525
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 63 SerglusercysasnleupheleuylsSerleuylsGlu 75
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1526 GACCTGGCCCTGAGCTGCTCTTCAAGAACATTAAGTAA 1564
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
US-10-311-035-36
; Sequence 36, Application US/10311035
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YUE, Henry
; APPLICANT: ELIOTT, Vicki
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: LAU, Preeti
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: DELEGEANE, Angelo M.
; APPLICANT: BAUGHN, Mariah R.

```



```
Oy 4 IlelyaspasnserrargAlaleuileglnArgmetGlymetThrValIlelysglnile 23
Db 63 CTGAAGGAGAAAGAAACCTGTTTATCCATTCATGGGTGAAGGATCAATAAATGCGCTTA 122
Oy 24 ThrAspAspLeuPheValITrPAsnValIleuAsnArgGluGluValAsnIleIlecyScys 43
Db 123 CTGATGTAATTTATACACAACAAGGCTGTAACCAAGAAAGATG----- 167
Oy 44 GluLySValGluGln-----AspAlaIleArgGlyIleIleHisMet 57
Db 168 GAGAAAGTAAACGTAATAATGCTACAGTATAGACCCGAGCTTGTGATGACTCC 227
Oy 58 IleleuLySgLySerGluSerCysAsnLeuPheLeuLySserLeuLySglu----- 75
Db 228 GTTATTCGAAAGGGGACACAGGATGCCAAATTTCATCACAATTTGTGAAGAAGAC 287
Oy 76 -----TrpAsnTyPProleu 80
Db 288 AGTTACCTGGCAGGACCGCTGGACTCTCAGCAGATCAACATCTGGAATTAACCTTAAT 347
Oy 81 PheGlnAspLeuAsnGly 86
Db 348 ATGCAAGACTCTCAAGGA 365

RESULT 10
US-09-724-676-11469
; Sequence 11469, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724.676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11469
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: n is a,c,g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (324)..(324)
; OTHER INFORMATION: n is a,c,g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (333)..(333)
; OTHER INFORMATION: n is a,c,g, or t
US-09-724-676-11469

Alignment Scores:
Pred. No.: 0.00144 Length: 358
Score: 91.50 Matches: 22
Percent Similarity: 51.28% Conserved: 18
Best Local Similarity: 28.21% Mismatches: 27
Query Match: 19.85% Indels: 11
Gaps: 2

US-09-697-089-2_COPY_1_88 (1-88) x US-09-724-676-11469 (1-358)
Oy 4 IlelyaspasnserrargAlaleuileglnArgmetGlymetThrValIlelysglnile 23
Db 63 CTGAAGGAGAAAGAAACCTGTTTATCCATTCATGGGTGAAGGATCAATAAATGCGCTTA 122
Oy 24 ThrAspAspLeuPheValITrPAsnValIleuAsnArgGluGluValAsnIleIlecyScys 43
Db 123 CTGATGTAATTTATACACAACAAGGCTGTAACCAAGAAAGATG----- 167
Oy 44 GluLySValGluGln-----AspAlaIleArgGlyIleIleHisMet 57
Db 168 GAGAAAGTAAACGTAATAATGCTACAGTATAGACCCGAGCTTGTGATGACTCC 227
Oy 58 IleleuLySgLySerGluSerCysAsnLeuPheLeuLySserLeuLySglu----- 75
Db 228 GTTATTCGAAAGGGGACACAGGATGCCAAATTTCATCACAATTTGTGAAGAAGAC 287
Oy 76 -----TrpAsnTyPProleu 80
Db 288 AGTTACCTGGCAGGACCGCTGGACTCTCAGCAGATCAACATCTGGAATTAACCTTAAT 347
Oy 81 PheGlnAspLeuAsnGly 86
Db 348 ATGCAAGACTCTCAAGGA 365

RESULT 10
US-09-724-676-11469
; Sequence 11469, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724.676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11469
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (324)..(324)
; OTHER INFORMATION: n is a,c,g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (333)..(333)
; OTHER INFORMATION: n is a,c,g, or t
US-09-724-676-11469

Alignment Scores:
Pred. No.: 0.00144 Length: 358
Score: 91.50 Matches: 22
Percent Similarity: 51.28% Conserved: 18
Best Local Similarity: 28.21% Mismatches: 27
Query Match: 19.85% Indels: 11
Gaps: 2

US-09-697-089-2_COPY_1_88 (1-88) x US-09-724-676-11469 (1-358)
Oy 4 IlelyaspasnserrargAlaleuileglnArgmetGlymetThrValIlelysglnile 23
Db 63 CTGAAGGAGAAAGAAACCTGTTTATCCATTCATGGGTGAAGGATCAATAAATGCGCTTA 122
Oy 24 ThrAspAspLeuPheValITrPAsnValIleuAsnArgGluGluValAsnIleIlecyScys 43
Db 123 CTGATGTAATTTATACACAACAAGGCTGTAACCAAGAAAGATG----- 167
Oy 44 GluLySValGluGln-----AspAlaIleArgGlyIleIleHisMet 57
Db 168 GAGAAAGTAAACGTAATAATGCTACAGTATAGACCCGAGCTTGTGATGACTCC 227
Oy 58 IleleuLySgLySerGluSerCysAsnLeuPheLeuLySserLeuLySglu----- 75
Db 228 GTTATTCGAAAGGGGACACAGGATGCCAAATTTCATCACAATTTGTGAAGAAGAC 281
```

```
Db 168 GAGAAAGTAAACGTAATAATGCTACAGTATAGACCCGAGCTTGTGATGACTCC 227
Oy 58 IleleuLySgLySerGluSerCysAsnLeuPheLeuLySserLeuLySglu 75
Db 228 GTTATTCGAAAGGGGACACAGGATGCCAAATTTCATCACAATTTGTGAA 281

RESULT 11
US-09-724-676A-11469
; Sequence 11469, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724.676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11469
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: n is a,c,g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (324)..(324)
; OTHER INFORMATION: n is a,c,g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (333)..(333)
; OTHER INFORMATION: n is a,c,g, or t
US-09-724-676A-11469

Alignment Scores:
Pred. No.: 0.00144 Length: 358
Score: 91.50 Matches: 22
Percent Similarity: 51.28% Conserved: 18
Best Local Similarity: 28.21% Mismatches: 27
Query Match: 19.85% Indels: 11
Gaps: 2

US-09-697-089-2_COPY_1_88 (1-88) x US-09-724-676A-11469 (1-358)
Oy 4 IlelyaspasnserrargAlaleuileglnArgmetGlymetThrValIlelysglnile 23
Db 63 CTGAAGGAGAAAGAAACCTGTTTATCCATTCATGGGTGAAGGATCAATAAATGCGCTTA 122
Oy 24 ThrAspAspLeuPheValITrPAsnValIleuAsnArgGluGluValAsnIleIlecyScys 43
Db 123 CTGATGTAATTTATACACAACAAGGCTGTAACCAAGAAAGATG----- 167
Oy 44 GluLySValGluGln-----AspAlaIleArgGlyIleIleHisMet 57
Db 168 GAGAAAGTAAACGTAATAATGCTACAGTATAGACCCGAGCTTGTGATGACTCC 227
Oy 58 IleleuLySgLySerGluSerCysAsnLeuPheLeuLySserLeuLySglu 75
Db 228 GTTATTCGAAAGGGGACACAGGATGCCAAATTTCATCACAATTTGTGAA 281

RESULT 12
US-09-513-999C-1335
; Sequence 1335, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J. B.
; APPLICANT: Ductert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59. US2. REG
; CURRENT APPLICATION NUMBER: US/09/513.999C
; CURRENT FILING DATE: 2000-02-24
```

```

; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 1335
; LENGTH: 362
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 45..362
; US-09-513-999C-1335

Alignment Scores:
Pred. No.: 0.00146 Length: 362
Score: 91.50 Matches: 22
Percent Similarity: 51.28% Conservative: 18
Best Local Similarity: 28.21% Mismatches: 27
Query Match: 19.85% Indels: 11
DB: Gaps: 2

US-09-697-089-2_COPY_1_88 (1-88) x US-09-513-999C-1335 (1-362)
QY 4 Illelyspasnserrargalaleuileglnargmetglymetrrvallileysglnile 23
DB 60 CTGAAGGAGAAAGAGAAAGCTGTTATCCATTCATGGGTGAAGGTACAAATGAATGCTTA 119
QY 24 ThrAspAspleuphevalITrpAsnValleuAsnArgGluGluValAsnIleIleCysCys 43
DB 120 CTGATGATCATTTATTACAGACAAAGGCTCTGACACGAGAGAGATG----- 164
QY 44 GluLysValGluGln-----AspAlaIlaArgGlyIleIleHisMet 57
DB 165 GAGAAAGTAAAGCTGAAATGCTACAGTTATGATTAAGACCCGAGCTTGATGACTCC 224
QY 58 IlleuLysGlySerGlySerGlySerCysAsnLeuPheLeuLysSerLeuLysGln 75
DB 225 GTTATTCGAAAGGCGACAGGCAATGTCCTGCAATTTGCATCATCATATTGTGAA 278

RESULT 13
US-09-724-676-11470
; Sequence 11470, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 11470
; LENGTH: 479
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: n is a,c,g, or t
; US-09-724-676-11470

Alignment Scores:
Pred. No.: 0.0021 Length: 479
Score: 91.50 Matches: 22
Percent Similarity: 51.28% Conservative: 18
Best Local Similarity: 28.21% Mismatches: 27
Query Match: 19.85% Indels: 11
DB: Gaps: 2

US-09-697-089-2_COPY_1_88 (1-88) x US-09-724-676-11470 (1-479)
QY 4 Illelyspasnserrargalaleuileglnargmetglymetrrvallileysglnile 23
DB 63 CTGAAGGAGAAAGAGAAAGCTGTTATTCATTCATGGGTGAAGGTACAAATGAATGCTTA 122
QY 24 ThrAspAspleuphevalITrpAsnValleuAsnArgGluGluValAsnIleIleCysCys 43
DB 123 CTGATGATCATTTATTACAGACAAAGGCTCTGAAACGAGAGAGATG----- 167
QY 44 GluLysValGluGln-----AspAlaIlaArgGlyIleIleHisMet 57
DB 168 GAGAAAGTAAAGCTGAAATGCTACAGTTATGATTAAGACCCGAGCTTGATGACTCC 227
QY 58 IlleuLysGlySerGlySerGlySerCysAsnLeuPheLeuLysSerLeuLysGln 75
DB 228 GTTATTCGAAAGGCGACAGGCAATGTCCTGCAATTTGCATCATCATATTGTGAA 281

RESULT 15
US-10-305-720-1076
; Sequence 1076, Application US/10305720
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Sellhame, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expres
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
```

```

QY 24 ThrAspAspleuphevalITrpAsnValleuAsnArgGluGluValAsnIleIleCysCys 43
DB 123 CTGATGATCATTTATTACAGACAAAGGCTCTGAAACGAGAGAGATG----- 167
QY 44 GluLysValGluGln-----AspAlaIlaArgGlyIleIleHisMet 57
DB 168 GAGAAAGTAAAGCTGAAATGCTACAGTTATGATTAAGACCCGAGCTTGATGACTCC 227
QY 58 IlleuLysGlySerGlySerGlySerCysAsnLeuPheLeuLysSerLeuLysGln 75
DB 228 GTTATTCGAAAGGCGACAGGCAATGTCCTGCAATTTGCATCATCATATTGTGAA 281

RESULT 14
US-09-724-676A-11470
; Sequence 11470, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 11470
; LENGTH: 479
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: n is a,c,g, or t
; US-09-724-676A-11470

Alignment Scores:
Pred. No.: 0.0021 Length: 479
Score: 91.50 Matches: 22
Percent Similarity: 51.28% Conservative: 18
Best Local Similarity: 28.21% Mismatches: 27
Query Match: 19.85% Indels: 11
DB: Gaps: 2

US-09-697-089-2_COPY_1_88 (1-88) x US-09-724-676A-11470 (1-479)
QY 4 Illelyspasnserrargalaleuileglnargmetglymetrrvallileysglnile 23
DB 63 CTGAAGGAGAAAGAGAAAGCTGTTATTCATTCATGGGTGAAGGTACAAATGAATGCTTA 122
QY 24 ThrAspAspleuphevalITrpAsnValleuAsnArgGluGluValAsnIleIleCysCys 43
DB 123 CTGATGATCATTTATTACAGACAAAGGCTCTGAAACGAGAGAGATG----- 167
QY 44 GluLysValGluGln-----AspAlaIlaArgGlyIleIleHisMet 57
DB 168 GAGAAAGTAAAGCTGAAATGCTACAGTTATGATTAAGACCCGAGCTTGATGACTCC 227
QY 58 IlleuLysGlySerGlySerGlySerCysAsnLeuPheLeuLysSerLeuLysGln 75
DB 228 GTTATTCGAAAGGCGACAGGCAATGTCCTGCAATTTGCATCATCATATTGTGAA 281
```

```

: SEQ ID NO 1076
: LENGTH: 2563
:
: TYPE: DNA
: ORGANISM: Homo sapiens
:
: FEATURE:
: NAME/KEY: misc. feature
:
: OTHER INFORMATION: GenBank ID No: g1160974
US-10-305-720-1076

```


GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 31, 2003, 11:41:11 ; Search time 2366.19 Seconds
(without alignments)
2004.811 Million cell updates/sec

Title: US-09-697-089-2_COPY_161_323`
Sequence: 1 LOSPCITEGSGCKSKTLLQ.....SAQALIREVLIKEALGILL 163

Scoring table:
BIOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 segs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame.p2n.model DEV=rlh
-Q=/cgn2_1/USPTO.spool/US09697089/runat_29012003_092753_19716/app_query.fasta_1.981
-DB=GenEmbl -OFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCTL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=Dlosum62 -TRANS=human40.cdi -LIST=45
-DOCLALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09697089_6CGN_1_1_3568_etunat_29012003_092753_19716 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_dat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_man:*
37: em_htg_vrl:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	829	100.0	891	6 AX318174	AX318174 Sequence
2	829	100.0	3133	9 AY032589	AY032589 Homo sapi
3	829	100.0	3219	9 AY035391	AY035391 Homo sapi
4	829	100.0	3355	9 AK095467	AK095467 Homo sapi
5	829	100.0	3360	9 BC031555	BC031555 Homo sapi
6	829	100.0	3396	6 AX318091	AX318091 Sequence
7	829	100.0	3366	9 AY027787	AY027787 Homo sapi
8	829	100.0	3581	9 AF376061	AF376061 Homo sapi
9	829	100.0	138909	9 CNS01DS3	AL1321653 BAC seque
10	829	100.0	160583	2 AC010968	AC010968 Homo sapi
11	623	75.2	185469	2 AC101793	AC101793 Mus muscu
12	236.5	28.5	4013	9 AB048534	AB048534 Homo sapi
13	236.5	28.5	5366	6 E23944	E23944 Apoptosis-1
14	236.5	28.5	5366	6 E24990	E24990 Apoptosis-1
15	236.5	28.5	5502	6 E23943	E23943 Excessive o
16	236.5	28.5	5984	6 E23943	E23943 Excessive o
17	236.5	28.5	5984	6 E24989	E24989 Apoptosis-1
18	236.5	28.5	5984	6 E38321	E38321 Monoclonal
19	236.5	28.5	6124	6 A64529	A64529 Sequence 21
20	236.5	28.5	6124	6 AX335820	AX335820 Sequence
21	236.5	28.5	6124	9 HSU19251	U19251 Homo sapien
22	236.5	28.5	6133	6 A64530	A64530 Sequence 2
23	236.5	28.5	6228	6 A64531	A64531 Sequence 23
24	236.5	28.5	82976	9 AC005031	AC005031 Homo sapi
25	236.5	28.5	131078	9 HSU80017	U80017 Homo sapien
26	236.5	28.5	155306	2 AC010272	AC010272 Homo sapi
27	236.5	28.5	155308	2 AC109487	AC109487 Homo sapi
28	236.5	28.5	155809	2 AC012369	AC012369 Homo sapi
29	236.5	28.5	155974	9 AC022119	AC022119 Homo sapi
30	236.5	28.5	168814	9 AC010237	AC010237 Homo sapi
31	235.5	28.4	190871	9 AC044797	AC044797 Homo sapi
32	225.5	27.2	716	9 HSNAP1	U1913 Homo sapien
33	220.5	26.6	6829	10 AF135494	AF135494 Mus muscu
34	220.5	26.6	117791	10 AF242431S1	AF242431 Mus muscu
35	220.5	26.6	168388	2 AC118378	AC118378 Rattus no
36	220.5	26.6	206808	2 AC093971	AC093971 Rattus no
37	219.5	26.5	41613	10 AF242433S1	AF242433 Mus muscu
38	216.5	26.1	4752	10 AF135490	AF135490 Mus muscu
39	216.5	26.1	4815	10 AF102871	AF102871 Mus muscu
40	216.5	26.1	4823	10 AF135489	AF135489 Mus muscu
41	216	26.1	5497	10 AF007769	AF007769 Mus muscu
42	216	26.1	90650	10 AF242432	AF242432 Mus muscu
43	216	26.0	1554	2 AC116741	AC116741 Mus muscu
44	215.5	26.0	1554	10 AF361881	AF361881 Rattus no
45	215.5	26.0	179252	10 AF131205	AF131205 Mus muscu

RESULT 1

ALIGNMENTS

AX318174	LOCUS	AX318174	891 bp	DNA	linear	PAT 14-DEC-2001
DEFINITION	Sequence 179 from Patent WO0190156.					
ACCESSION	AX318174					
VERSION	AX318174.1	GI:17900865				
KEYWORDS	.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
AUTHORS	1 Reed,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H., Oliveira,V.A., Hayashi,H. and Pawlowski,K.					
TITLE	Catd domain containing polypeptides, encoding nucleic acids, and methods of use					
JOURNAL	Patent: WO 0190156-A 179 29-NOV-2001; The Burnham Institute (US)					
FEATURES	location/Qualifiers					
source	1..891					
	/organism="Homo sapiens"					
	/db_xref="taxon:9606"					
	<1..>891					
CDS	/note="unnamed protein product"					
	/codon_start=1					
	/protein_id="CAD19350.1"					
	/db_xref="GI:17900866"					
	/translation="LQSPCTIEGSEGGKSTLLQRIAMLWGSKKALTRKKFYELRLSRKQGLFETICQPLDIPCTIRKQPMMLLKLRLRVFLPDGYNDRPNPELEIALLENHREKMWLVITTECLRIHTRFGALITAVGMDTESDALIREVLKELAGLLIQKSRCLRLNMLKTPLEVITACIQOMGSEPHSHQTLFFPYDLIQKKHRRKGVASDPFRSLDRGDLGEGVFSHKRFEDELQVSSVNEDEVLLTTGDKYTAORRKKPKYKFFKSPQETAYAGRRLSS"					
BASE COUNT	237 a 228 c 217 g 209 t					
ORIGIN						
Alignment Scores:						
Pred. No. :	1,87e-92	Length:	891			
Score:	829..00	Matches:	163			
Percent Similarity:	100..00%	Conservative:	0			
Best local Similarity:	100..00%	Mismatches:	0			
Query Match:	100..00%	Indels:	0			
DB:	6	Gaps:	0			
US-09-697-089-2_COPY_161_323 (1-163) x AX318174 (1-891)						
OY	1	LeuGInSerProCysAlIleIleGluGlyUsErGlyLySgLyLysSerThrLeuEngIn	20			
Db	1	CTTCAGAGGCCCTGCATCATTTGAAGGGAAATGTGGCAAAAGCAAGTCCACTCTGCTGCAG	60			
OY	21	ArgIleAlaMetLeuTrpGlySerGlyCysLySAlaLeuThrLysPheLysPheVal	40			
Db	61	CGCATTTGCCATCTCTGGGGGCTCGGAAAGTCCAAAGGCTCTGACCAGATTCAAAATTCGTC	120			
OY	41	PhePheLeuArgLeuSerArgAlaGInGlyLyLeuPheGluThrLeuCysAspGInLeu	60			
Db	121	TTCCTTCCTCCGCTCTCAGCAGGGGCCAGGCTGACATTTTGAANAACCTCTGTATCAACTC	180			
OY	61	LeuAspIleProGlyThrIleArgLySgInThrPheMetAlaMetLeuLeuLySLeuArg	80			
Db	181	CTGGATATACCTCGGCACAATCAGAAAGCAGACATTCATGCGCATGCTGCTGAAGCTGGCG	240			
OY	81	GInArgValLeuPheLeuLeuAspGlyTrpAsnGluPheLySProGInAsnGlyProGlu	100			
Db	241	CAGAGGGTCTTTCTTCCTTCCTTCATGATGACTACAAATTCACCCCAAGAACTGCCAGAA	300			
OY	101	IleGluAlaLeuIleLySgInAsnHisArgPheLySAsnMetValIleValThrThrThr	120			
Db	301	ATCGAAGCCCTGATATAAGGAAAAACCCGCTTCAGAAACATGCTCATGCTACCACTACC	360			
OY	121	ThrGluCysLeuArgHisIleArgGInPheGlyAlaLeuThrAlaGluValGlyAspMet	140			
Db	361	ACTGATGTGCTCAGAGCACATACGCGAGTTGTTGTCCTGCATGCTGACGAGTGCGGATATAG	420			

[illegible]

Score: 829.00 Matches: 163
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-697-089-2_COPY_161_323 (1-163) x AY032589 (1-3133)

```
QY 1 LeuGlnSerProCysIleIleGluGlyGluSerGlyGlySerThrLeuGln 20
DB 516 CTTGAGAGCCCTGCATCATATTGAAGGGGAATCTGGCAAGCAAGTCCACTCTGCTGCAG 575
QY 21 ArgIleAlaMetLeuTyrGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
DB 576 CGCATTTGCATGCTCTGGGGCTCCGGAAAGTCAAGGCTCGACCAATTCAAATTCCTC 635
QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLysLeuPheGluThrLeuCysAspGlnLeu 60
DB 636 TTCTTCCCTCCCTCAGAGGGCCAGGGGTGACTTTTGAACCCCTCTGATCACTC 695
QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 80
DB 696 CTGATATACCTGGACACATACGAGACGACATTCATGCCATCTGCTGAAGCTGGCG 755
QY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 100
DB 756 CAGAGGGTCTTTTCCCTCTTGATGGCTACAAATGAAATTCAGCCCAAGTCCGCCAGAA 815
QY 101 IleguAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValIThrThr 120
DB 816 ATCGAAGCCCTGATAAAGAAACCCAGCTTCAAGAACATGATGTCACCCACTACC 875
QY 121 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140
DB 876 ACTGATGCTCCCTGAGGACATACGAGAGTGTGGTCCCTGACTGCTGAGAGTGGGGATATG 935
QY 141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 160
DB 936 ACAGAAGACAGCGCCAGGCTCTCATCCGAAAGTCTGATCAAGAGACTTGTCTGAAGC 995
QY 161 LeuLeuLeu 163
DB 996 TTGTTGCTC 1004

RESULT 3
LOCUS AY035391 3219 bp mRNA linear PRI 24-JUL-2001
DEFINITION Homo sapiens ICE-protease activating factor mRNA, complete cds.
ACCESSION AY035391
VERSION AY035391.1 GI:14334214
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Poyet,J.L., Srinivasula,S.M., Thani,M., Razmaza,M.,
Fernandes-Alnemri,T. and Alnemri,E.S.
Identification of Ipa1, a human caspase-1-activating protein
related to Araf-1
J. Biol. Chem. 276 (30), 28309-28313 (2001)
TITLE
JOURNAL MEDLINE 21359454
PUBMED 11390368
REFERENCE Poyet,J.-L., Srinivasula,S.M., Fernandes-Alnemri,T. and
Alnemri,E.S.
Direct Submission
JOURNAL Submitted (16-MAY-2001) Microbiology and Immunology, Thomas
Jefferson University, 233 S. 10th Street, Philadelphia, PA 19107,
USA
FEATURES
source location/Qualifiers
1..3219
/organism="Homo sapiens"
```

/db_xref="taxon:9606"
/chromosome="2"
/map="p21-22"
145..3219
/note="IPAF; CED4/Apaf-1 family member; caspase-associated
recruitment domain containing protein"
/codon_start=1
/product="ICE-protease activating factor"
/protein_id="AAK59843.1"
/db_xref="GI:14334215"

CDS

```
BASE COUNT 934 a 696 c 748 g 841 t
ORIGIN
```

Alignment Scores:

Pred. No.: 9 31e-92 Length: 3219
Score: 829.00 Matches: 163
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-697-089-2_COPY_161_323 (1-163) x AY035391 (1-3219)

```
QY 1 LeuGlnSerProCysIleIleGluGlyGluSerGlyGlySerThrLeuGln 20
DB 625 CTTGAGAGCCCTGCATCATATTGAAGGGGAATCTGGCAAGCAAGTCCACTCTGCTGCAG 684
QY 21 ArgIleAlaMetLeuTyrGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
DB 685 CGAATTTGCCATGCTCTGGGGCTCCGGAAAGTCAAGGCTCGACCAATTCAAATTCCTC 744
QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLysLeuPheGluThrLeuCysAspGlnLeu 60
DB 745 TTCTTCCCTCCCTCAGAGGGCCAGGGGTGACTTTTGAACCCCTCTGATCACTC 804
QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 80
DB 805 CTGATATACCTGGACACATACGAGACGACATTCATGCCATCTGCTGAAGCTGGCG 864
QY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 100
DB 865 CAGAGGGTCTTTTCCCTCTTGATGGCTACAAATGAAATTCAGCCCAAGTCCGCCAGAA 924
QY 101 IleguAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValIThrThr 120
DB 925 ATCGAAGCCCTGATAAAGAAACCCAGCTTCAAGAACATGATGTCATGCACCACTACC 984
QY 121 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140
DB 985 ACTGATGCTCCCTGAGGACATACGAGAGTGTGGTCCCTGACTGCTGAGAGTGGGGATATG 1044
QY 141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 160
DB 1045 ACAGAAGACAGCGCCAGGCTCTCATCCGAAAGTCTGATCAAGAGACTTGTCTGAAGC 1104
```

```

Qy      161 LeuDeuLeu 163
      |||||
Db      1105 TTGTGCTC 1113

RESULT 4
AK095467
LOCUS   Homo sapiens cDNA FLJ38148 fls, clone D90ST2003791, highly similar
DEFINITION
ACCESSION AK095467 3355 bp mRNA linear PRI 15-JUL-2002
VERSION   Homo sapiens ICB-protease activating factor mRNA.
KEYWORDS  oligo capping; fls (full insert sequence).
SOURCE    Homo sapiens CD34+ Cells cDNA to mRNA, clone_11b:D90ST2
           clone:D90ST2003791.
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS  Minomura,K., Magatsuma,M., Kanda,K., Kondo,H., Yokoi,T.,
          Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K.,
          Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,
          Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
          Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
          Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
          Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
          Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
          Nagahara,K., Masubo,Y., Nagai,K. and Isogai,T.
          NEDO human cDNA sequencing project
          Unpublished
          2 (bases 1 to 3355)
          Isogai,T. and Yamamoto,J.
          Direct Submission
          Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
          Kazusa-Kamatari, Kisarazu, Chiba 229-0812, Japan
          (E-mail:genomese@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
          NEDO human cDNA sequencing project supported by Ministry of
          Economy, Trade and Industry of Japan; cDNA full insert sequencing:
          Research Association for Biotechnology (RAB); cDNA library
          construction: Helix Research Institute (HRI) (supported by Japan
          Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
          HRI, and Biotechnology Center, National Institute of Technology and
          Evaluation; clone selection for full insert sequencing: HRI and
          RAB; annotation: HRI and RAB.
          Location/Qualifiers
          1..3355
             /organism="Homo sapiens"
             /db_xref="taxon:9606"
             /clone="D90ST2003791"
             /cell_type="CD34+ Cells"
             /clone_11b="D90ST2"
             /note="Cloning vector: PME18SFL3-mRNA from CD34+ cells
             after 9-days ODF induction.-primary culture, CD34+ Cells"

BASE COUNT  986 a 726 c 774 g 869 t

ORIGIN
Alignment Scores:
Pred. No.:      9.81e-92      Length:      3355
Score:          829.00      Matches:      163
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             9          Gaps:      0

US-09-697-089-2_COPY_161_323 (1-163) x AK095467 (1-3355)
Qy      1 LeuGInserProcysIleIleGluGluGluSerGlyLysGlyLysSerThrLeuLeuGln 20
      |||||
Db      742 CTTGAGGCGCCCTGCATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACCTCTGAG 801

Qy      21 ArgTleAlaMetLeuTppGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
      |||||
Db      802 CGAATTCCCATGCTCTG66GCTCCGGAAGTGCAAGGCTGACCAAGTCAAAATTCGTC 861

```

```

Qy      41 PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu 60
      |||||
Db      862 TTCTTCTCCGCTCAGCAGAGGCCAGGTCGATTTTGAACCCCTGTGATCAACTC 921

Qy      61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80
      |||||
Db      922 CTGATATACCTGGCACATCATCAGAGACAGACATTCATGCGCATGCTGAACTCGCG 981

Qy      81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGlnLysProGlnAsnGlyProGlu 100
      |||||
Db      982 CAGAGGCTTCTTCTCTTCTTGATGCTGACATATTAATTCAGCCCAAGACTGCCAGAA 1041

Qy      101 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr 120
      |||||
Db      1042 ATCGAAGCCCTGATTAAGAAAACACCCGCTTCAGAAACATGCTATCGTCCACCTACC 1101

Qy      121 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140
      |||||
Db      1102 ACTGAGTGCCCTGAGGCGACATACGCGCATGCTGCTCCCTGACTGAGTGCGGATATG 1161

Qy      141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 160
      |||||
Db      1162 ACAGAAGCACGCGCCAGGCTCTATCCGAGAACTGATGATCAAGAGCTGTGAAGGC 1221

Qy      161 LeuDeuLeu 163
      |||||
Db      1222 TTGTGCTC 1230

RESULT 5
BC031555
LOCUS   Homo sapiens 3360 bp mRNA linear PRI 26-JUN-2002
DEFINITION
ACCESSION BC031555 3360 bp mRNA linear PRI 26-JUN-2002
VERSION   MGC:35330 IMAGE:5179909, mRNA, complete cds.
KEYWORDS  BC031555.1 GI:21594975
          MGC.
SOURCE    human.
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
          1 (bases 1 to 3360)
          Strausberg,R.
          Direct Submission
          Submitted (06-JUN-2002) National Institutes of Health, Mammalian
          Gene Collection (MGC), Cancer Genomics Office, National Cancer
          Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
          USA
          NIH-MGC Project URL: http://mgc.nci.nih.gov
          Contact: MGC help desk
          Email: gc@bbs.femail.nih.gov
          Tissue Procurement: Life Technologies, Inc.
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
          DNA Sequencing by: Baylor College of Medicine Human Genome
          Sequencing Center
          Center code: BCM-HGSC
          Web site: http://www.hgsc.bcm.tmc.edu/cdna/
          Contact: amg@bcm.tmc.edu
          Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
          Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
          Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK plate: 50 Row: a Column: 10
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis.
FEATURES
source      1..3360
             /organism="Homo sapiens"
             /db_xref="LocusID:38484"
             /db_xref="taxon:9606"

```

/clone="MGC:35330 IMAGE:5179909"
/tissue_type="Brain, Lung, Testis, adult, pooled whole"
/clone_lib="NTH_MGC_115"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
332. .3306
/codon_start=1
/product="caspase recruitment domain protein 12"
/protein_id="AAH31555.1"
/db_xref="GI:21594976"

/translation="MNFIDKNSRALIQRMGNTVTKQTDDLFVNNVNIREEVNITICE
KVEDDAARGIIHMLTKGSESCNLFELSKEMNYPLEQDLNGOSLFHQTSBGDLDDLA
QDLKDIYHTPSFLNFPYPLGEDIDITFNKSPFTRPVLRKQDHHNRVQLNLGLDA
LQSPCITIEGSESGKSTLQRIAMMGSGKALTKRFEVLELISRAQGLFEFTLDD
QLDIPGTRIKQRTFMALIKRQAVLELDQYNEFKQNCPEITALLKENRFRNMYI
VTTTECLRHIRQFGALTAIEYGDMTEDSAOLIREVILIKELAEGLLIQIOKSRCLRNL
MKTPLEPVITCAIQMGSEFHSHTQTLFHFYDILLQKNHKKRGAASQFISLSDH
CGDIALRGVFSHKDFEIQDVSVNEVDLITGLCKYTAQRFKPKYKFFKFSQERT
AGRLSSILTSHEPEVTKGNGYLQKNVLSIDITSTYSLRYTSGSSVEATRAVMKH
LAAYOHGCLGLSLAKRPLMROESLOSVMNTEOEILKAININSFECGHIHQEST
SKASLSOEFEPFGOKSLIYNSGNIPYLPDFEHLRPNCSALDPIKIDPYGMAAS
EKAEDTGGIIMEAPETIIPSRVSLFPMKQERFLLEVLRDPSKLNKODIRTLGK
IFSSATSLRLQIKRCAGVAGSLSVLSTCKNIYSLEWASPLTIEDERHITVSYNLKT
LSIHDLQNRPLPGJLTDLSGLNKLTLMDNIMNEDAKIKLAEGLKMLKMLFHL
THLSIDIGEMDYIVKSLSSPECDLEEIQLVSCCSANAIVKILAOINLNLVLTSLDLS
ENYLEKDGNEALHELIDRMNVLEQITLALPMGCDVGSLSILKHLIEVPOVLKGL
KNMRLTDEIRILCAFPKGNPLKNFQOLNLAGNVSDDGMLAFMGVEENLKQIVFFDF
STKEFLDPPLAVRLKSOVLKSLTFLQERLRLVGMQFDDDDLSVITGARFLVTA"

BASE COUNT 1011 a 718 c 768 g 863 t
ORIGIN

Alignment Scores:

Pred. No.: 9.82e-92 Length: 3360
Score: 829.00 Matches: 163
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-697-089-2_copy_161_323 (1-163) x BC031555 (1-3360)

Qy 1 LeuGlnSerProCysIleIleGlnGlyGlnSerGlyGlyGlySerThrLeuLeuGln 20
Db 712 CTTGAGAGACCCCTGCATCATTTGAAGGGAATCTGGCAAGCAAGTCCACTCTGCTGACG 771
Qy 21 ArgIleAlaMetLeuTrpGlySerGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 40
Db 772 CGAATTGCCATGCTCTGGGCGCTCCGGAAGTGCAGGCTGACCAAGTCAAAATTCGTC 831
Qy 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGlnThrLeuGlyAspGlnLeu 60
Db 832 TTCTTCTCTCCGCTCAGAGAGGCCAGGGTGACTTTTGAAGCCCTGTGATCAACTC 891
Qy 61 LeuAspIleProGlyThrIleArgGlyGlnThrPheMetAlaMetLeuLeuLeuArg 80
Db 892 CTGGATATACCTGGACACATCAGAGACGACATTCATGCCATCTCTGAAAGTGGCG 951
Qy 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGlnPheGlyProGlnAsnCysProGln 100
Db 952 CAGAGAGGCTTCTTCCCTTCTGATGGCTACATGAAATTCAGGCCCAAGACTGCCAGAA 1011
Qy 101 IlegIuAlaLeuIleGlyGlnAsnHisArgPheGlyAsnMetValIleValThrThrThr 120
Db 1012 ATCGAAGCCCTGATTAAGAAACCCAGGCTTCAAGACATGGTATGTGTACCACTAC 1071
Qy 121 ThrGlnCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGlnValAlGlyAspMet 140
Db 1072 ACTGAGTGCCTGAGGACATACGCGAGTTGTGGCTCTGACTGCTGAGAGTGGGAGATATG 1131
Qy 141 ThrGlnAspSerAlaGlnAlaLeuIleArgGlnValLeuIleGlyGlnLeuAlaGlnGly 160
Db 1132 ACAGAAAGACAGCCCGCAGGCTCTCATCCGAGAAAGTGTGATCAAGAGACTTGTGAAAGC 1191

Qy 161 LeuLeuLeu 163
Db 1192 TTGTTGCTC 1200

RESULT 6

AX318091 3396 bp DNA linear PAT 14-DEC-2001
LOCUS Sequence 96 from Patent WO0190156.
DEFINITION AX318091
ACCESSION AX318091
VERSION AX318091.1 GI:17900820
KEYWORDS

SOURCE

ORGANISM Homo sapiens
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 Reed,J.C., Plo,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,
Oliveira,V.A., Hayashi,H. and Pawlowski,K.
CARD domain containing polypeptides, encoding nucleic acids, and
methods of use
Patent: WO 0190156-A 96-29-NOV-2001;
The Burnham Institute (US)

FEATURES

source

CDS

1..3396
/organism="Homo sapiens"
/db_xref="taxon:9606"
277..3351
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD19340.1"
/db_xref="GI:17900821"
/translation="MNFIDKNSRALIQRMGNTVTKQTDDLFVNNVNIREEVNITICE
KVEDDAARGIIHMLTKGSESCNLFELSKEMNYPLEQDLNGOSLFHQTSBGDLDDLA
QDLKDIYHTPSFLNFPYPLGEDIDITFNKSPFTRPVLRKQDHHNRVQLNLGLDA
LQSPCITIEGSESGKSTLQRIAMMGSGKALTKRFEVLELISRAQGLFEFTLDD
QLDIPGTRIKQRTFMALIKRQAVLELDQYNEFKQNCPEITALLKENRFRNMYI
VTTTECLRHIRQFGALTAIEYGDMTEDSAOLIREVILIKELAEGLLIQIOKSRCLRNL
MKTPLEPVITCAIQMGSEFHSHTQTLFHFYDILLQKNHKKRGAASQFISLSDH
RGDIALRGVFSHKDFEIQDVSVNEVDLITGLCKYTAQRFKPKYKFFKFSQERT
AGRLSSILTSHEPEVTKGNGYLQKNVLSIDITSTYSLRYTSGSSVEATRAVMKH
LAAYOHGCLGLSLAKRPLMROESLOSVMNTEOEILKAININSFECGHIHQEST
SKASLSOEFEPFGOKSLIYNSGNIPYLPDFEHLRPNCSALDPIKIDPYGMAAS
EKAEDTGGIIMEAPETIIPSRVSLFPMKQERFLLEVLRDPSKLNKODIRTLGK
IFSSATSLRLQIKRCAGVAGSLSVLSTCKNIYSLEWASPLTIEDERHITVSYNLKT
LSIHDLQNRPLPGJLTDLSGLNKLTLMDNIMNEDAKIKLAEGLKMLKMLFHL
THLSIDIGEMDYIVKSLSSPECDLEEIQLVSCCSANAIVKILAOINLNLVLTSLDLS
ENYLEKDGNEALHELIDRMNVLEQITLALPMGCDVGSLSILKHLIEVPOVLKGL
KNMRLTDEIRILCAFPKGNPLKNFQOLNLAGNVSDDGMLAFMGVEENLKQIVFFDF
STKEFLDPPLAVRLKSOVLKSLTFLQERLRLVGMQFDDDDLSVITGARFLVTA"

BASE COUNT 992 a 737 c 793 g 874 t
ORIGIN

Alignment Scores:

Pred. No.: 9.96e-92 Length: 3396
Score: 829.00 Matches: 163
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-697-089-2_copy_161_323 (1-163) x AX318091 (1-3396)

Qy 1 LeuGlnSerProCysIleIleGlnGlyGlnSerGlyGlyGlySerThrLeuLeuGln 20
Db 757 CTTGAGAGACCCCTGCATCATTTGAAGGGAATCTGGCAAGCAAGTCCACTCTGCTGACG 816
Qy 21 ArgIleAlaMetLeuTrpGlySerGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 40
Db 817 CGCATTCGATGCTCTGGGCGCTCCGGAAGTGCAGGCTGACCAAGTCAAAATTCGTC 876
Qy 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGlnThrLeuGlyAspGlnLeu 60
Db 877 TTCTTCTCTCCGCTCAGAGAGGCCAGGGTGACTTTTGAAGCCCTGTGATCAACTC 936

BASE COUNT	992 a	737 c	793 g	874 t
ORIGIN	<p> LAAYVHGCLIGLSTIAKRPRLROBSLOSVMNTTEOEILTKA1NINSPFEGGILHYOES SKSLASDSEFPAPFROGKSLYINSGNIPIYLEDPEPHLEPNCSALDFITLDPYGGAMSW EKALEDYTGIMHEAPETYPISRAVSLPEFMKQEFFRLEYLRQFSKLNKODYINLTK IFSSATSLRLQIKRCAGAVASLSVLTCKNITYSLAMEASPLTIEDRHTTYNINLT LSIHDLNORLPGGILTDLSGLNKLMLTILMDINIKIMBEDAIKIAEGIKNLKMLFHL THSIDGEMDYIVKSLSSPECDLEEIOLVMSCCLSAAYVILKONLNLVKSITLSDS ENYERKDGNEALHILIDRMVYLDQTLNIPWGDVSGSLSLIKHLEVPOLYKGL KNMRLDPEETRIICGAFPKGKNDIKRFPOLNLAGNVSVDGLAFMGVEENIKOLVFPDF STKFLFDLPALVRKLSOYLSKFTPLQZARLVGMQFDDDLIVTTIGAKFLVTA" </p>			
Alignment Scores:	<p> Pred. No.: 9,96e-92 Length: 3396 Score: 829.00 Matches: 163 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0 DB: Gaps: 0 </p>			
US-09-697-089-2_COPY_161_323 (1-163) x AY027787 (1-3396)				
Qy 1	<p> LeuGlnSerProCysIleIleGlnGlyGlnSerGlyGlyGlySerThrLeuLeuGln 20 Db 757 CTTGAGAGCCCGCGATCATTTGAAGGGGATGTGGCAAGCAATCCACTGCTGCAG 816 </p>			
Qy 21	<p> ArgIleIaMetLeuTirPglYserGlyCysLysAlaLeuThrLysPheLysPheVal 40 Db 817 CGCATTTGCCATGCTCTGGGGGCGTCCGGAAAGTGCACAGGCTCTGCACCAAGTTCCAAATTCGTC 876 </p>			
Qy 41	<p> PhePheLeuArgLeuSerArgIaGlnGlyLeuPheGlnThrLeuCysAspGlnLeu 60 Db 877 TTCTTCTTCGCTGCTCAGAGGGGCCAGGGGTGGACTTTTGAAGCCCTCTGTATCACTC 936 </p>			
Qy 61	<p> LeuAspIleProGlyThrIleArgLysGlnThrPheMetIaMetLeuLysLeuArg 80 Db 937 CTGGATATACCTGGGACATCGAAGAGCAGACATTCATGAGCCATGCTGTGAAGCTGGCGG 996 </p>			
Qy 81	<p> GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 100 Db 997 CAGAGGATCTTTCTTCCTTCCTTGATGGCTACATGTAATTCAGCCCCCAAGACGCCCCAGAA 1056 </p>			
Qy 101	<p> IleGluAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThrThr 120 Db 1057 ATCGAAGCCCTGATTAAGGAAACCAACCGCTTCAAGAACATGTGATGCTACCACTACC 1116 </p>			
Qy 121	<p> ThrGlnCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140 Db 1117 ACTGATGCTCTAGGCACATACGCGAGTTGGTGGCCCTGACGCGCGAGAGTGGGGGATATAG 1176 </p>			
Qy 141	<p> ThrGluAspSerAlaGlnAlaLeuIleArgGluValIleLysGlnLeuAlaGlnGly 160 Db 1177 ACAGAGAGACAGCGCCACGCTCTCATCCGAGAAAGTGTGATCAACAGAGACTGCTGAAGGC 1236 </p>			
Qy 161	<p> LeuLeuLeu 163 </p>			
Db 1237	<p> TTGTTCCTC 1245 </p>			
RESULT 8				
AF376061				
LOCUS				
DEFINITION	<p> Homo sapiens caspase recruitment domain protein 12 mRNA, complete cds. </p>			
ACCESSION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE	<p> Gingras,M.-C., Olu,J. and Margolin,J.F. Differential expression of the caspase recruitment domain protein </p>			

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

12 (CARD12) during monocytic differentiation
Unpublished
2 (bases 1 to 3581)
Gingras, M.-C., Otu, J. and Margolin, J. F.
Direct Submission
Submitted (03-MAY-2001) Pediatric/Texas Children's Cancer Center,
Baylor College of Medicine, 6621 Fannin St. MC3-3320, Houston, TX
77030, USA

FEATURES
Source

Location/Qualifiers
1..3581

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="2"

/map="2p21-22"

/cell_line="0937"

/cell_type="peripheral blood-derived CD14 mature monocyte"

490..3564

/note="CARD12"

/codon_start=1

/product="caspase recruitment domain protein 12"

/protein_id="AAK53443.1"

/db_xref="GI:14040075"

/translation="MNFIDKNSRALIQMGMTVIKQITDLEFVNVNIREVNITICE
KVEDDARGIIMHLKSGESCNFLKSLKEMNPLFODLNGSLFQTSQDIDDLA
ODKDLVHTPEFNEPLGEDIIDIFPNKSTPEVLMRKDOHHHRYEQLNLGLA
LOSPCIEGSGKSKTLRIAMMGSKKATLKEFVPELISRAQSGLEFELCD
QLDIPGTRKQTMAMILKRLQRYELFDGYNERPONCEPITALIKENRERKMYI
VTTTECLRHIFQFALAEVDMEDSAQALIEVILKEALBELLQIQSKRLRL
MKTPLFVITCAIQMGSEFHSHTQTLFHFYDILLQKNHKGKGAASPFISLH
CGDLALBEGVSHKDFEIDQVSYNEDELITGLCKYTAQFKPKKFEKFSQEYT
AGRRSLSLTSEBEVYKNGVYLOKMYISIDISTYSLARTYSGKSEVETRAVMK
LAAYHOCCLIGLSTAKRPLMRQESLOSVMKTRQELIKAINISFVDCGHIHQEST
SKSLASQFEAFQFGKSLYINSNGIPDLFPEFHLPCASALDFIKLDFEGKMAAS
EKAEDVGGHMEAPETVYIPRAVSLEFNNKQEFRLVTLRDFSKINKQDIYLGK
IFSSATSLRLQIKRCAGVAGSLSVLSTCKNIYSIMVEASPLTEDEBHTSVNLT
LSIHDLNORLPGLDLSIGLNKLNKLTIMONIKMNEEDAKIKLEGKLNKMLFHL
THSIDIGEMDIYKLSLSEPCDELEIQLVSCCLSAUNAVKILAEONLNLVSTLIDS
ENYLEKDNENALHELDIMVNLLEDTALMLPMGCDVCGSSILKHLIEVQYIKIGI
KNRMLTEIRIILCAFEGKPNLKNFQOLNLAAGVSSDGMALFEGVENLKVLFDFE
STKEFLDPALVRLKLSOVLSKLFLQLQEARLVGWOFDDDLSTVITGARFLVYA"

502..741

/note="Region: caspase recruitment domain"

BASE COUNT 1033 a 781 c 843 g 924 t

ORIGIN

misc_feature

BASE COUNT 1033 a 781 c 843 g 924 t

ORIGIN

Alignment Scores:

Pred. No.: 1.06e-91

Score: 829.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 9

Gaps: 0

US-09-697-089-2_COPY_161_323 (1-163) x AF376061 (1-3581)

Oy 1 LeuGlnSerProCysIleIleGlnGlyIleSerGlyLysGlySerThrLeuGln 20

Db 970 CTTGAGAGCCCTGCATATGTAAGGGAATCTGGCAAGGCAATCTGCTGCAAG 1029

Oy 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40

Db 1030 CGCAATGGCAGCTCTGCGGCGCCGGAAGTGCAAGGCTGACCAAGTCAAAATTCGTC 1089

Oy 41 PhePheLeuAlaGlyLeuSerArgAlaGlnGlyLeuPheGlnThrLeuCysAspGlnLeu 60

Db 1090 TTCTTCCCTCCGCTCAGAGGCGCCAGGCTGACCTTTTGAACCCCTGTCGATCAACTC 1149

Oy 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysArg 80

Db 1150 CTGGATATACCTGGCAGCATCGAAGACACATTCATGCGCATCTGCTGAAGCTGCGG 1209

Oy 81 GlnArgValIleuPheLeuLeuAspGlyTyrAsnGlnIlePheLysProGlnAsnGlyProGln 100

Db 1150 CTGGATATACCTGGCAGCATCGAAGACACATTCATGCGCATCTGCTGAAGCTGCGG 1209

Oy 81 GlnArgValIleuPheLeuLeuAspGlyTyrAsnGlnIlePheLysProGlnAsnGlyProGln 100

Db 1210 CAGAGGCTCTTTTCCCTCTTGATGCTACAAATGAATCAAGCCCAAGTCCAGAGA 1269

Oy 101 IlegIAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThr 120

Db 1270 ATCGAAGCCCTGATTAAGAAAACACCGCTTCAAGAACATGTCATGCTACCCCTAC 1329

Oy 121 ThrGluCysLeuArgHisIleLeuArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140

Db 1330 ACTGAGTGCCTGAGCAGACATACGCGAGTGTGCTGCTGACTGCTGAGGTGGGGATATG 1389

Oy 141 ThrGluAspSerArgAlaGlnAlaLeuIleLeuArgGluValIleLysGlnLeuAlaGlu 160

Db 1390 ACAGAAAGACAGCGCCAGGCTCTCATCCGAGAAAGTCGATCAAGAGAGCTGCTGAAGGC 1449

Oy 161 LeuLeuLeu 163

Db 1450 TTGTTGCTC 1458

Oy 161 LeuLeuLeu 163

Db 1450 TTGTTGCTC 1458

Oy 161 LeuLeuLeu 163

Db 1450 TTGTTGCTC 1458

Oy 161 LeuLeuLeu 163

Db 1450 TTGTTGCTC 1458

Oy 161 LeuLeuLeu 163

Db 1450 TTGTTGCTC 1458

Oy 161 LeuLeuLeu 163

Db 1450 TTGTTGCTC 1458

Oy 161 LeuLeuLeu 163

Db 1450 TTGTTGCTC 1458

Oy 161 LeuLeuLeu 163

Db 1450 TTGTTGCTC 1458

Oy 161 LeuLeuLeu 163

Db 1450 TTGTTGCTC 1458

Oy 161 LeuLeuLeu 163

Db 1450 TTGTTGCTC 1458

Oy 161 LeuLeuLeu 163

Db 1450 TTGTTGCTC 1458

Oy 161 LeuLeuLeu 163

Db 1450 TTGTTGCTC 1458

Oy 161 LeuLeuLeu 163

Db 1450 TTGTTGCTC 1458

Oy 161 LeuLeuLeu 163

Db 1450 TTGTTGCTC 1458

Oy 161 LeuLeuLeu 163

Db 1450 TTGTTGCTC 1458

Oy 161 LeuLeuLeu 163

Db 1450 TTGTTGCTC 1458

Oy 161 LeuLeuLeu 163

Db 1450 TTGTTGCTC 1458

Oy 161 LeuLeuLeu 163

Db 1450 TTGTTGCTC 1458

Oy 161 LeuLeuLeu 163

Db 1450 TTGTTGCTC 1458

QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGlnThrLeuCysAspGlnLeu 60
 |||||
 Db 74971 TTCTTCCTCCGCTCAGCAGGCGCCAGGAGACTTTTGAACCCCTCGTGCATCACTC 74912
 QY 61 LeuAspIleProGlyThrIleArgGlyGlnThrPheMetAlaMetLeuLeuGlyLeuArg 80
 |||||
 Db 74911 CTGATATACCTGGCACAATCAGAACACATTCATGGCCATGCTGTAACCTGCGG 74852
 QY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGlnPheLysProGlnAsnGlyProGlu 100
 |||||
 Db 74851 CAGAGGTTCTTTCTCTTCCTGATGCTCATAATTCAGCCCGAGAACTGCCCGAGAA 74792
 QY 101 IleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThrThr 120
 |||||
 Db 74791 ATGCAACCCCTGATAAAGAAAACACCGCTCAAGAAACATGTCATGTCACCATAC 74732
 QY 121 ThrGlyCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140
 |||||
 Db 74731 ACTGAGTGCCTGAGGACACATACGCGAGTTGTGCTCCTGACTGCTGAGTGCGGATATG 74672
 QY 141 ThrGlnAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGlnLeuAlaGlnGly 160
 |||||
 Db 74671 ACAGAAACAGCCGCCAGCTCTCATCCGAGAACTGCTGATCAAGAGCTTCTGAAGGC 74612
 QY 161 LeuLeuLeu 163
 |||||
 Db 74611 TTGTTCCTC 74603

RESULT 10
 AC010968 160583 bp DNA linear HTG 18-AUG-2000
 LOCUS
 DEFINITION Homo sapiens chromosome 2 clone RP11-9302, WORKING DRAFT SEQUENCE,
 11 unordered pieces.
 AC010968
 AC010968.5 GI:9845170
 VERSION HTG: HTGS_PHASE1; HTGS_DRAFT.
 KEYWORDS Homo sapiens.
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 160583)
 Waterston, R.H.
 The sequence of Homo sapiens clone
 Unpublished
 2 (bases 1 to 160583)
 Waterston, R.H.
 Direct Submission
 Submitted (28-SEP-1999) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 On Aug 18, 2000 this sequence version replaced gi:8439959.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

COMMENT

----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc/index.shtml
 ----- Project Information -----
 Center project name: H_NH0093002
 ----- Summary Statistics -----
 Sequencing vector: M13; 59%
 Sequencing vector: plasmid; 41%
 Chemistry: Dye-Primer ET; 47% of reads
 Chemistry: Dye-terminator Big Dye; 53% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: bases at least Q40
 Consensus quality: bases at least Q30
 Consensus quality: bases at least Q20
 Insert size: 147000; agarose-fp
 Insert size: 159583; sum-of-contrigs
 Quality coverage: 6.64 in Q20 bases; agarose-fp
 Quality coverage: 6.38 in Q20 bases; sum-of-contrigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 11 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 1080: contig of 1080 bp in length
 * 1081 1180: gap of unknown length
 * 1181 2476: contig of 1296 bp in length
 * 2477 2576: gap of unknown length
 * 2577 5035: contig of 2459 bp in length
 * 5036 5135: gap of unknown length
 * 5136 9606: contig of 4471 bp in length
 * 9607 9706: gap of unknown length
 * 9707 17078: contig of 7372 bp in length
 * 17079 17178: gap of unknown length
 * 17179 27158: contig of 9980 bp in length
 * 27159 27258: gap of unknown length
 * 27259 45137: contig of 17879 bp in length
 * 45138 45237: gap of unknown length
 * 45238 65522: contig of 20285 bp in length
 * 65523 65623: gap of unknown length
 * 65624 91496: contig of 25876 bp in length
 * 91497 91598: gap of unknown length
 * 91599 116836: contig of 25237 bp in length
 * 116837 160583: gap of unknown length
 * 160584 160583: contig of 43648 bp in length.

FEATURES

source

1. 160583
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="2"
 /clone="RP11-9302"
 1. 1080
 /note="assembly_name:Contig9"
 1181. 2476
 /note="assembly_name:Contig12"
 2577. 5035
 /note="assembly_name:Contig13"
 5136. 9606
 /note="assembly_name:Contig14"
 9707. 17078
 /note="assembly_name:Contig15"
 17179. 27158
 /note="assembly_name:Contig16"
 27259. 45137
 /note="assembly_name:Contig17"
 45238. 65522
 /note="assembly_name:Contig18
 clone_end:T7
 vector_side:right"
 65623. 91496
 /note="assembly_name:Contig19"
 91599. 116835
 /note="assembly_name:Contig20
 clone_end:SP6
 vector_side:right"
 116936. 160583
 /note="assembly_name:Contig21"

BASE COUNT 44349 a 33843 c 33703 g 47641 t 1047 others

ORIGIN

Alignment Scores:

Pred. No.: 1.24e-89 length: 160583
 Score: 829.00 Matches: 163
 Percent Similarity: 100.00% Conserves: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-09-697-089-2_COPY_161_323 (1-163) x AC010968 (1-160583)


```

QY      1 LeuGlnSerProCysIleIleGluGlyGlySerGlyLysGlyLysSerThrLeuLeuGln 20
DB      49406 CTTCCAGAGCCCTTCATCTTATAGGGGATGTCGCAAGAGCCCTCTGCGCAG 49465
QY      21 ArgIleAlaMetLeuTrpLysSerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
DB      49466 CCGCATTTGCATCTCTGGGGCTCCGGAAAGTCCAAAGCTTCAAGTTCAATTTCGTC 49525
QY      41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 60
DB      49526 TTCTTCCTCCGCTCAGCAGGCGCCAGGGGTGCATTTTGAACCCCTGTGATCAGCTC 49585
QY      61 LeuAspIleProGlyThrThrLeuArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80
DB      49586 CTTGATATACCTGGSCACATTCAGAAAGACATTCATGCGCATGCTGTGAAGCTGCGG 49645
QY      81 GlnATGValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 100
DB      49646 CAGAGGGTTCTTTCTCTTCTTATGCTACATGATGATCAACCCAGAACTGCCAGAA 49705
QY      101 IleglAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThrThr 120
DB      49706 ATCGAAGCCCTGATTAAGGAAACACCGCTTCAGAAACATGTCATGTCACCACTACC 49765
QY      121 ThrGluCysLeuArgHisIleLeuArgGlnPheGlyAlaLeuThrAlaGluValLysPheT 140
DB      49766 ACTGAGTGGCTTACGACACATTCAGGAGTTGGTGGCTGTACGCTGAGAGTGGGGATTAAG 49825
QY      141 ThrGluAspSerAlaGlnAlaLeuIleLeuArgGluValIleLysGlnLeuValLysGly 160
DB      49826 ACAGAAAGACAGGCCCGAGCTTCATCCAGAAAGTCTGATCAAGAGAGCTTCTGAGGC 49885
QY      161 LeuLeuLeu 163
DB      49886 TTGTTGCTC 49894

RESULT 11
AC101793/c
LOCUS   AC101793      185469 bp    DNA        linear    HTG 21-AUG-2002
DEFINITION Mus musculus clone RP24-178L2, WORKING DRAFT SEQUENCE, 43 unordered
           pieces.
ACCESSION AC101793.2 GI:22381529
VERSION   AC101793.2
KEYWORDS  HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE    house mouse.
ORGANISM  Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 185469)
AUTHORS  Birren,B., Nusbaum,C. and Lander,E.
JOURNAL   Unpublished
TITLES    2 (bases 1 to 185469)
REFERENCE 2 (bases 1 to 185469)
AUTHORS  Anderson,S., Barna,N., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
           Birren,B., Linton,L., Bastien,V., Boguslavsky,L., Boukhalter,B.,
           Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
           Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
           Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Fato,S.,
           Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
           Glinde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
           Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
           Jones,C., Kamat,A., Karatas,A., Kells,C., Labocque,K.,
           Lamazares,R., Landers,T., Lehoczyk,D., Levine,R., Liu,G.,
           Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
           McCarthy,M., McKernan,P., McKernan,K., McPheters,R., Meldrum,J.,
           Menes,L., Mihova,T., Mlenka,V., Murphy,T., Naylor,J., Nguyen,C.,
           Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
           Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
           Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
           Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupack,R.,
           Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
           Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,

```

```

TITLES    Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
           Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
           Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
JOURNAL   Direct Submission
REFERENCE  Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
           Research, 320 Charles Street, Cambridge, MA 02141, USA
AUTHORS   3 (bases 1 to 185469)
           Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
           Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhalter,B.,
           Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
           Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
           Fato,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,
           Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
           Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
           Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
           Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,
           McCarthy,M., Meldrum,J., Menes,L., Mihova,T., Mlenka,V.,
           Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
           O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
           Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
           Roman,J., Roy,A., Schauer,S., Schupack,R., Seaman,S., Severy,P.,
           Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
           Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
           Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
           Zembek,L., Zimmer,A. and Zody,M.

TITLES    Direct Submission
JOURNAL   Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome
           Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT   On Aug 21, 2002 this sequence version replaced gi:17060568.
           All repeats were identified using RepeatMasker:
           Smit, A.F.A. & Green, P. (1996-1997)
           http://ftp.genome.washington.edu/RM/RepeatMasker.html

TITLES    Genome Center
JOURNAL   Center: Whitehead Institute/ MIT Center for Genome Research
COMMENT   Center code: WIBR
           Web site: http://www-seq.wi.mit.edu
           Contact: sequence.submissions@genome.wi.mit.edu

TITLES    Project Information
JOURNAL   Center project name: L17408
COMMENT   Center clone name: 178_L_2
           ----- Summary Statistics
           Sequencing vector: Plasmid; n/a; 100% of reads
           Chemistry: Dye-terminator Big Dye; 100% of reads
           Assembly program: Phrap; version 0.960731
           Consensus quality: 173992 bases at least Q40
           Consensus quality: 177954 bases at least Q30
           Consensus quality: 180012 bases at least Q20
           Insert size: 168000; agarose-fp
           Insert size: 181269; sum-of-continigs
           Quality coverage: 7.1 in Q20 bases; agarose-fp
           Quality coverage: 6.6 in Q20 bases; sum-of-continigs
           -----
           * NOTE: This is a 'working draft' sequence. It currently
           * consists of 43 contigs. The true order of the pieces
           * is not known and their order in this sequence record is
           * arbitrary. Gaps between the contigs are represented as
           * runs of N, but the exact sizes of the gaps are unknown.
           * This record will be updated with the finished sequence
           * as soon as it is available and the accession number will
           * be preserved.
           *
           1          60: contig of 60 bp in length
           *          61 160: gap of 100 bp
           *          824: contig of 664 bp in length
           *          825 924: gap of 100 bp
           *          925      1843: contig of 919 bp in length
           *          1844 1943: gap of 100 bp
           *          1944      2615: contig of 672 bp in length
           *          2616 2715: gap of 100 bp
           *          2716      3318: contig of 603 bp in length
           *          3319 3418: gap of 100 bp
           *          3419      4524: contig of 1106 bp in length
           *          4525 4624: gap of 100 bp
           *          5485: contig of 861 bp in length

```



```

Db 1675 TTGAACCTGTGCATGTGTGTGGAGGTTGAAAGCTGGAAAGTGAAGACGGCTCCTCTGAAG 1734
Qy 21 Argilealmetleutrglyserglyscylsalaleuthrllyspheyl 40
Db 1735 AAAATAGCTTTCTGTGTGGCATGTGATGCTGTCCCTGTTAAACAGGTTCCAGCTGTT 1794
Qy 41 PhepheleuArgleuser-----Arglaaglnglylyleuphegluthrlleucysasp 58
Db 1795 TTCTACCTCTCCCTTAGTTCCACACAGACAGAGGGGCTGCCAGTATCATCTGTGAC 1854
Qy 59 Glnleuleuaspilpeproglythrilearglysglnthrlphemelalmetleuleuls 78
Db 1855 CAGCTCCCTAGAGAAAGAAAGACTGTCTACTGAATGTGCATGAGAAACATTTCCAGCAG 1914
Qy 79 LeuarglnArgValleupheleuleuaspglytyrAsnGluPhe-----LysProgin 96
Db 1915 TTTAAAGAAATCAGTCTTATCTTTAGTACTACAAAGAAATATGTTCAATCCCTCA 1974
Qy 97 AsncysprogluileglualaleuilelysgluAsnHlsArgPheLysAsnmetValile 116
Db 1975 -----GTCATAGGAAACTGATTCAAAAAACCACTTATCCCGACCTGCTATTG 2025
Qy 117 ValthrThrThrThrglucylseuArgHlslearglnphe 130
Db 2026 ATTGCTGTCCGTACAAACAGGGCCAGGACATCCGCCGATAC 2067

RESULT 14
E24990 5366 bp DNA linear PAT 18-JUN-2001
LOCUS Apoptosis-inhibiting protein, gene encoding the same and cDNA
DEFINITION E24990
FEATURES
VERSION E24990.1 GI:13024688
KEYWORDS JP 1999116599-A/2.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 5366)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Apoptosis-inhibiting protein, gene encoding the same and cDNA
JOURNAL Patent: JP 1999116599-A 2 27-APR-1999;
COMMENT SCIENCE & TECH AGENCY
OS Homo sapiens (human)
PN JP 1999116599-A/2
PD 27-APR-1999
PF 14-OCT-1997 JP 1997280831
PR
PI SHIGEHRO IKEDA, KENJI YAMAMOTO
PC C07K14/52, C07K16/28, C12N15/09, C12Q1/68, C12P21/02, C12P21/02,
PC C12R1:19),
PC C12N15/00
CC Strandedness: Double;
CC Topology: Linear;
FH Key 1. 5366 Location/Qualifiers
FT source /organism="Homo sapiens (human)".
FEATURES
source 1. 5366 Location/Qualifiers
/db_xref="taxon:9606"
BASE COUNT 1483 a 1173 c 1222 g 1488 t
ORIGIN
Alignment Scores:
Pred. No.: 1.45e-18 Length: 5366
Score: 236.50 Matches: 53
Percent Similarity: 58.96% Conservative: 26
Best Local Similarity: 39.55% Mismatches: 48
Query Match: 28.53% Indels: 7
DB: 6 Gaps: 3
US-09-697-089-2_COPY_161_323 (1-163) x E24990 (1-5366)

```

```

Qy 1 LeugInserProCysIlellegluIngluIuserglyLysSerThrleuIn 20
Db 1675 TTGAACCTGTGCATGTGTGTGGAGGTTGAAAGCTGGAAGTGAAGACCGTCTCTGAAG 1734
Qy 21 Argilealmetleutrglyserglyscylsalaleuthrllyspheyl 40
Db 1735 AAAATAGCTTTCTGTGTGGCATGTGATGCTGTCCCTGTTAAACAGGTTCCAGCTGTT 1794
Qy 41 PhepheleuArgleuser-----Arglaaglnglylyleuphegluthrlleucysasp 58
Db 1795 TTCTACCTCTCCCTTAGTTCCACACAGACAGAGGGGCTGCCAGTATCATCTGTGAC 1854
Qy 59 Glnleuleuaspilpeproglythrilearglysglnthrlphemelalmetleuleuls 78
Db 1855 CAGCTCCCTAGAGAAAGAAAGACTGTCTACTGAATGTGCATGAGAAACATTTCCAGCAG 1914
Qy 79 LeuarglnArgValleupheleuleuaspglytyrAsnGluPhe-----LysProgin 96
Db 1915 TTTAAAGAAATCAGTCTTATCTTTAGTACTACAAAGAAATATGTTCAATCCCTCA 1974
Qy 97 AsncysprogluileglualaleuilelysgluAsnHlsArgPheLysAsnmetValile 116
Db 1975 -----GTCATAGGAAACTGATTCAAAAAACCACTTATCCCGACCTGCTATTG 2025
Qy 117 ValthrThrThrThrglucylseuArgHlslearglnphe 130
Db 2026 ATTGCTGTCCGTACAAACAGGGCCAGGACATCCGCCGATAC 2067

RESULT 15
A64509 5502 bp DNA linear PAT 29-MAR-1999
LOCUS Sequence 1 from Patent WO9726331.
DEFINITION A64509
ACCESSION A64509
VERSION A64509.1 GI:3717908
KEYWORDS
ORGANISM unidentified.
SOURCE unidentified.
REFERENCE 1 (bases 1 to 5502)
AUTHORS Korneluz R.G., Mackenzie, A.E., Roy, N., Robertson, G. and Tamai, K.
TITLE USE OF NEURONAL APOPTOSIS INHIBITOR PROTEIN (NAIP)
JOURNAL Patent: WO 9726331-A 1 24-JUL-1997;
UNIV OTTAWA (CA)
COMMENT Other publication AU 1614997 19970811.
FEATURES
source 1. 5502 Location/Qualifiers
/db_xref="taxon:32644"
BASE COUNT 1558 a 1229 c 1204 g 1511 t
ORIGIN
Alignment Scores:
Pred. No.: 1.5e-18 Length: 5502
Score: 236.50 Matches: 53
Percent Similarity: 58.96% Conservative: 26
Best Local Similarity: 39.55% Mismatches: 48
Query Match: 28.53% Indels: 7
DB: 6 Gaps: 3
US-09-697-089-2_COPY_161_323 (1-163) x A64509 (1-5502)
Qy 1 LeugInserProCysIlellegluIngluIuserglyLysSerThrleuIn 20
Db 1779 TTGAACCTGTGCATGTGTGTGGAGGTTGAAAGCTGGAAGTGAAGACCGTCTCTGAAG 1838
Qy 21 Argilealmetleutrglyserglyscylsalaleuthrllyspheyl 40
Db 1839 AAAATAGCTTTCTGTGTGGCATGTGATGCTGTCCCTGTTAAACAGGTTCCAGCTGTT 1898
Qy 41 PhepheleuArgleuser-----Arglaaglnglylyleuphegluthrlleucysasp 58
Db 1899 TTCTACCTCTCCCTTAGTTCCACACAGACAGAGGGGCTGCCAGTATCATCTGTGAC 1958

```


THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 31, 2003, 10:49:01 ; Search time 193.092 Seconds
(without alignments)
1901.038 Million cell updates/sec

Title: US-09-697-089-2_COPY_161_323
Perfect score: 829
Sequence: 1 LQSPCTIEGSGKSKTLQ.....SAQALIREVLKEALAEGLL 163

Scoring table:
BLOSUM62
Xgapop 10.0 , Ygapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+g2n.model -DEV=xlh
-O=/cgn2.1/USPRO_SPOOL/US09697089/runat_29012003_092753_19709/app_query.fasta.1.981
-DB=N.Geneseq.101002 -OFMT=fasta -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09697089@cgn.1.1_276@runat_29012003_092753_19709 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAPP -LARGESQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMOUT=120
-WARN_TIMOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N.Geneseq.101002:*
1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	829	100.0	891	24	ABK22766	Human CDNA encodin
2	829	100.0	2215	22	AAH78218	Nucleotide sequenc
3	829	100.0	3133	22	AA503945	Human caspase recr
4	829	100.0	3213	22	AAH78219	Nucleotide sequenc
5	829	100.0	3396	24	ABK22731	Human CDNA encodin
6	829	100.0	3545	22	AAH98254	Murine EST-derived
7	829	100.0	3615	22	AA503946	Human caspase recr
8	276	33.3	522	22	AA526575	Human CDNA encodin
9	236.5	28.5	5366	20	AA538001	Conadotropic hormo
10	236.5	28.5	5366	20	AA538001	Conadotropic hormo
11	236.5	28.5	5502	17	AAAT30092	Human apoptosis in
12	236.5	28.5	5502	18	AAAT71263	Neuronal apoptosis
13	236.5	28.5	5984	20	AA558000	Neuronal apoptosis
14	236.5	28.5	5984	20	AA558000	Conadotropic hormo
15	236.5	28.5	5984	21	AA538008	Human apoptosis in
16	236.5	28.5	6124	18	AAAT71265	Human NALP CDNA.
17	236.5	28.5	6124	24	ABL67992	Neuronal apoptosis
18	236.5	28.5	6133	18	AAAT71264	Ovary cancer relat
19	236.5	28.5	6228	18	AAAT71266	Neuronal apoptosis
20	120.5	14.5	888	24	ABK22763	Human CDNA encodin
21	120.5	14.5	3030	24	ABK22727	Human CDNA #1 enc
22	120.5	14.5	3063	24	ABK22771	Human CDNA #2 enc
23	120.5	14.5	4322	22	AA165591	Nucleotide sequenc
24	120.5	14.5	37443	22	AA165592	Nucleotide sequenc
25	111	13.4	4141	20	AA209251	Murine CARD-4L cDN
26	111	13.4	4141	22	AA230006	Mouse CARD-4L (lon
27	111	13.4	4141	24	AA140764	DNA of murine CAR
28	107	12.9	1470	24	AA140757	DNA of human CARD-
29	107	12.9	2859	24	AA140755	Human CARD-4S part
30	107	12.9	3080	20	AA209248	Human CARD-4S (ho
31	107	12.9	3080	22	AA230003	CDNA of human CARD
32	107	12.9	3080	24	AA140756	Human CARD-4L (lon
33	107	12.9	3382	22	AA130002	Human CARD-4L (lon
34	107	12.9	3382	24	AA140754	CDNA of human CARD
35	107	12.9	4415	21	AA95791	Apoptosis related
36	107	12.9	4570	22	AA531622	Human polynucleoti
37	107	12.9	4610	22	AAH18313	Human CDNA sequenc
38	107	12.9	5250	22	AA526606	Human polynucleoti
39	107	12.9	32042	20	AA209252	Human CARD-4 DNA.
40	107	12.9	32042	22	AA230011	Human CARD-4 gene.
41	107	12.9	32042	24	AA140765	Genomic DNA of hum
42	104.5	12.6	3300	24	AA147129	Pylin domain conta
43	102.5	12.4	1557	24	AA147143	Human NALP exon 13
44	100.5	12.1	250	20	AA502906	Human APRC polypep
45	100.5	12.1	2460	24	ABA94363	Human APRC polypep

ALIGNMENTS

RESULT 1
ABK22766
ID ABK22766 standard; CDNA: 891 BP.
XX
AC ABK22766;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human CDNA encoding CLAN NACHT.
XX
KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
KW autoimmune disease; inflammation; keratinocyte hyperplasia;
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
KW leukoenemia; allergy; arthritis; lupus; Schriegen's syndrome;
KW Crohn's disease; graft-versus-host disease; stroke;
KW myocardial infarction; heart failure; neurodegenerative disease;

KM Parkinson's disease; Alzheimer's disease; HIV;
KW human immunodeficiency virus infection.
OS Homo sapiens.
XX WO200190156-A2.
XX
XX
XX 29-NOV-2001.
XX
XX 24-MAY-2001; 2001WO-US17158.
XX
XX 24-MAY-2000; 2000US-0579240.
PR 10-OCT-2000; 2000US-0686347.
PR 14-MAR-2001; 2001US-275980P.
PR 23-MAY-2001; 2001US-0864921.
XX
XX (BURN-) BURHAM INST.
XX
XX Reed JC, Plo FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
PI Oliveira VAM, Hayashi H, Pawlowski K;
XX
XX WPI: 2002-083086/11.
DR P-PSDB: AAU80872.
XX
XX New caspase recruitment domain (CARD)-containing polypeptides and
PT encoding nucleic acids, useful for treating abnormal cell proliferation
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
PT arthritis or stroke
XX
XX Claim 1; Page 200-201; 216pp; English.
XX
XX The invention relates to an isolated caspase recruitment domain (CARD)
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
CC from it, and the polynucleotides encoding them. Also included are a
CC recombinant vector comprising the polynucleotide, recombinant cells
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
CC and insect cells) and an anti-CARD antibody. The CARD-containing
CC polypeptide and CARD-encoding nucleic acid are useful for treating a
CC pathology characterised by abnormal cell proliferation (e.g. cancer),
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In
CC particular, the polypeptide and nucleic acid are useful for treating
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
CC muscle cell proliferation in arteries following balloon angioplasty
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukemias,
CC allergies, arthritis, lupus, Crohn's syndrome, Crohn's disease,
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
CC disease) or immunodeficiency associated disease (e.g. human
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
CC in a variety of diagnostic applications. The present sequence is a
CC cDNA encoding a CARD domain containing protein.
XX
XX
SQ Sequence 891 BP; 237 A; 228 C; 217 G; 209 T; 0 other:

Alignment Scores:
Pred. No.: 1.07e-99 Length: 891
Score: 829.00 Matches: 163
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0

US-09-697-089-2_COPY_161_323 (1-163) x ABR22766 (1-891)
QY 1 LeuGlnSerProCysIleIleGlnGlyGluSerGlyLysGlyLysSerThrLeuLeuGln 20
DB 1 CTTAGAGCCCTCGATCATTTGAAGGGAATCTGGCAAGCAAGTCCACTCTGCTGAG 60
QY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
DB 61 CGCATTTGCATGCTCTGGGGCTCCGGAAGATGCAAGGCTCTGACCAATTCATAATTCCTC 120
QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGlnThrLeuCysAspGlnLeu 60

DB 121 TTTCTTCCTCCGCTCAGCAGGGCCAGGGTGCACTTTTGAACCTCTGTGATCAACTC 180
QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 80
DB 181 CTGGATATACCTGGCCACATCAGGAAGCAAGACATTTCATGGCCATCTCTGAAGCTGGG 240
QY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGlnPheLysProGlnAsnCysProGlu 100
DB 241 CAGAGGGTTCTTTCTCTTCTTATGCTACATGAAATTCAGCCCAAGACCTGCCCAAA 300
QY 101 ILeGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr 120
DB 301 ATCGAAGCCCTGATAAAGGAAACCCAGCTTCAAGAACATGCTCATGTCACCACTACC 360
QY 121 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140
DB 361 ACTGAGTGCCTGAGGACACATACGAGATTGGTGGCTGACTGAGAGTGGGGATATG 420
QY 141 ThrGluAspSerArgAlaGlnAlaLeuIleArgGluValIleLysGluLeuAlaGlnGly 160
DB 421 ACAGAAGACAGGCCCCAGGCTCTCATCCGAGAAGTGTGATCAAGAGACTTGTCAAGGC 480
QY 161 LeuLeuLeu 163
DB 481 TTGTTGCTC 489

RESULT 2
ID AAH78218 standard; DNA; 2215 BP.
XX
XX AAH78218;
AC
XX 26-NOV-2001 (first entry)
DE
XX Nucleotide sequence of a human secreted polypeptide.
XX
XX Human; secreted polypeptide; nervous disease; muscular disease; tumour;
KW gastrointestinal ulceration; spinal cord disease; trachea disease;
KW thyroid gland disease; ovary disease; prostate disease; heart disease;
KW renal gland disease; small intestine disease; thymus disease;
KW lymph node disease; muscular system disease; colon disease;
KW lipase deficiency; cystic fibrosis; pancreatitis; clot formation;
KW myocardial infarction; angioplasty; liver disease; coagulation disorder;
KW microbial disease; immune disorder; inflammation; transplant rejection;
KW bone thickness; bone density; ferroxidase loss; apoptosis;
KW vascular smooth cell proliferation; vaccine; ss.
XX
XX Homo sapiens.
OS
XX
XX
XX Key Location/Qualifiers
FH 1.2214
FT CDS
FT /tag= a
FT /product= "secreted polypeptide"
FT /note= "no termination codon given"
XX
XX WO200166690-A2.
XX
XX 13-SEP-2001.
XX
XX 05-MAR-2001; 2001WO-US07143.
XX
XX 06-MAR-2000; 2000US-0187107.
PR 13-MAR-2000; 2000US-0188916.
PR 03-OCT-2000; 2000US-0236874.
PR 03-OCT-2000; 2000US-0237846.
XX
XX (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;
XX WPI: 2001-570768/64.

DR P-PSDB: AAG67526.

XX Novel isolated secreted polypeptide useful for treating nervous and
PT muscular diseases, gastrointestinal ulceration, coagulation and immune
PT disorders, microbial diseases, inflammation and transplant rejection -

XX Claim 2; Page 52-53; 102pp; English.

XX The present sequence encodes a human secreted polypeptide. The
CC secreted polypeptides and polynucleotides are useful for treating
CC nervous and muscular diseases, for inhibiting tumour formation and
CC metastasis, for treating gastrointestinal ulceration, for preventing
CC and treating diseases in spinal cord, thyroid gland, ovary prostate,
CC renal gland, small intestine, heart, trachea, thymus, lymph node,
CC muscular system and colon, for treating lipase deficiency in cystic
CC fibrosis and pancreatitis, for treating undesirable clot formation
CC such as myocardial infarction, during angioplasty and all surgical
CC procedures that require decreased blood clot formation, for treating
CC liver diseases, coagulation disorders and microbial diseases, for
CC treating immune disorders, for treating inflammation and transplant
CC rejection, for enhancing bone thickness and increasing bone density,
CC for reducing the loss of essential ferroxiolases, for suppressing
CC apoptosis, and for regulating vascular smooth cell proliferation. They
CC may also be used as vaccines.

XX Sequence 2215 BP; 621 A; 522 C; 519 G; 553 T; 0 other;

Alignment Scores:

Pred. No.: 3,94e-99 Length: 2215
Score: 829.00 Matches: 163
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-697-089-2_COPY_161_323 (1-163) x AAH78218 (1-2215)

OY 1 LeuGlnSerProCySAllellleGluGluSerGlyGlySerThrLeuGln 20

DB 439 CTTCAGAGCCCTGCATATGGAAGGGAATCTGGCAAGCAATCTCTGTCAG 498

OY 21 ArgIleAlaMetLeuTrpGlySerGlyScylsAlaLeuThrLysPheLysPheVal 40

DB 499 CGAATGGCATGCTCTGGGGCTCCGGAAGTGCAGGCTGACCAAGTCAATTCTGTC 558

OY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 60

DB 559 TTCTTCCCTCCGTCACAGAGGCCCGAGGCTGATTTTGAACCTCTGATCACTGC 618

OY 61 LeuAspIleProGlyThrIleArgGlyGlnThrPheMetAlaMetLeuLeuLysLeuArg 80

DB 619 CTGGATATACCTGGCACAATACGAGAACGACATTCATGAGCCATCTCTGAAGCTGCGG 678

OY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 100

DB 679 CAGAGGGTTCTTTCTCTTCTGATGGCTACAAATGAAATTCAGGCCCAAGTCCAGAGA 738

OY 101 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValIleThrThr 120

DB 739 ATCGAAGCCCTGATMAAGAAACCCACCGCTTCAAGAACATGCTCATGCCACTACCC 798

OY 121 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyLysMet 140

DB 799 ACTGATGCTCCGAGGACATACGAGGAGTTTGGTCCCTGACTGCTGAGAGTGGGGATATG 858

OY 141 ThrGluAspSerAlaGlnAlaLeuIleArgGlnValLeuIleLysGluLeuAlaGluCly 160

DB 889 ACAGAAAGACAGAGGCCAGGCTCTATCCGAGAGTGTGATCAAGAGACTTGTCTAAAGC 918

OY 161 LeuLeuLeu 163

DB 919 TTGTGTGCTC 927

RESULT 3

AAS03945

ID AAS03945 standard; cDNA: 3133 BP.

AC AAS03945;

DT 12-SEP-2001 (first entry)

DE Human caspase recruitment domain 12 (CARD-12) cDNA.

XX Caspase recruitment domain; CARD-12; apoptosis; stress-related pathway;
KW cancer; viral infection; poxvirus; adenovirus; autoimmune disorder;
KW systemic lupus erythematosus; arthritis; neurological disorder; stroke;
KW Alzheimer's disease; amyotrophic lateral sclerosis; haematologic disease;
KW aplastic anaemia; myocardial infarction; inflammatory disorder;
KW Crohn's disease; insulin-dependent diabetes; contact dermatitis;
KW psoriasis; graft rejection; bacterial infection; lepromatous leprosy;
KW tuberculosis; ischaemic brain injury; hypoxic brain injury; ss;
KW kidney ischaemia; reperfusion injury; acute bacterial meningitis;
KW excitotoxic brain damage; liver disease.

OS Homo sapiens.

FX Key Location/Qualifiers

FX CDS 36..3110

FT /tag=a

FT /product="Human CARD-12"

XX WO200130971-A2.

XX 03-MAY-2001.

XX 26-OCT-2000; 2000WO-US29643.

XX 27-OCT-1999; 99US-0161822.

XX (MILL-) MILENNIUM PHARM INC.

XX Bertin J, Robison KE;

XX WPI; 2001-308628/32.

XX P-PSDB; AAU02880.

PS Claim 2; Fig 1; 93pp; English.

XX The sequence represents a cDNA which encodes the human caspase
CC recruitment domain 12 (CARD-12) polypeptide. CARD domains are found in a
CC number of proteins that transmit signals that activate apoptosis and
CC inflammatory pathways in response to stress and other stimuli. Therefore,
CC CARD-12 and its corresponding nucleic acid may be used in treatment and
CC diagnosis of patients suffering from disorders associated with an
CC abnormal level (an increase or a decrease) of apoptotic cell death or
CC abnormal activity of stress-related pathways. The disorders include
CC cancer, viral infections (e.g. caused by poxviruses, adenoviruses),
CC autoimmune disorders (e.g. systemic lupus erythematosus, arthritis),
CC neurological disorders (e.g. Alzheimer's disease, amyotrophic lateral
CC sclerosis), haematologic diseases (e.g. aplastic anaemia, myocardial
CC infarction, stroke), inflammatory and immune system disorders (e.g.
CC Crohn's disease, insulin-dependent diabetes, contact dermatitis,
CC psoriasis, graft rejection), bacterial infections (e.g. tuberculosis,
CC lepromatous leprosy), ischaemic and hypoxic brain injury, kidney
CC ischaemia/reperfusion injury, excitotoxic brain damage, acute bacterial
CC meningitis and liver disease.

SO Sequence 3133 BP; 903 A; 691 C; 729 G; 810 T; 0 other;

Alignment Scores:

Pred. No.: 6.48e-99 Length: 3133

Score: 829.00 Matches: 163
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0

US-09-697-089-2_COPY_161_323 (1-163) x AAS03945 (1-3133)

QY 1 LeuGlnSerProCysIleIleGlnGlySerGlyLysSerThrLeuLeuGln 20
 DB 516 CTTAGAGCCCTGCATCATGTAAGGGGAATCTGGCAAGGCAAGTCACCTCTGCTGAG 575
 QY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
 DB 576 CGCATGGCATGCTCTGGGGCTCCGGAAAGTGAAGGCTGTGACCAAGTTCAAAATTGCTC 635
 QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGlnThrLeuCysAspGlnLeu 60
 DB 636 TTCCTCCCTCCGTCAGAGGGCCAGGGTGGACTTTTGAACCCCTCTGTGATCAACTC 695
 QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 80
 DB 696 CTGATATACCTGGCACAATCAGAGCAAGCATTCATGCCATGCTGCTGAAGCTGGG 755
 QY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGlnPheLysProGlnAsnCysProGln 100
 DB 756 CAGAGGGTCTTTCTCTCTGATGGCTACAAATGAAATTCAGCCCAAGTCCAGAA 815
 QY 101 IleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThr 120
 DB 816 ATCCAAACCCCGATAAAGAAACACCCTTCAAGAAACATGGTCATGTCACACATACC 875
 QY 121 ThrGlnLysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGlnValGlyAspMet 140
 DB 876 ACTAGAGCCCTGAGACACATCGGCAAGTTGGTCCCTGCATGCTGAGAGTGGGGATATG 935
 QY 141 ThrGlnAspSerAlaGlnAlaLeuIleArgGlnValLeuIleLysGlnLeuAlaGlnGly 160
 DB 936 ACAGAAACAGACGCCAGGCTCTCATCGAGAGTGTGATCAAGAGAGCTGTGAAGGC 995
 QY 161 LeuLeuLeu 163
 DB 996 TTGTTGCTC 1004

RESULT 4
 AAH78219
 ID AAH78219 standard; DNA: 3213 BP.
 AC AAH78219;
 XX 26-NOV-2001 (first entry)
 DE Nucleotide sequence of a human secreted polypeptide.
 XX Human: secreted polypeptide; nervous disease; muscular disease; tumour;
 KW gastrointestinal ulceration; spinal cord disease; trachea disease;
 KW thyroid gland disease; ovary disease; prostate disease; heart disease;
 KW renal gland disease; small intestine disease; thymus disease;
 KW lymph node disease; muscular system disease; colon disease;
 KW lipase deficiency; cystic fibrosis; pancreatitis; clot formation;
 KW myocardial infarction; angioplasty; liver disease; coagulation disorder;
 KW microbial disease; immune disorder; inflammation; transplant rejection;
 KW bone thickness; bone density; ferroxidase loss; apoptosis;
 KW vascular smooth cell proliferation; vaccine; ss.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT CDS 1..3213
 FT /*tag= a
 FT /product= "secreted polypeptide"
 XX
 PN MO200166690-A2.

XX 13-SEP-2001.
 PD 05-MAR-2001; 2001MO-US07143.
 XX 06-MAR-2000; 2000US-0187107.
 PR 13-MAR-2000; 2000US-0188916.
 PR 03-OCT-2000; 2000US-0236874.
 PR 03-OCT-2000; 2000US-0237846.
 XX (SMK) SMITHKLINE BEECHAM CORP.
 PA (SMK) SMITHKLINE BEECHAM PLC.
 DR Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;
 DR WPI: 2001-570768/64.
 PT P-PSDB; AAG67527.
 PT Novel isolated secreted polypeptide useful for treating nervous and
 PT muscular diseases, gastrointestinal ulceration, coagulation and immune
 PT disorders, microbial diseases, inflammation and transplant rejection -
 PS Claim 2; Page 53-54; 102pp; English.
 XX The present sequence encodes a human secreted polypeptide. The
 CC secreted polypeptides and polynucleotides are useful for treating
 CC nervous and muscular diseases, for inhibiting tumour formation and
 CC metastasis, for treating gastrointestinal ulceration, for preventing
 CC and treating diseases in spinal cord, thyroid gland, ovary, prostate,
 CC renal gland, small intestine, heart, trachea, thymus, lymph node,
 CC muscular system and colon, for treating lipase deficiency in cystic
 CC fibrosis and pancreatitis, for treating undesirable clot formation
 CC such as myocardial infarction, during angioplasty and all surgical
 CC procedures that require decreased blood clot formation, for treating
 CC liver diseases, coagulation disorders and microbial diseases, for
 CC treating immune disorders, for treating inflammation and transplant
 CC rejection, for enhancing bone thickness and increasing bone density,
 CC for reducing the loss of essential ferroxidases, for suppressing
 CC apoptosis, and for regulating vascular smooth cell proliferation. They
 CC may also be used as vaccines.
 XX

Sequence 3213 BP: 916 A; 704 C; 756 G; 837 T; 0 other;
 Alignment Scores:
 Pred. No.: 6,72e-99 Length: 3213
 Score: 829.00 Matches: 163
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0

US-09-697-089-2_COPY_161_323 (1-163) x AAH78219 (1-3213)

QY 1 LeuGlnSerProCysIleIleGlnGlySerGlyLysSerThrLeuLeuGln 20
 DB 619 CTTAGAGCCCTGCATCATGTAAGGGGAATCTGGCAAGGCAAGTCACCTCTGCTGAG 678
 QY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
 DB 679 CGATTCGCATGCTCTGGGGCTCCGGAAAGTGAAGGCTGTGACCAAGTTCAAAATTGCTC 738
 QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGlnThrLeuCysAspGlnLeu 60
 DB 739 TTCCTCCCTCCGTCAGAGGGCCAGGGTGGACTTTTGAACCCCTGTGATCAACTC 798
 QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 80
 DB 799 CTGATATACCTGGCACAATCAGAGCAAGCATTCATGCCATGCTGTAAGCTGGG 858
 QY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGlnPheLysProGlnAsnCysProGln 100
 DB 859 CAGAGGGTCTTTCTCTCTGATGGCTACAAATGAAATTCAGCCCAAGTCCAGAA 918

QY 101 ILEGUAlaleuilelsgluasnHisArqPheLysAsnMetValIleValThrThrThr 120
DB 919 ATCGAAGCCCTGATTAAGAAACACCCCTTCAAGACATGTGATCTCCACTACC 978
QY 121 ThrGluCysLeuArqHisIleArqGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140
DB 979 ACTGAGTCCCTGAGCAGATACGGCAGATTGGTCCCTGACTGCTGAGGTGGGGATANG 1038
QY 141 ThrGluAspSerAlaGlnAlaLeuileArqGluValIlelelsgluLeuAlaGluGly 160
DB 1039 ACAGAAGACAGCCGCCAGGCTCTCATCCAGAAAGTGATCAAGAGCCTTGTAAGGC 1098
QY 161 LeuLeuLeu 163
DB 1099 TTGTGCTC 1107
RESULT 5
ABK22731
ID ABK22731 standard; cDNA: 3396 BP.
XX
AC ABK22731;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human cDNA encoding CLAN A.
XX
KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
KW autoimmune disease; inflammation; keratinocyte hyperplasia;
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;
KW Crohn's disease; graft-versus-host disease; stroke;
KW myocardial infarction; heart failure; neurodegenerative disease;
KW Parkinson's disease; Alzheimer's disease; HIV;
KW human immunodeficiency virus infection.
XX
OS Homo sapiens.
XX
PN WO200190156-A2.
XX
PD 29-NOV-2001.
XX
PE 24-MAY-2001; 2001WO-US17158.
XX
PR 24-MAY-2000; 2000US-0579240.
PR 10-OCT-2000; 2000US-0686347.
PR 14-MAR-2001; 2001US-275980P.
PR 23-MAY-2001; 2001US-0864921.
XX
PA (BURN-) BURNHAM INST.
PI Reed JC, Plo FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
PI Oliveira VAM, Hayashi H, Pawlowski K;
XX
XX WPI: 2002-083086/11.
DR P-PSDB: AA080861.
XX
XX New caspase recruitment domain (CARD)-containing polypeptides and
PT encoding nucleic acids, useful for treating abnormal cell proliferation
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
PT arthritis or stroke
XX
XX Claim 1; Page 166-171; 216pp; English.
XX
XX The invention relates to an isolated caspase recruitment domain (CARD)
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
CC from it, and the polynucleotides encoding them. Also included are a
CC recombinant vector comprising the polynucleotide, recombinant cells
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
CC and insect cells) and an anti-CARD antibody. The CARD-containing
CC polypeptide and CARD-encoding nucleic acid are useful for treating a
CC pathology characterised by abnormal cell proliferation (e.g. cancer),

CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In
CC particular, the polypeptide and nucleic acid are useful for treating
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
CC muscle cell proliferation in arteries following balloon angioplasty
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
CC disease) or immunodeficiency associated disease (e.g. human
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
CC in a variety of diagnostic applications. The present sequence is a
CC cDNA encoding a CARD domain containing protein.
XX
SQ Sequence 3396 BP; 992 A; 737 C; 793 G; 874 T; 0 other.
Alignment Scores:
Pred. No.: 7,27e-99 Length: 3396
Score: 829.00 Matches: 163
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 24
US-09-697-089-2_COPY_161_323 (1-163) x ABK22731 (1-3396)
QY 1 LeuGlnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeuLeuGln 20
DB 757 CTTTCAGAGCCCTTGATCATCTTAAGGGGAATGTGGCAAGGACCTTGCTGCGAG 816
QY 21 ArgIleAlaMetLeuThrPylSerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
DB 817 CGCATTTGCATCTCTGGGGGCTCCGGAAAGTGCMAAGCCTTACCAAGTTCAAATTGCG 876
QY 41 PhePheLeuArqLeuSerArqAlaGlnGlyLysLeuPheGluThrLeuCysAspGlnLeu 60
DB 877 TTTCTTCCTCCGCTCAGCAGGCGCCAGGGGTGACATTTTGAACCTCTGTGATCAATC 936
QY 61 LeuAspIleProGlyThrIleArqLysGlnThrPheMetAlaMetLeuLeuLysLeuArq 80
DB 937 CTGGATATACCTGGCAATCATCAGAAAGCAGACATTATGCGCATGCTGTAAGCTGCGG 996
QY 81 GlnArqValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 100
DB 997 CAGAGGGTTCTTTTCTCTTCTTATGCTACATTAATTAACCCACAGACTGCCAGAA 1056
QY 101 ILEGUAlaleuilelsgluasnHisArqPheLysAsnMetValIleValThrThrThr 120
DB 1057 ATCGAAGCCCTGATTAAGAAACACCCCTTCAAGAACATGTCATGTCACACTACC 1116
QY 121 ThrGluCysLeuArqHisIleArqGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140
DB 1117 ACTGAGTCCCTGAGCAGATACGGCAGATTGGTCCCTGACTGCTGAGGTGGGGATANG 1176
QY 141 ThrGluAspSerAlaGlnAlaLeuileArqGluValIlelelsgluLeuAlaGluGly 160
DB 1177 ACAGAAGACAGCCGCCAGGCTCTCATCCAGAAAGTGATCAAGAGCCTTGTAAGGC 1236
QY 161 LeuLeuLeu 163
DB 1237 TTGTGCTC 1245
RESULT 6
AAH98254
ID AAH98254 standard; cDNA: 3545 BP.
XX
XX AAH98254;
XX
DT 12-OCT-2001 (first entry)
XX
DE Murine EST-derived coding sequence SEQ ID NO: 111.
XX
KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;

KW diagnostics; forensic test; gene mapping; genetic disorder;
 KW biodiversity; gene therapy; nutrition; ss.
 XX Mus musculus.
 PN WO200154477-A2.
 XX 02-AUG-2001.
 XX 25-JAN-2001; 2001WO-US02687.
 XX 25-JAN-2000; 2000US-0491404.
 PR 17-JUL-2000; 2000US-0617746.
 PR 03-AUG-2000; 2000US-0631451.
 PR 15-SEP-2000; 2000US-0663870.
 XX (HYSEQ-) HYSEQ INC.
 XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
 PI Cao Y, Dermanac RA, Zhang J, Werhman T;
 XX WPI: 2001-476164/51.
 DR P-PSDB: AAM23595.
 XX Isolated polypeptide for treatment of diseases, diagnostics, raising
 PT antibodies and research use -
 XX Claim 1; Page 250-251; 1275pp; English.
 XX The present invention provides the protein and coding sequences of novel
 CC proteins from a variety of organisms, including human, dog, cat, horse,
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
 CC from the organism of interest. They can be used in diagnostics,
 CC forensics, gene mapping, identification of mutations, to assess
 CC biodiversity and for nutritional purposes. The present sequence is a CDNA
 CC of the invention.
 XX .SQ Sequence 3545 BP; 1038 A; 755 C; 816 G; 936 T; 0 other;
 XX
 Alignment Scores:
 Pred. No.: 7 73e-99 Length: 3545
 Score: 829.00 Matches: 163
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0
 US-09-697-089-2_COPY_161_323 (1-163) x AAH98254 (1-3545)
 QY 1 LeuGlnSerProCysIleIleGlnGlyIleuSerGlyLysGlyLysSerThrLeuLeuGln 20
 DB 712 CTTGAGAGCCCTGATGATGGAAGGGAATCTGCAAGCAATCCACCTGTGCGAG 771
 QY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
 DB 772 CGCATTTGCCATGCTCTGGGGCTCCGGAAGTCCAGGCTGCAAGCAAGTTCAAATTCGTC 831
 QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuLysPheLeu 60
 DB 832 TTCTTCCCTCCGCTCAGCAGAGGCCAGGGTGACTTTTGAACCCCTGTGATCAACTC 891
 QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80
 DB 892 CTGGATTAATACCTGGCAGCAATCAGAGACACATTCATGGCCATGCTCTGAAGCTGGG 951
 QY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 100
 DB 952 CAGAGGGGTTCTTCTTCTTCTGATGGCTACATGAATCAAGCCCAACATGCGCCAGAA 1011
 QY 101 IleGluAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThrThr 120
 DB 1012 ATCGAAGCCCTGATTAAGGAAACCCACCGCTTCAAGACATGCTCATGTCACCACTACG 1071

QY 121 ThrGluCysLeuArgHisIleArgGlnPheGluAlaLeuThrAlaGluValGlyAspMet 140
 DB 1072 ACTGAGTCCCTGAGGCAATACAGGAGTGTGGTCCCTGACTGCTGAGCTGGGGATATG 1131
 QY 141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 160
 DB 1132 ACAGAAAGACAGGCCCGCCAGGCTCTCATCCGAGAAAGTGTGATCAAGAGACTTGTGAAGGC 1191
 QY 161 LeuLeuLeu 163
 DB 1192 TTGTGTCTC 1200
 RESULT 7
 ID AAS03946 standard; DNA; 3615 BP.
 AC AAS03946:
 XX AAS03946:
 XX 12-SEP-2001 (first entry)
 DE Human caspase recruitment domain 12 (CARD-12) genomic DNA.
 KW Caspase recruitment domain; CARD-12; apoptosis; stress-related pathway;
 KW cancer; viral infection; poxvirus; adenovirus; autoimmune disorder;
 KW systemic lupus erythematosus; arthritis; neurological disorder; stroke;
 KW Alzheimer's disease; amyotrophic lateral sclerosis; haematologic disease;
 KW aplastic anaemia; myocardial infarction; inflammatory disorder;
 KW Crohn's disease; insulin-dependent diabetes; contact dermatitis;
 KW psoriasis; graft rejection; bacterial infection; lepromatous leprosy;
 KW tuberculosis; ischaemic brain injury; hypoxic brain injury; ds;
 KW kidney ischaemia; reperfusion injury; acute bacterial meningitis;
 KW excitotoxic brain damage; liver disease.
 XX Homo sapiens.
 XX Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 1..3615
 FT /tag= a
 FT /product= "Human CARD-12"
 XX WO200130971-A2.
 XX 03-MAY-2001.
 PD 26-OCT-2000; 2000WO-US29643.
 PF 27-OCT-1999; 99US-0161822.
 PR (MILL-) MILLENNIUM PHARM INC.
 PA Bertin J, Robison KE;
 XX P-PSDB: AAU02881.
 DR WPI: 2001-308628/32.
 DR 12-SEP-2001
 PT Isolated caspase recruitment domain-12 polypeptide and nucleic acids
 PT encoding them, useful for treating and diagnosing disorders associated
 PT with abnormal apoptosis such as cancer, arthritis and Alzheimer's
 PT disease -
 XX Disclosure: Fig 2; 93pp; English.
 PS The sequence represents a genomic DNA which encodes the human caspase
 CC recruitment domain 12 (CARD-12) polypeptide. CARD domains are found in a
 CC number of proteins that transmit signals that activate apoptosis and
 CC inflammatory pathways in response to stress and other stimuli. Therefore,
 CC CARD-12 and its corresponding nucleic acid may be used in treatment and
 CC diagnosis of patients suffering from disorders associated with an
 CC abnormal level (an increase or a decrease) of apoptotic cell death or
 CC abnormal activity of stress-related pathways. The disorders include
 CC cancer, viral infections (e.g. caused by poxviruses, adenoviruses),
 CC autoimmune disorders (e.g. systemic lupus erythematosus, arthritis),

CC neurological disorders (e.g. Alzheimer's disease, amyotrophic lateral sclerosis), haematologic diseases (e.g. aplastic anaemia, myocardial infarction, stroke), inflammatory and immune system disorders (e.g. Crohn's disease, insulin-dependent diabetes, contact dermatitis, psoriasis, graft rejection), bacterial infections (e.g. tuberculosis, lepromatous leprosy), ischaemic and hypoxic brain injury, kidney ischaemia/reperfusion injury, excitotoxic brain damage, acute bacterial meningitis and liver disease.

XX Sequence 3615 BP: 1041 A; 811 C; 845 G; 918 T; 0 other;

Alignment Scores:

Pred. No.:	7.95e-99	Length:	3615
Score:	829.00	Matches:	163
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09-697-089-2_copy_161_323 (1-163) x AAS03946 (1-3615)

QY 1 LeuGlnSerProCysIleIleGluGlyIleuSerGlyIysGlyLysSerThrLeuGln 20
Db 952 CTTCAAGACCCCTGCATCATTCGAAGGCAATCTGGCAAGGCAAGTCCACTCTCTGCAG 1011
QY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysIysAlaLeuThrLysPheVal 40
Db 1012 CGAATTGCCATGCTCTGGGGCTCCGGAAAGTGCAGAGCTCTGACCAAGTCCAAATTCTTC 1071
QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspLeu 60
Db 1072 TTCTTCCTCCGCTCAGACAGGGCCAGGGTGGACTTTTGAACCTCTGATCAACTC 1131
QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80
Db 1132 CTGGATATACCTGGACCAATAGAGAGCAATCATGCCATCTGCTGAAGCTGCGG 1191
QY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAspProGlu 100
Db 1192 CAGAGGGTCTTTCTCTTGGATGGCTACAAATGAAATTCAGCCCAAGCTGCCAGAA 1251
QY 101 IleGluAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThr 120
Db 1252 ATCGAAGCCCTGATTAAGAAACACCGCTTCAAGAAACATGGTCATGCCACTACC 1311
QY 121 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140
Db 1312 ACTGAGTCCCTGAGGACATAGAGCAGATTGTGCTGCTGACTGCTGAGAGTGGGATATG 1371
QY 141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGlnLeuAlaGluLys 160
Db 1372 ACAGAAAGACAGCCCAAGCTCTCATCCGAGAAGTGTGATCAAGGAGCTTGCAAGG 1431
QY 161 LeuLeuLeu 163
Db 1432 TTGTTGCTC 1440

RESULT 8

AAS26575 standard; cDNA: 522 BP.

XX AAS26575;

XX 07-NOV-2001 (first entry)

XX Human cDNA encoding a novel secreted protein, Seq ID 754.

XX Human: immunosuppressive; antiarthritic; ss; antirheumatic;

KW cytosolic; cardiant; vasotropic; cerebroprotective; nootropic;

KW neuroprotective; antibacterial; vitucide; fungicide; ophthalmological;

KW vulnerary; secreted protein; rheumatoid arthritis;

KW hyperproliferative disorder; cardiovascular disorder; cardiac arrest;

KW cerebrovascular disorder; cerebral ischaemia; angiogenesis;

KW nervous system disorder; Alzheimer's disease; infection; ocular disorder;

KW corneal infection; wound healing; epithelial cell proliferation;

KW skin ageing; food additive; preservative; antiproliferative.

XX Homo sapiens.

XX WO20015322-A2.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US01341.

XX 31-JAN-2000; 2000US-0179065.

XX 04-FEB-2000; 2000US-0180628.

XX 24-FEB-2000; 2000US-0184664.

XX 02-MAR-2000; 2000US-0186350.

XX 16-MAR-2000; 2000US-0189874.

XX 17-MAR-2000; 2000US-0190076.

XX 18-APR-2000; 2000US-0198123.

XX 19-MAY-2000; 2000US-0205515.

XX 07-JUN-2000; 2000US-0209467.

XX 28-JUN-2000; 2000US-0214886.

XX 30-JUN-2000; 2000US-0215135.

XX 07-JUL-2000; 2000US-0216647.

XX 07-JUL-2000; 2000US-0216880.

XX 11-JUL-2000; 2000US-0217487.

XX 11-JUL-2000; 2000US-0217496.

XX 14-JUL-2000; 2000US-0218290.

XX 26-JUL-2000; 2000US-0220963.

XX 26-JUL-2000; 2000US-0220964.

XX 14-AUG-2000; 2000US-0224518.

XX 14-AUG-2000; 2000US-0224519.

XX 14-AUG-2000; 2000US-0225213.

XX 14-AUG-2000; 2000US-0225214.

XX 14-AUG-2000; 2000US-0225266.

XX 14-AUG-2000; 2000US-0225267.

XX 14-AUG-2000; 2000US-0225268.

XX 14-AUG-2000; 2000US-0225270.

XX 14-AUG-2000; 2000US-0225447.

XX 14-AUG-2000; 2000US-0225757.

XX 14-AUG-2000; 2000US-0225758.

XX 14-AUG-2000; 2000US-0225759.

XX 18-AUG-2000; 2000US-0226279.

XX 22-AUG-2000; 2000US-0226681.

XX 22-AUG-2000; 2000US-0226868.

XX 22-AUG-2000; 2000US-0227182.

XX 23-AUG-2000; 2000US-0227009.

XX 30-AUG-2000; 2000US-0228924.

XX 01-SEP-2000; 2000US-0229287.

XX 01-SEP-2000; 2000US-0229343.

XX 01-SEP-2000; 2000US-0229344.

XX 01-SEP-2000; 2000US-0229345.

XX 05-SEP-2000; 2000US-0229509.

XX 05-SEP-2000; 2000US-0229513.

XX 06-SEP-2000; 2000US-0230437.

XX 06-SEP-2000; 2000US-0230438.

XX 08-SEP-2000; 2000US-0231242.

XX 08-SEP-2000; 2000US-0231243.

XX 08-SEP-2000; 2000US-0231244.

XX 08-SEP-2000; 2000US-0231413.

XX 08-SEP-2000; 2000US-0231414.

XX 08-SEP-2000; 2000US-0232080.

XX 08-SEP-2000; 2000US-0232081.

XX 12-SEP-2000; 2000US-0231968.

XX 14-SEP-2000; 2000US-0232397.

XX 14-SEP-2000; 2000US-0232398.

XX 14-SEP-2000; 2000US-0232399.

XX 14-SEP-2000; 2000US-0232400.

XX 14-SEP-2000; 2000US-0232401.

XX 14-SEP-2000; 2000US-0233063.

XX 14-SEP-2000; 2000US-0233064.

XX 14-SEP-2000; 2000US-0233065.

XX 21-SEP-2000; 2000US-0234223.

PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 13-OCT-2000; 2000US-0239393.
PR 13-OCT-2000; 2000US-0239397.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241121.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 01-NOV-2000; 2000US-0241826.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249267.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251968.
PR 05-DEC-2000; 2000US-0256179.
PR 05-DEC-2000; 2000US-0251749.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.

PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI: 2001-488783/53.
DR P-PSDB; AAU16588.
XX
PT New nucleic acid molecules encoding 461 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives -
XX
PS Claim 1; SEQ ID No 754; 980pp; English.

CC The invention relates to isolated nucleic acid molecules and their
CC encoded secreted proteins. The nucleic acids and proteins are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They
CC are also used in diagnosing a pathological condition or susceptibility
CC to a pathological condition. Antibodies to the proteins can also
CC be used in alleviating symptoms associated with the disorders and in
CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked
CC immunosorbant assays (ELISA). Disorders which are diagnosed or treated
CC include autoimmune diseases e.g. rheumatoid arthritis,
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC e.g. cerebral ischemia, angiodenesis, nervous system disorders e.g.
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi
CC and ocular disorders e.g. corneal infection, and many other
CC disorders listed in the specification. The polypeptides can also
CC be used to aid wound healing and epithelial cell proliferation, to
CC prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors and other nutritional components. The present
CC sequence encodes a novel secreted protein of the invention.

Alignment Scores:

Pred. No.: 6.88e-27 Length: 522
Score: 276.00 Matches: 69
Percent Similarity: 81.1% Conservative: 4
Best Local Similarity: 76.67% Mismatches: 13
Query Match: 33.29% Indels: 6
DB: 22 Gaps: 1

US-09-697-089-2_COPY_161_323 (1-163) x AAS26575 (1-522)

QY 1 LeuGlnSerProCysIleIleGluGluSerGlyLysGlyLysSerThrLeuGln 20
DB 246 CTTGAGACCCCTTCATCATATTGAAGGGGAATCTGGCAAGGCAAGTCATTCCTGCTCAG 305
QY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheVal 40
DB 306 CGCATTCGCATGCTCTGGGGCTCCGGAAGTGAAGGAGCTGTGACCAAGTTCAANTTCGT 365
QY 40 Lphe-PheLeuArgLeuSerArgAlaGlnGly-GlyLeuPheGluThrLeuCysASPglu 59
DB 366 CTTCTTCCTCTCTGTCAGCAGGCGCCAGGCTGAGACTTTTGAACCCCTGTGATCAAA 425
QY 60 LeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLys 79
DB 426 TTCCG-GGTATACCGGAGCA-TTCAGAGAGGAGACATTACAGCCNGGT---GCTGAGGTG 480
QY 80 ArgGlnArgValLeuPheLeuLeu 87
DB 481 CGGCAAGAGGTTCTTTTCNTCTTG 504
RESULT 9
AAS58001

ID AAX58001 standard; cDNA to mRNA; 5366 BP.
XX AAX58001;
AC
XX
XX 20-JUL-1999 (first entry)
DT
XX
XX Gonadotropic hormone coding sequence.
DE
XX Gonadotropic hormone coding sequence.
XX
XX Gonadotropic hormone; excessive ovulation animal; transgenic animal;
KW totipotent cell; somatic cell chromosome; ds.
XX
XX Homo sapiens.
OS
XX JP1113444-A.
PN
XX 27-APR-1999.
PD
XX 14-OCT-1997; 97JP-0280830.
PF
XX 14-OCT-1997; 97JP-0280830.
PR
XX 14-OCT-1997; 97JP-0280830.
XX
XX (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
PA (SAKA/) SAKAI H.
DR WPI; 1999-320709/27.
XX P-PSDB; AAY14080.
DR
XX An excessive ovulation animal - useful for improving the
PT productivity of animals
PS
XX Claim 1; Page 9-11; 18pp; Japanese.
XX
XX This sequence encodes a gonadotropic hormone.
CC The invention relates to an excessive ovulation animal, which is a
CC transgenic animal with a totipotent cell containing a DNA fragment
CC containing a promoter sequence and a gonadotropic hormone coding
CC sequence. The DNA fragment is in the somatic cell chromosome. The
CC excessive ovulation animal is useful for improving the productivity of
CC animals. The method can improve the productivity of a useful animal.
XX
SQ Sequence 5366 BP; 1483 A; 1173 C; 1222 G; 1488 T; 0 other;

Alignment Scores:
Pred. No.: 3,266-20 Length: 5366
Score: 236.50 Matches: 53
Percent Similarity: 58.96% Conservative: 26
Best Local Similarity: 39.55% Mismatches: 48
Query Match: 28.53% Indels: 7
DB: Gaps: 3
US-09-697-089-2_COPY_161_323 (1-163) x AAX58001 (1-5366)
QY 1 LeuGlnSerProCysIleIleGlnGlyIuSerGlyLysGlyLysSerThrLeuGln 20
Db 1675 TTGAACCTCTGCATCTGTGGGCACTGGATGCTGCCCTGTTAAACAGGTTCCAGCTGTT 1734
QY 21 ArgIleAlaMetLeuTrpGlySerGlyLysGlyLysAlaLeuThrLysPheIleVal 40
Db 1735 AAAATAGCTTTTCTGTGGGCACTGGATGCTGCCCTGTTAAACAGGTTCCAGCTGTT 1794
QY 41 PhePheLeuArgLeuSer-----ArgAlaGlnGlyLeuPheGluThrLeuGlyAsp 58
Db 1795 TTTCACCTCTCCCTTAGTCCACGACGACGAGGCGCTGGCCAGTATCTGTAC 1854
QY 59 GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLys 78
Db 1855 CAGCTCCTAGAGAAAGAGATCTGTACTGAAATGTGCATGAGGACATTTATCCAGCAG 1914
QY 79 LeuArgGlnArgValIleuPheLeuLeuAspGlyIleArgLysGlnPhe-----LysProGln 96
Db 1915 TTAAAGATTCAGGCTTATTTCTTTAGATGACTTACAAAGAAATATGTCTCAATCCCTCAA 1974
QY 97 AsnGlyProGluIleGluAlaLeuIleLysGlnLysAsnHisArgPheLysAsnMetValIle 116

Db 1975 -----GTCATAGGAAGAACTGATTCAGAAAAAACACATATCCCGAGACTGCTATGTG 2025
QY 117 ValThrThrThrGluCysLeuArgHisIleArgGlnPhe 130
Db 2026 ATTGCTGTCCGTAACAAGAGGCGCAGGACATCCCGCATAC 2067
RESULT 10
AAX56273
ID AAX56273 standard; cDNA to mRNA; 5366 BP.
XX AAX56273;
AC
XX 20-JUL-1999 (first entry)
DT
XX
XX Human apoptosis inhibiting protein encoding cDNA #2.
DE
XX Human apoptosis inhibitory protein; apoptotic disease; diagnosis;
KW Human; apoptosis inhibitory protein; apoptotic disease; diagnosis;
KW spinal muscular atrophy; ds.
XX
XX Homo sapiens.
OS
XX JP1116599-A.
PN
XX 27-APR-1999.
PD
XX 14-OCT-1997; 97JP-0280831.
PF
XX 14-OCT-1997; 97JP-0280831.
PR
XX 14-OCT-1997; 97JP-0280831.
XX
XX (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
PA
XX WPI; 1999-323531/27.
DR P-PSDB; AAY09540.
XX
XX New apoptosis inhibitory protein - useful for determining mechanism
PT of various apoptotic diseases e.g. human spinal muscular atrophy
XX
XX Claim 8; Page 13-15; 16pp; Japanese.
XX
XX The present sequence encodes a human apoptosis inhibitory protein.
CC The apoptosis inhibitory protein is useful for the elucidation of
CC the mechanism of various apoptosis diseases such as human spinal
CC muscular atrophy and the diagnosis, the prevention and the treatment
CC of such diseases.
XX
SQ Sequence 5366 BP; 1483 A; 1173 C; 1222 G; 1488 T; 0 other;

Alignment Scores:
Pred. No.: 3,266-20 Length: 5366
Score: 236.50 Matches: 53
Percent Similarity: 58.96% Conservative: 26
Best Local Similarity: 39.55% Mismatches: 48
Query Match: 28.53% Indels: 7
DB: Gaps: 3
US-09-697-089-2_COPY_161_323 (1-163) x AAX56273 (1-5366)
QY 1 LeuGlnSerProCysIleIleGlnGlyIuSerGlyLysGlyLysSerThrLeuGln 20
Db 1675 TTGAACCTCTGCATCTGTGGGCACTGGATGCTGCCCTGTTAAACAGGTTCCAGCTGTT 1734
QY 21 ArgIleAlaMetLeuTrpGlySerGlyLysGlyLysAlaLeuThrLysPheIleVal 40
Db 1735 AAAATAGCTTTTCTGTGGGCACTGGATGCTGCCCTGTTAAACAGGTTCCAGCTGTT 1794
QY 41 PhePheLeuArgLeuSer-----ArgAlaGlnGlyLeuPheGluThrLeuGlyAsp 58
Db 1795 TTTCACCTCTCCCTTAGTCCACGACGACGAGGCGCTGGCCAGTATCTGTAC 1854
QY 59 GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLys 78
Db 1855 CAGCTCCTAGAGAAAGAGATCTGTACTGAAATGTGCATGAGGACATTTATCCAGCAG 1914

DR WPI: 1997-38535/35.
XX New neuronal inhibitor of apoptosis - useful for diagnosing and
PT treating, e.g. cancer, AIDS or amyotrophic lateral sclerosis
XX
XX Example 4; Fig 5A-L; 102pp; English.
PS
XX A new neuronal apoptosis inhibitor protein (NAIP) cDNA clone
CC (AA71263) was isolated from a human foetal spinal cord cDNA library
CC by probing with the genomic insert in cosmid 25086, containing a
CC CAPT locus. An additional coding sequence (AA71264), including
CC exon 14a (see also AA71265 and AA71266), was subsequently obtd.
CC The NAIP DNA sequence including exon 14a appears to be a
CC predominant gene isoform which is not deleted or mutated in spinal
CC muscular atrophy (SMA) patients. The NAIP gene was mapped to
CC 5q13.1. NAIP (see also AA720032 and AA720033) is a negative regulator
CC of apoptosis, partic. neuronal apoptosis and, when deficient or
CC absent, contributes to neurodegenerative phenotypes such as SMA and
CC amyotrophic lateral sclerosis.
XX
SQ Sequence 5502 BP; 1560 A; 1226 C; 1206 G; 1510 T; 0 other;

Alignment Scores:
Pred. No.: 3.38e-20 Length: 5502
Score: 236.50 Matches: 53
Percent Similarity: 58.96% Conservative: 26
Best Local Similarity: 39.55% Mismatches: 48
Query Match: 28.53% Indels: 7
DB: 18 Gaps: 3

US-09-697-089-2_COPY_161_323 (1-163) x AA71263 (1-5502)
QY 1 LeuGlnSerProCysIleIleGlnGlyGlnSerGlyLysGlyLysSerThrLeuGln 20
DB 1779 TTGAACCTGTCATGTCGTGTGGAGGTGAAGCTGGAAGACGGCTCTCTGGAAG 1838
QY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
DB 1839 AAAATAGCTTTTCTGTGGCATCTGATGCTCTCCCTGTTAAACAGGTTCCAGCTGGTT 1898
QY 41 PhePheLeuArgLeuSer-----ArgAlaGlnGlyGlyLeuPheGlnThrLeuGln 58
DB 1899 TTCTACCTCTCCCTAGTTCACACAGACAGAGGGGCTGGCAGTATCATCTGTGAC 1958
QY 59 GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLys 78
DB 1959 CAGCTCCCTAGAGAAAGAGATCTGTACTGAATGTCATGAGAGACATTATCCAGCAG 2018
QY 79 LeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPhe-----LysProGln 96
DB 2019 TTAAGAAATCAAGCTTATCTTCTTTAGATGACTACAAAGAAATATGTTCAATCCCTCAA 2078
QY 97 AsnCysProGluIleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIle 116
DB 2079 -----GTCATAGGAAGAACTGATCAAAAAAACCACTATCCCGGACTGCTATTG 2129
QY 117 ValThrThrThrThrGlnCysLeuArgHisIleArgGlnPhe 130
DB 2130 ATTGCTGTCCGTACAAACAGGGCCAGGACATCCGCCGATAC 2171

RESULT 13
AAK58000 ID AAK58000 standard; cDNA to mRNA; 5984 BP.
XX
XX AAK58000;
DE 20-JUL-1999 (first entry)
XX Gonadotropic hormone coding sequence.
XX Gonadotropic hormone; excessive ovulation animal; transgenic animal;
KM totipotent cell; somatic cell chromosome; ds.
XX

OS Homo sapiens.
XX JP11113444-A.
XX
XX 27-APR-1999.
XX
XX 14-OCT-1997; 97JP-0280830.
XX
XX 14-OCT-1997; 97JP-0280830.
XX
XX 14-OCT-1997; 97JP-0280830.
XX
XX (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
XX (SAKA/) SAKAI H.
DR WPI: 1999-320709/27.
DR P-PSDB: AAV14079.
PT An excessive ovulation animal - useful for improving the
PT productivity of animals
XX
XX Claim 1; Page 7-9; 18pp; Japanese.
XX
XX This sequence encodes a gonadotropic hormone.
XX The invention relates to an excessive ovulation animal, which is a
XX transgenic animal with a totipotent cell containing a DNA fragment
XX containing a promoter sequence and a gonadotropic hormone coding
XX sequence. The DNA fragment is in the somatic cell chromosome. The
XX excessive ovulation animal is useful for improving the productivity of
XX animals. The method can improve the productivity of a useful animal.
SQ Sequence 5984 BP; 1777 A; 1267 C; 1267 G; 1673 T; 0 other;

Alignment Scores:
Pred. No.: 3.81e-20 Length: 5984
Score: 236.50 Matches: 53
Percent Similarity: 58.96% Conservative: 26
Best Local Similarity: 39.55% Mismatches: 48
Query Match: 28.53% Indels: 7
DB: 20 Gaps: 3

US-09-697-089-2_COPY_161_323 (1-163) x AAK58000 (1-5984)
QY 1 LeuGlnSerProCysIleIleGlnGlyGlnSerGlyLysGlyLysSerThrLeuGln 20
DB 1675 TTGAACCTGTCATGTCGTGTGGAGGTGAAGCTGGAAGACGGCTCTCTGGAAG 1734
QY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
DB 1735 AAAATAGCTTTTCTGTGGCATCTGATGCTCTCCCTGTTAAACAGGTTCCAGCTGGTT 1794
QY 41 PhePheLeuArgLeuSer-----ArgAlaGlnGlyGlyLeuPheGlnThrLeuGln 58
DB 1795 TTCTACCTCTCCCTTAGTTCACACAGACAGAGGGGCTGGCAGTATCATCTGTGAC 1854
QY 59 GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLys 78
DB 1855 CAGCTCCCTAGAGAAAGAGATCTGTACTGAATGTCATGAGAACTATGTTCAATCCCTCAA 1914
QY 79 LeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPhe-----LysProGln 96
DB 1915 TTAAGAAATCAAGCTTATCTTCTTTAGATGACTACAAAGAAATATGTTCAATCCCTCAA 1974
QY 97 AsnCysProGluIleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIle 116
DB 1975 -----GTCATAGGAAGAACTGATCAAAAAAACCACTTATCCCGGACTGCTATTG 2025
QY 117 ValThrThrThrThrGlnCysLeuArgHisIleArgGlnPhe 130
DB 2026 ATTGCTGTCCGTACAAACAGGGCCAGGACATCCGCCGATAC 2067

RESULT 14
AAK56272 ID AAK56272 standard; cDNA to mRNA; 5984 BP.
XX

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 31, 2003, 11:50:07 ; Search time 1331.94 Seconds

(without alignments)
1981.965 Million cell updates/sec

Title: US-09-697-089-2_COPY_161_323

Perfect score: 829

Sequence: 1 LQSPCTIEGSGKSTLLQ.....SAQALIREVLIKEALBGLL 163

Scoring table:
BIOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+g2n.model -DEV=xlh
-O=/cgn2_1/USPTO.spool/US09697089/Runat_29012003_092754_19729/app_query.fasta.1.981
-DB=ST -QFMT=faaap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=1 -MATRIX=blowsum62 -TRANS=humand40.cdi -LIST=45
-DOCLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09697089 -GCN.1_1_185 -grunat.29012003_092754_19729 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAP -LARGEOUTERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THRADE=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estinu:*
5: em_estov:*
6: em_estopl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	622	75.0	650	10	BB627584
2	318	38.4	619	17	BH2671584
3	274	33.1	518	17	BH348412
4	272	32.8	817	17	BH358172
5	231.5	27.9	1058	13	BM477340
6	226	27.3	697	17	BH293386
7	139.5	16.8	546	17	AZ362463
8	135	16.3	668	17	AZ762115
9	133.5	16.1	515	14	BQ365804
10	123	14.8	728	9	AL652549
11	121.5	14.7	556	17	AZ941653
12	120	14.5	345	13	BG994836
13	116	14.0	586	13	BG994334
14	110	13.3	361	10	AW504276
15	105.5	12.7	939	12	BE887277
16	103	12.4	981	17	AZ138405
17	98.5	11.9	302	9	AA853292
18	96	11.6	146	13	B1685879
19	95.5	11.5	1156	12	BE731237
20	94.5	11.4	959	10	BE468715
21	94	11.3	870	12	BG745278
22	93.5	11.3	782	17	AZ137956
23	93	11.2	409	9	AA997492
24	91	11.0	1039	17	CNS02NVI
25	90.5	10.9	523	17	AZ171618
26	88.5	10.7	3368	11	BC012172
27	88.5	10.7	3369	11	BC012789
28	87	10.5	538	17	AZ192862
29	86.5	10.4	844	17	AZ209193
30	86	10.4	894	9	AL544013
31	85.5	10.3	708	10	BE374417
32	85.5	10.3	891	17	AZ202697
33	85	10.3	464	12	BE932231
34	85	10.3	691	9	AI344276
35	84	10.1	418	13	BJ228034
36	84	10.1	473	9	AT698228
37	84	10.1	670	10	BB633515
38	83	10.0	699	9	AL505087
39	83	10.0	993	12	BE902227
40	83	10.0	1098	13	BM547125
41	82	9.9	420	17	AZ161566
42	81.5	9.8	831	17	BH467737
43	81	9.8	682	13	BJ215942
44	80.5	9.7	639	9	AU239615
45	80.5	9.7	639	12	BF325534

ALIGNMENTS

RESULT 1
LOCUS BB627584
DEFINITION BB627584 RIKEN full-length enriched, adult male urinary bladder Mus
ACCESSION BB627584
VERSION BB627584.1 GI:16465218
KEYWORDS
SOURCE
ORGANISM house mouse.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 650)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanaagaki,T., Hara,A.,
Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,T., Kono,H., Kouda

(<http://www.chori.org/bacpac/rat230.htm>). For BAC library availability, please contact Pieter de Jong (pdjong@mail.cho.org).

Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orering_information.htm). BAC end page: http://www.tigr.org/tldb/bac_ends/rat/bac_end_intro.html

Plate: 19 row: B column: 22
Seq primer: SP6
Class: BAC ends.

FEATURES

source

location/Qualifiers
1. 619
/organism="Rattus norvegicus"
/strain="BN/SSNhsd/MCM"
/db_xref="taxon:10116"
/clone="CH230-19B2"
/clone_lib="CHORI-230 Segment 1"
/sex="Female"
/cell_type="Brain"
/note="Vector: PTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI; CHORI-230 Rat (BN/SSNhsd/MCM) BAC library produced by Pieter de Jong"

BASE COUNT 163 a 141 c 158 g 157 t
ORIGIN

Alignment Scores:

Pred. No.:	3.85e-32	Length:	619
Score:	318.00	Matches:	62
Percent Similarity:	85.06%	Conservative:	12
Best Local Similarity:	71.26%	Mismatches:	13
Query Match:	38.36%	Indels:	0
DB:	17	Gaps:	0

US-09-697-089-2_COPY_161_323 (1-163) x BH267158 (1-619)

QY 1 LeuGlnSerProGlyIleIleGluGlyIleuSerGlyIleuSerThrLeuGln 20

DB 263 CTGAAGACTCCCTGCTATTGAGGAGGAGTGGCAAGGAGGAGTCCCTGCTGCA 204

QY 21 ArgIleAlaMetLeuTrpGlySerGlyIleuSerGlyIleuSerThrLeuGln 40

DB 203 AAAATGCGCATGCTGTGGGCTATGAGATGCGCCAGCTCTGACCAATTCAATGCTC 144

QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyIleuPheGluTrpLeuGlnLeu 60

DB 143 TTCTTCATCCCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 84

QY 61 LeuAspIleProGlyThrIleArgGlnThrPheMetAlaMetLeuLeuLeuArg 80

DB 83 GTGAACATACCTGACTCATGAGCAACCAACCTTCAGGCTGCTGCTGAGTTACAC 24

QY 81 GlnArgValIleuPheLeuLeu 87

DB 23 AAGAAAGTCTCTTTCTCTC 3

RESULT 3 BH348412 518 bp DNA linear GSS 03-DEC-2001

LOCUS CH230-42F7.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone

DEFINITION BH348412 CH230-42F7, DNA sequence.

ACCESSION BH348412 GSS. BH348412.1 GI:17279146

VERSION BH348412.1 GI:17279146

KEYWORDS Norway rat.

SOURCE Rattus norvegicus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 518) Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de Jong, P. and Fraser, C. M.

TITLE Rat BAC End Sequences from Library CHORI-230 EcoRI segment

JOURNAL Unpublished (1999)

COMMENT Other_GSSs: CH230-42F7.TJ

Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhaog@tigr.org

Clones are derived from the rat BAC library CHORI-230 (<http://www.chori.org/bacpac/rat230.htm>). For BAC library availability, please contact Pieter de Jong (pdjong@mail.cho.org).

Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orering_information.htm). BAC end page: http://www.tigr.org/tldb/bac_ends/rat/bac_end_intro.html

Plate: 42 row: F column: 7
Seq primer: T7
Class: BAC ends.

FEATURES

source

location/Qualifiers
1. 518
/organism="Rattus norvegicus"
/strain="BN/SSNhsd/MCM"
/db_xref="taxon:10116"
/clone="CH230-42F7"
/clone_lib="CHORI-230 Segment 1"
/sex="Female"
/cell_type="Brain"
/note="Vector: PTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI; CHORI-230 Rat (BN/SSNhsd/MCM) BAC library produced by Pieter de Jong"

BASE COUNT 133 a 124 c 146 g 115 t
ORIGIN

Alignment Scores:

Pred. No.:	2.47e-26	Length:	518
Score:	274.00	Matches:	55
Percent Similarity:	91.94%	Conservative:	2
Best Local Similarity:	88.71%	Mismatches:	5
Query Match:	33.05%	Indels:	0
DB:	17	Gaps:	0

US-09-697-089-2_COPY_161_323 (1-163) x BH348412 (1-518)

QY 101 IleGluAlaLeuIleuGlyIleuGlyIleuGlyIleuGlyIleuGlyIleuGlyIleu 120

DB 2 ATCGAGGCGCCGTGTAAGAAACCATGCTTCAAGAACATGCTATGCTACACGCC 61

QY 121 ThrGluSerLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140

DB 62 ACGAGTGCTGAGGACATGACACACGCTGCGCCCTGACTGTGAGGTGGAGATATG 121

QY 141 ThrGluSerLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 160

DB 122 ACCGAGACACGCCGCGGAGTTCATCGGAGAGTGTGATTAATGAATGCTGAGGCC 181

QY 161 LeuLeu 162

DB 182 TTGTTG 187

RESULT 4 BH358172 817 bp DNA linear GSS 03-DEC-2001

LOCUS CH230-18E7.TJB CHORI-230 Segment 1 Rattus norvegicus genomic clone

DEFINITION BH358172 CH230-18E7, DNA sequence.

ACCESSION BH358172 GSS. BH358172.1 GI:17288906

VERSION BH358172.1 GI:17288906

KEYWORDS Norway rat.

SOURCE Rattus norvegicus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 817) Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de

RESULT 6
BH293386
LOCUS
DEFINITION BH293386 697 bp DNA linear GSS 30-NOV-2001
CH230-44G15.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
ACCESSION BH293386
VERSION BH293386.1 GI:17205794
KEYWORDS GSS.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 697)
Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shwartsbeyn
, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de
Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)
OTHER GSS: CH230-44G15.TJ
COMMENT
TITLE JOURNAL
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 44 Row: 6 Column: 15
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1..697
/organism="Rattus norvegicus"
/strain="BN/SSNhsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-44G15"
/clone_lib="CHORI-230 Segment 1"
/sex="Female"
/cell_type="Brain"
/note="Vector: pPARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SSNhsd/MCW) BAC library produced by
Pieter de Jong"

BASE COUNT 182 a 165 c 190 g 160 t
ORIGIN

Alignment Scores:
Pred. No.: 1,05e-19 Length: 697
Score: 226.00 Matches: 50
Percent Similarity: 89.47% Conservative: 1
Best Local Similarity: 87.72% Mismatches: 6
Query Match: 27.26% Indels: 1
DB: 17 Gaps: 0

US-09-697-089-2_COPY_161_323 (1-163) x BH293386 (1-697)

QY 106 LysGluSnHISArgPheLysAspMetValIleValThrThrThrThrGluCysLeuArg 125
DB 11 AAGGAAACCAATGCG-TTTAAGAACATGCTGTCACACACCGAGTGCCTGAGG 69

QY 126 HisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMetThrGluAspSerAla 145
DB 70 CACATTCAGACACGTTGGCGCCCTGACTGTGAGTGGAGATATGACCGAAGACAGCCCC 129

QY 146 GlnAlaIleuIleArgGluValLeuIleLysGluLeuAlaGluGlyLeuLeu 162
DB 130 CGAGTTCATCCGGAAGTCTGATAAATGAACTGCGCTGAAGGCTTGTG 180

RESULT 7
AZ362463/c
LOCUS
DEFINITION AZ362463 546 bp DNA linear GSS 02-OCT-2000
1M0107N03R Mouse 10kb plasmid U06C1M library Mus musculus genomic
clone U06C1M0107N03 R, DNA sequence.
ACCESSION AZ362463
VERSION AZ362463.1 GI:10476163
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 546)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
COMMENT
TITLE JOURNAL
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0107 row: N column: 03
Seq primer: CACACAGGAACACGTATGACC
Class: plasmid ends
High quality sequence stop: 546.
Location/Qualifiers
1..546
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U06C1M0107N03"
/clone_lib="Mouse 10kb plasmid U06C1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male); was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMDA2 (gll473j1419b1AFL29072.1) a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the Insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 151 a 111 c 139 g 144 t 1 others
ORIGIN

Alignment Scores:
Pred. No.: 3.17e-08 Length: 546
Score: 139.50 Matches: 37
Percent Similarity: 51.75% Conservative: 22
Best Local Similarity: 32.46% Mismatches: 48
Query Match: 16.83% Indels: 7
DB: 17 Gaps: 3

US-09-697-089-2_COPY_161_323 (1-163) x AZ362463 (1-546)


```

source
1. .556
/organism="Mus musculus"
/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="MGC2M0201C01"
/clone_lib="Mouse 10kb plasmid UDGCM library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PMD42ny; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1473214|db|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT      134 a      150 c      159 g      113 t
ORIGIN
Alignment Scores:
Pred. No.:      8.54e-06      Length:      556
Score:          121.50      Matches:      49
Percent Similarity: 40.33%      Conservative: 24
Best Local Similarity: 27.07%      Mismatches: 63
Query Match:    14.66%      Indels:      45
DB:              17      Gaps:          8

US-09-697-089-2_COPY_161_323 (1-163) x A2941653 (1-556)
QY      6  11lellgluglyguserglyysglysserthleuenglnargylleAlaMetleu 25
Db      507 CTGGTGGTGGGCGAAGGCGAGGCAAGTCTTCTGCGAGCGTTGGACCTCTG 448
QY      26  TTPGlySerClyysClyssAlaLeuThrLysPheLysValIlePheLeuArgLeu 45
Db      447 TGGGCAACAGGG-----AGGAGCTTCACAGAGTTCCTTCATTTCCCATTCAGCTGC 394
QY      46  SerArgAlaGln-----GlyGlyLeuPheGlyThrLeu 56
Db      393 CGACAGTTGCATGCTGGCCAAACCGCTGCCATGAGAGCGCTGTTGAGCCACTGC 334
QY      57  CysAspIleLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetleu 76
Db      333 TGC-----TGGCCTGATGTCGCTAGGACGATGCTTCACG--TTCCTT 292
QY      77  LeuLysLeuArgGlnArgValIleuPheLeuLeuAspGlyTyrAsnGluPheLys----- 94
Db      291 CTTGACCATCTGACCGTGTCTTAACTTCATGCTGGACGAGTTCGAATTCACGCG 232
QY      95  -----ProGlnAsnCysProGluIleGluAlaLeuIleLysGluAsnHisArg 110
Db      231 TTTCACGACCGGCGGAGCGCACTGCTCCAAATGACCC----- 193
QY      111 PheLysAsnMetValIleValThrThrThrGluCysLeuArgHisIleArgGlnPhe 130
Db      192 -----ACGTCAGTCACAGACTGCTGCTTCATTCCTTCACAGGG 154
QY      131 G1yAlaLeu-----ThrAlaGluValG1yAspMetThrGluAspSerAlaGlnAlaLeu 148
Db      153 AACTTGTGAAGATGCTGCAGAGGTGCTGACACAGCCGTCGGATGGTGTGTCAGCCGTC 94
QY      149 11eArgLuuValleuIleLysGluLeu-----AlaGluGlyLeuLeu 162

```

```

Db      93  CTCAGGAAGTTCGTCGACAGAGTTGCAACTGAAGGCTTCTCTGAAGAGGCAATCCAA 34
QY      163 1eu 163
Db      33  CTG 31

RESULT 12
BC994836/c 345 bp mRNA linear EST 13-JUN-2001
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 345)
REFERENCE
AUTHORS
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.V.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL
MEDLINE
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?PI=PMO&t2=PMO-HT1166-
150201-002-d06&t3=2001-02-15&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 24
High quality sequence stop: 345.
Location/Qualifiers
1. 345
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT1166"
/dev_stage="Adult"
/notes="Organ: head_neck; Vector: puc18; Site: 1; Smal;
Site: 2; Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      95 a      87 c      88 g      75 t
ORIGIN
Alignment Scores:
Pred. No.:      7.09e-06      Length:      345
Score:          120.00      Matches:      23
Percent Similarity: 62.75%      Conservative: 9
Best Local Similarity: 45.10%      Mismatches: 19
Query Match:    14.48%      Indels:      0
DB:              13      Gaps:          0

US-09-697-089-2_COPY_161_323 (1-163) x BC994836 (1-345)
QY      1  LeuGlnSerProCysIleIleGluGlyGlySerGlyLysSerThrLeuLeuGln 20
Db      173 TTGAACCTGTCATGTCGTGGAGGCTGAAGCTGAAGTGAAGAGCGTCTCTGTAAG 114

```

21 Arg11e1a1metleutrp1gserglyscyslalsala1euthrlyspheyl 40
Db 113 AAAATAGCTTTCTGTGGCATCTGATCTGCCCTGTAAACAGGTTCCAGCTGGT 54
Oy 41 Phep1e1a1g1e1u1s1e1r1g1a1g1n1g1y1 51
Db 53 TTCTACACCTCCCTTGAGTCCACGACGACAGGT 21

RESULT 13
Bg994334/c 586 bp mRNA linear EST 13-JUN-2001
LOCUS PM0-HT1166-130201-003-cl1 HT1166 Homo sapiens cDNA, mRNA sequence.
Bg994334
Bg994334.1 GI:14398404
VERSION EST.
KEYWORDS
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 586)
REFERENCE
AUTHORS
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/ICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM0&cl2=PM0-HT1166-
130201-003-cl1&cl3=2001-02-13&cl4=1)
Seq primer: puc 18 forward
High quality sequence start: 3
High quality sequence stop: 586.
Location/Qualifiers
1..586
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT1166"
/dev_stage="Adult"
/note="Organ: head,neck; Vector: puc18; Site_1: Sma1;
Site_2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 156 a 145 c 137 g 147 t 1 others
ORIGIN

Alignment Scores:
Pred. No.: 5.03e-05 Length: 586
Score: 116.00 Matches: 21
Percent Similarity: 69.05% Conservative: 8
Best Local Similarity: 50.00% Mismatches: 13
Query Match: 13.99% Indels: 0
DB: 13 Gaps: 0

US-09-697-089-2_COPY_161_323 (1-163) x Bg994334 (1-586)
Oy 1 leu1nserprocy1le1le1g1u1g1u1sergly1s1g1y1s1e1r1hr1leu1n 20

158 TTGACTCTGTCATGTCGTGTGAGGTTGAGTGAAGGAGAAACGGTCTCTGTAAG 99
Db 21 Arg11e1a1metleutrp1gserglyscyslalsala1euthrlyspheyl 40
Db 98 AAAATAGCTTTCTGTGGCATCTGATCTGCCCTGTAAACAGGTTCCAGCTGGT 39
Oy 41 Phep1e1a1g1e1u1s1e1r1g1a1g1n1g1y1 51
Db 38 TTCTAC 33

RESULT 14
AM504276 361 bp mRNA linear EST 02-MAR-2000
LOCUS UT-HF-BN0-alp-g-07-0-UT.r1 NIH_MGC_50 Homo sapiens cDNA clone
DEFINITION IMAGE:3080628 5', mRNA sequence.
AM504276
AM504276.1 GI:7141931
VERSION EST.
KEYWORDS
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 361)
REFERENCE
AUTHORS
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cga@bbs-rcmail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.C. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNI at:
www-bio.lnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
Location/Qualifiers
1..361
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="3080628"
/clone_lib="NIH_MGC_50"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (IRT)"
/note="Vector: pUT3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(3.5-4.4kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 56 a 119 c 104 g 80 t 2 others
ORIGIN

Alignment Scores:
Pred. No.: 0.000167 Length: 361
Score: 110.00 Matches: 36
Percent Similarity: 42.34% Conservative: 11
Best Local Similarity: 32.43% Mismatches: 40
Query Match: 13.27% Indels: 24
DB: 10 Gaps: 4

US-09-697-089-2_COPY_161_323 (1-163) x AM504276 (1-361)
Oy 7 ile1g1u1g1u1sergly1s1g1y1s1e1r1hr1leu1n1a1e1metleutrp 26
Db 17 ATCTGGGTGATGCTGGGGTGGGCAAGTCCATGCTGCTACACGGCTCAGACCTCTGG 76
Oy 27 gly1sergly1s1g1y1s1a1e1u1thr1lyspheyl1phep1e1u1arg1e1u1s1e1r 46
Db 77 GCCACGGCCGGCTGAGACGACGAGGGGTCAAAATTCCTTCCACTTTCGCTGCCGATGTTC 136

QY 47 Argala-----glnlglyleuphenglthrleucys 57
Db 137 AGCTGCTCAAGAAAGTACAGGCTGTCTGTCTGACAGACCTGCTTCAAGACCTACTGTC 196
QY 58 Aspglnleuleuaspilleglthrlearglysglnthrphemetalametleuleu 77
Db 197 -----TACCCAGAGCGGAGACCCCAAGAGGTGT---GCTTCTCTGCTG 238
QY 78 LysleuArglnArgValleuphelleuleuaspilgltYrAsngluPhe----- 93
Db 239 CGCTTCCCCCAGNTGGCTCTTCACTTCGATGNCCTGACGAGCTGCACCTCGACCTTG 298
QY 94 -----LysproGlnAsnCysPro 99
Db 299 GACCTGAGCGCGGCTGCTGACAGCTCTGCCCC 331
RESULT 15
BE887277 939 bp mRNA linear EST 20-OCT-2000
LOCUS 601508592F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909958 5',
DEFINITION mRNA sequence.
ACCESSION BE887277
VERSION BE887277
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 939)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM9724 row: h column: 23
High quality sequence stop: 613.
Location/Qualifiers
1. 939
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3909958"
/clone_id="NIH_MGC_71"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb.
BASE COUNT 185 a 295 c 276 g 183 t
ORIGIN
Alignment Scores:
Pred. No.: 0.00247 Length: 939
Score: 105.50 Matches: 38
Percent Similarity: 45.79% Conservative: 11
Best Local Similarity: 35.51% Mismatches: 43
Query Match: 12.73% Indels: 15
DB: 12 Gaps: 3
US-09-697-089-2_COPY_161_323 (1-163) x BE887277 (1-939)
QY 7 lileglnlglylusergilylysglyserthrleuleuGlnArgIleAlaMetLeuTrp 26
Db 129 ATCCGTGGGTGATGCTGGGTGGGCAAGTCATGCTGCTACAGCGGCTGACAGCCTCTGG 188
QY 27 GlyserglyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeu-Se 46

Db 189 ::::: ||| ||||| ||| ||| ::::: ||
GCCACGGGCGCGCTAGACGACGAGGGGTCAAATCTTCTTCACTTTCGCTGCGCATGTC 248
QY 46 rArgIaGln-----gLyGlyLeuPheGlnThrleucysasp-glnleuleuaspI 63
Db 249 AGCTGCTCAAGAAAGTACAGGCTGTGTCTGACGAGCTGCTTCAACACTACTGTC 308
QY 63 lProGlyThrIleArglysglnthrphemetalametleuleuLysleuArglnArgv 83
Db 309 TACCCAGAGCGGAGACCAAGAGAGGTGT---GCTTCTCTGCTGCGCTTCCCCACGCTGG 365
QY 83 alleuPheuleuaspilgltYrAsngluPhe-----L 94
Db 366 CCTTCTCACCTTGTGATGCTGAGAGCTGCACCTGCACTGAGACTGAGACCGCGTGC 425
QY 94 yspProGlnAsnCysPro 99
Db 426 CTGACAGCTCTGCCCC 442

Search completed: January 31, 2003, 16:18:52
Job time : 1335.94 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 31, 2003, 11:43:51 : Search time 36.8989 Seconds
(without alignments)
1354.737 Million cell updates/sec

Title: US-09-697-089-2_COPY_161_323

Perfect score: 829
Sequence: 1 LQSPCIEGSGKGRSLQ.....SAQALREVLIKEALBELL 163

Scoring table:

BIOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=x1h
-O=/cgn2_1/USPRO.spool/US09697089/runat_29012003_092754_19735/app_query.fasta_1.981
-DB=Issued_Patents.NA -OPMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LDOPTCL=0
-LDOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsun62 -TRANS=human40.cdi
-LIST=45 -DOCAIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pcio -NORM=ext -HEAPSIZE=500 -MIMLEN=0 -MAXLEN=2000000000
-USER=US09697089_ECGN_1_1_37_etunal_29012003_092754_19735 -NCPU=6 -ICPU=3
-NO_XLIPY -NO_MMAP -LARGESOURCY -NEG_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAOP=10 -YGAPEXT=0.5 -DELop=6 -DELEXT=7

Database :

Issued_Patents_NA.*
1: /cgn2_6/ptodata/2/1na/5A.COMB.seq.*
2: /cgn2_6/ptodata/2/1na/5B.COMB.seq.*
3: /cgn2_6/ptodata/2/1na/6A.COMB.seq.*
4: /cgn2_6/ptodata/2/1na/6B.COMB.seq.*
5: /cgn2_6/ptodata/2/1na/PCUTUS.COMB.seq.*
6: /cgn2_6/ptodata/2/1na/Backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	236.5	28.5	5502	3 US-08-836-134-1	Sequence 1, Appli
2	236.5	28.5	5502	4 US-09-493-784-1	Sequence 1, Appli
3	111	13.4	4141	4 US-09-245-281-42	Sequence 42, Appl
4	111	13.4	4141	4 US-09-207-359B-7	Sequence 42, Appl
5	107	12.9	1470	4 US-09-099-041A-27	Sequence 27, Appl
6	107	12.9	1470	4 US-09-245-281-27	Sequence 27, Appl
7	107	12.9	1470	4 US-09-207-359B-27	Sequence 27, Appl
8	107	12.9	2859	4 US-09-099-041A-9	Sequence 9, Appli
9	107	12.9	2859	4 US-09-245-281-9	Sequence 9, Appli
10	107	12.9	2859	4 US-09-207-359B-9	Sequence 9, Appli
11	107	12.9	3080	4 US-09-099-041A-25	Sequence 25, Appl
12	107	12.9	3080	4 US-09-245-281-25	Sequence 25, Appl

13	107	12.9	3080	4 US-09-207-359B-25	Sequence 25, Appl
14	107	12.9	3382	4 US-09-099-041A-7	Sequence 7, Appli
15	107	12.9	3382	4 US-09-245-281-7	Sequence 7, Appli
16	107	12.9	3382	4 US-09-207-359B-7	Sequence 7, Appli
17	107	12.9	32042	4 US-09-245-281-44	Sequence 44, Appl
18	100.5	12.1	250	2 US-08-824-701A-8	Sequence 8, Appli
19	82	9.9	626	3 US-09-019-942-4	Sequence 4, Appli
20	82	9.9	626	4 US-09-470-271-4	Sequence 4, Appli
21	78	9.4	3393	1 US-08-295-502-1	Sequence 1, Appli
22	78	9.4	3393	5 PCT-US95-10691-1	Sequence 1, Appli
23	78	9.4	4441	4 US-09-641-999-2	Sequence 2, Appli
24	78	9.4	4543	2 US-08-519-547A-5	Sequence 5, Appli
25	76.5	9.2	7881	2 US-08-751-189-1	Sequence 1, Appli
26	76.5	9.2	7881	2 US-09-060-836-1	Sequence 1, Appli
27	76.5	9.2	7881	4 US-09-184-445-1	Sequence 1, Appli
28	75.5	9.1	732	4 US-08-919-573-3	Sequence 3, Appli
29	75.5	9.1	735	4 US-08-919-573-1	Sequence 1, Appli
30	71.5	8.6	4014	4 US-09-541-782-1	Sequence 1, Appli
31	71.5	8.6	4014	4 US-09-723-820-1	Sequence 1, Appli
32	71.5	8.6	5278	4 US-08-961-527-227	Sequence 227, App
33	71	8.6	834	4 US-09-134-001C-2775	Sequence 2775, Ap
34	70.5	8.5	1761	4 US-09-504-358-19	Sequence 19, Appl
35	70.5	8.5	1761	4 US-09-954-314-19	Sequence 19, Appl
36	70.5	8.5	11471	4 US-09-504-358-16	Sequence 16, Appl
37	70.5	8.5	11471	4 US-09-954-314-16	Sequence 16, Appl
38	69.5	8.4	2634	2 US-08-907-166-7	Sequence 7, Appli
39	69.5	8.4	6464	4 US-09-221-017B-168	Sequence 168, App
40	69.5	8.4	13440	4 US-08-961-527-128	Sequence 128, App
41	69.5	8.4	4411529	4 US-09-103-840A-1	Sequence 59, Appli
42	69	8.3	1776	4 US-09-149-476-59	Sequence 1, Appli
43	69	8.3	4371	1 US-08-803-972-1	Sequence 1, Appli
44	69	8.3	4371	1 US-08-803-972-1	Sequence 1, Appli
45	68.5	8.3	1620	4 US-09-360-197-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-836-134-1
: Sequence 1, Application US/08836134A
: Patent No. 6020127
: GENERAL INFORMATION:
: APPLICANT: Mackenzie, Alex E.
: APPLICANT: Korneluk, Robert G.
: APPLICANT: Mahadevan, Mani S.
: APPLICANT: McLean, Michael
: APPLICANT: Roy, Natalie
: APPLICANT: Ikeda, John-e
: TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and
: Patent No. 6020127
: TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy
: FILE REFERENCE: 3477-112, 033477/139914
: CURRENT APPLICATION NUMBER: US/08/836.134A
: CURRENT FILING DATE: 1997-06-20
: NUMBER OF SEQ ID NOS: 23
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 5502
: TYPE: DNA
: ORGANISM: Homo sapiens
US-08-836-134-1

Alignment Scores:
Pred. No.: 2.63e-22
Score: 236.50
Percent Similarity: 58.96%
Best Local Similarity: 39.55%
Query Match: 28.53%
DB: 3
Gaps: 3
Length: 5502
Matches: 53
Conservative: 26
Mismatches: 48
Indels: 7

US-09-697-089-2_COPY_161_323 (1-163) x US-08-836-134-1 (1-5502)
Oy 1 LeuGlnSerProCysIleIleGluGlyIleuSerGlyLysGlySerThrLeuGln 20

```

Db 1779 TTGAACCTCTGCATGTGTGGAGGTGAAGCTGGAAAGAGCGTCCCTCTGAG 1838
OY 21 ArgillealettLeuTprGlySerGlyLysCysLysAlaLeuThrLysPheVal 40
Db 1839 AAAATACCTTTTCTGTGGCATCTGCATCTGCTCCCTGTTAAACAGATTCACCTGTT 1898
OY 41 PhePheLeuArgLeuSer-----ArgAlaGlnGlyLeuPheGlnThrLeuCysAsp 58
Db 1899 TTCTACCTCTCCCTTACTTACACCAAGACAGAGGGCGTGGCCAGTATCATCTGTGAC 1958
OY 59 GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLys 78
Db 1959 CAGCTCTAGAGAAAGAGAGATCTGTACTGAAATGTGATGAGCAACATTATTCACAGCAG 2018
OY 79 LeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGlnPhe-----LysProGln 96
Db 2019 TTAAAGATCATGAGTCTATTCTTTTATGATGACTACAAAGAAATATGTCAATCCCTCAA 2078
OY 97 AsnCysProGlnIleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIle 116
Db 2079 -----GTCAATGAGAAACTGATTCAAAAAAACCACTTATCCGACCTGCTATTG 2129
OY 117 ValThrThrThrThrGlyCysLeuArgHisIleArgGlnPhe 130
Db 2130 ATTGCTGTCCGTACAAACAGGGCCAGGACATCCGCGATAC 2171

RESULT 2
US-09-493-784-1
; Sequence 1, Application US/09493784
; Patent No. 6429011
; GENERAL INFORMATION:
; APPLICANT: Mackenzie, Alex E.
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mahadevan, Mani S.
; APPLICANT: McLean, Michael
; APPLICANT: Roy, Natalie
; APPLICANT: Ikeda, John
; TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and
; Patent No. 6429011
; FILE REFERENCE: 3477-112, 033477/139914
; CURRENT APPLICATION NUMBER: US/09/493,784
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 08/836,134
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 5502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-493-784-1

Alignment Scores:
Pred. No.: 2,63e-22 Length: 5502
Score: 236.50 Matches: 53
Percent Similarity: 58.96% Conservative: 26
Best Local Similarity: 39.55% Mismatches: 48
Query Match: 28.53% Indels: 7
Gaps: 3

US-09-697-089-2_COPY_161_323 (1-163) x US-09-493-784-1 (1-5502)
OY 1 LeuGlnSerProCysIleIleGlnGlyLysSerGlyLysSerThrLeuLeuGln 20
Db 1779 TTGAACCTCTGCATGTGTGGAGGTGAAGCTGGAAAGAGCGTCCCTCTGAG 1838
OY 21 ArgillealettLeuTprGlySerGlyLysCysLysAlaLeuThrLysPheVal 40
Db 1839 AAAATACCTTTTCTGTGGCATCTGCATCTGCTCCCTGTTAAACAGATTCACCTGTT 1898
OY 41 PhePheLeuArgLeuSer-----ArgAlaGlnGlyLeuPheGlnThrLeuCysAsp 58
Db 1899 TTCTACCTCTCCCTTACTTACACCAAGACAGAGGGCGTGGCCAGTATCATCTGTGAC 1958
OY 59 GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLys 78
Db 1959 CAGCTCTAGAGAAAGAGAGATCTGTACTGAAATGTGATGAGCAACATTATTCACAGCAG 2018
OY 79 LeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGlnPhe-----LysProGln 96
Db 2019 TTAAAGATCATGAGTCTATTCTTTTATGATGACTACAAAGAAATATGTCAATCCCTCAA 2078
OY 97 AsnCysProGlnIleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIle 116
Db 2079 -----GTCAATGAGAAACTGATTCAAAAAAACCACTTATCCGACCTGCTATTG 2129
OY 117 ValThrThrThrThrGlyCysLeuArgHisIleArgGlnPhe 130
Db 2130 ATTGCTGTCCGTACAAACAGGGCCAGGACATCCGCGATAC 2171

RESULT 3
US-09-245-281-42
; Sequence 42, Application US/09245281
; Patent No. 6369196
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/09/245,281
; EARLIER FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: US 09/207,359
; EARLIER FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: US 09/099,041
; EARLIER FILING DATE: 1998-06-17
; EARLIER APPLICATION NUMBER: US 09/019,942
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 4141
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (261)...(3119)
US-09-245-281-42

Alignment Scores:
Pred. No.: 5.2e-05 Length: 4141
Score: 111.00 Matches: 45
Percent Similarity: 41.21% Conservative: 23
Best Local Similarity: 27.27% Mismatches: 63
Query Match: 13.39% Indels: 34
Gaps: 7

US-09-697-089-2_COPY_161_323 (1-163) x US-09-245-281-42 (1-4141)
OY 9 GlyLysSerGlyLysGlyLysSerThrLeuLeuGlnArgIleAlaMetLeuTprGlySer 28
Db 864 GGGAGCGGGAGTGGCGCAAGTCCATGCTGTGCGAGAGTTCGACAGACCTCTGGGCGTCA 923
OY 29 GlyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSerArgAla 48
Db 924 GGCAGGTTCACCTTCACAGCAACAAATTTCTTCTCCACTCCGCTGCCAGATTCAGCTGC 983
OY 49 -----GlnGlyLeuPheGlnThrLeuCysAspGln 59
Db 984 TTCAAGAGAGACGACATGATGATCTGCAGAGACCTGCTTCAAGCAATTCCTGC----- 1037
OY 60 LeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeu 79
Db 1038 -----TACCGGAGACAGACCCCGAGAGAGGTTC--TCTCTTGTGCTGCTTT 1085
```

```

Db 1899 TTCTACCTCTCCCTTACTTACACCAAGACAGAGGGCGTGGCCAGTATCATCTGTGAC 1958
OY 59 GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLys 78
Db 1959 CAGCTCTAGAGAAAGAGAGATCTGTACTGAAATGTGATGAGCAACATTATTCACAGCAG 2018
OY 79 LeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGlnPhe-----LysProGln 96
Db 2019 TTAAAGATCATGAGTCTATTCTTTTATGATGACTACAAAGAAATATGTCAATCCCTCAA 2078
OY 97 AsnCysProGlnIleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIle 116
Db 2079 -----GTCAATGAGAAACTGATTCAAAAAAACCACTTATCCGACCTGCTATTG 2129
OY 117 ValThrThrThrThrGlyCysLeuArgHisIleArgGlnPhe 130
Db 2130 ATTGCTGTCCGTACAAACAGGGCCAGGACATCCGCGATAC 2171

RESULT 3
US-09-245-281-42
; Sequence 42, Application US/09245281
; Patent No. 6369196
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/09/245,281
; EARLIER FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: US 09/207,359
; EARLIER FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: US 09/099,041
; EARLIER FILING DATE: 1998-06-17
; EARLIER APPLICATION NUMBER: US 09/019,942
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 4141
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (261)...(3119)
US-09-245-281-42

Alignment Scores:
Pred. No.: 5.2e-05 Length: 4141
Score: 111.00 Matches: 45
Percent Similarity: 41.21% Conservative: 23
Best Local Similarity: 27.27% Mismatches: 63
Query Match: 13.39% Indels: 34
Gaps: 7

US-09-697-089-2_COPY_161_323 (1-163) x US-09-245-281-42 (1-4141)
OY 9 GlyLysSerGlyLysGlyLysSerThrLeuLeuGlnArgIleAlaMetLeuTprGlySer 28
Db 864 GGGAGCGGGAGTGGCGCAAGTCCATGCTGTGCGAGAGTTCGACAGACCTCTGGGCGTCA 923
OY 29 GlyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSerArgAla 48
Db 924 GGCAGGTTCACCTTCACAGCAACAAATTTCTTCTCCACTCCGCTGCCAGATTCAGCTGC 983
OY 49 -----GlnGlyLeuPheGlnThrLeuCysAspGln 59
Db 984 TTCAAGAGAGACGACATGATGATCTGCAGAGACCTGCTTCAAGCAATTCCTGC----- 1037
OY 60 LeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeu 79
Db 1038 -----TACCGGAGACAGACCCCGAGAGAGGTTC--TCTCTTGTGCTGCTTT 1085
```



```
OY      80 ArgGlnArgValIleuPheLeuLeuaspGlyTyrAsnGlnPheLys----- 94
Db      1086 CCCACACAGCCCTTTCACCTTTTACCGCGCTGGATGAGCTGCACACTTCAGACTTCGACCTG 1145
OY      95 -----ProGlnAsnCysProGluIleGlnAlaLeuIleLysGlnAsnHisArgPhe 111
Db      1146 AGCCGCGTCCGGATAGCTGCTGCCCGCCCTGGAGCGC----- 1181
OY      112 LysAsnMetValIleValIleThrThrThrThrGluCysLeuArgHisIleArgGlnPheGly 131
Db      1182 GCTCACCTTGTCTGCTGCTGCTGCTAACCTCTTAAGTGGAGGCTGCTCAAGAGGTGCGCGC 1241
OY      132 ---AlaLeuThrAlaGlnValGlyAspMetThrGluAspSerAlaGlnAlaLeuLeuArg 150
Db      1242 AAATGCTCAGCTGCTGCACAGAGC-----GTGAGAGTCCCCCGCCAGCTCCTGGCAGAA 1295
OY      151 GluValIleuLeuLys 155
Db      1296 AAGTGTCTGCTCCGCG 1310
```

RESULT 4

```
US-09-207-359B-42
; Sequence 42, Application US/09207359B
; Patent No. 6469140
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/207,359B
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 4141
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (261)...(3119)
US-09-207-359B-42
```

Alignment Scores:

```
Pred. No.: 5.2e-05 Length: 4141
Score: 111.00 Matches: 45
Percent Similarity: 41.21% Conservative: 23
Best Local Similarity: 27.27% Mismatches: 63
Query Match: 13.39% Indels: 34
DB: 4 Gaps: 7
```

US-09-697-089-2_COPY_161_323 (1-163) x US-09-207-359B-42 (1-4141)

```
OY      9 GlyIuSerGlyLysGlyLysSerThrIleuLeuGlnArgIleAlaMetLeuTrpLysSer 28
Db      864 GGGGAGCGGGGAGTGGGAGTCCATGCTGCTGCAGAGGTTCACAGAGCTTCGGGCGCTCA 923
OY      29 GlyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLysSerArgLa 48
Db      924 GGCAGGTGACCTCCACAGCCCAATTCCTTCCACTTCGCCGTGCCGCACTTCAGCTGC 983
OY      49 -----GlnGlyLysLeuPheGluThrLeuLysAspGln 59
Db      984 TTCAGAGAGAGACATGCTGAGTGCAGAGACGCTGCTTCAACCATTTCTGC----- 1037
OY      60 LeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysIleu 79
Db      1038 -----TACCCGAGACAGAGACCCGAGAGAGGTGTTT---TCTTCTTCTGCGCTTT 1085
OY      80 ArgGlnArgValIleuPheLeuLeuaspGlyTyrAsnGlnPheLys----- 94
```

```
Db      1086 CCCACACAGCCCTTTCACCTTTTACCGCGCTGGATGAGCTGCACACTTCGACCTG 1145
OY      95 -----ProGlnAsnCysProGluIleGlnAlaLeuIleLysGlnAsnHisArgPhe 111
Db      1146 AGCCGCGTCCGGATAGCTGCTGCCCGCCCTGGAGCGC----- 1181
OY      112 LysAsnMetValIleValIleThrThrThrThrGluCysLeuArgHisIleArgGlnPheGly 131
Db      1182 GCTCACCTTGTCTGCTGCTGCTGCTAACCTCTTAAGTGGAGGCTGCTCAAGAGGTGCGCGC 1241
OY      132 ---AlaLeuThrAlaGlnValGlyAspMetThrGluAspSerAlaGlnAlaLeuLeuArg 150
Db      1242 AAATGCTCAGCTGCTGCACAGAGC-----GTGAGAGTCCCCCGCCAGCTCCTGGCAGAA 1295
OY      151 GluValIleuLeuLys 155
Db      1296 AAGTGTCTGCTCCGCG 1310
```

RESULT 5

```
US-09-099-041A-27
; Sequence 27, Application US/09099041A
; Patent No. 6340576
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/09/099,041A
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 1470
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-099-041A-27
```

```
Alignment Scores:
Pred. No.: 3.98e-05 Length: 1470
Score: 107.00 Matches: 35
Percent Similarity: 42.34% Conservative: 12
Best Local Similarity: 31.53% Mismatches: 40
Query Match: 12.91% Indels: 24
DB: 4 Gaps: 4
```

US-09-697-089-2_COPY_161_323 (1-163) x US-09-099-041A-27 (1-1470)

```
OY      7 IlegIuGlyLysGlyLysSerThrIleuLeuGlnArgIleAlaMetLeuTrp 26
Db      481 ATCTGGGTGATGATGCGGGTGGGCAAGTCCATGCTGTAACAGCGGCTCAGAGCTCTGG 540
OY      27 GlySerGlyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLysSer 46
Db      541 GCCAGGGCGGGCTAGACGACGAGGGGTCAAAATTCCTTCCACTTTCGCTGCCGCAATGTT 600
OY      47 ArgAla-----GlnGlyLysLeuPheGluThrLeuLys 57
Db      601 AGCTGCTTCAAGAAAGTACAGAGCTGTGTGTGCAGAGACCTGCTTCAAGCACTACAGTCG 660
OY      58 AspGlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeu 77
Db      661 -----TACCAGAGCGGAGACCCCGAGAGAGTGT---GCCCTTCTGCTG 702
OY      78 LysLeuArgGlnArgValIleuPheLeuLeuaspGlyTyrAsnGlnPhe----- 93
Db      703 CGCTTCCCCACAGTGGCCCTTTCACCTTCGATGGCTGAGACAGCTGCATCGAGACTTG 762
OY      94 -----LysProGlnAsnCysPro 99
Db      763 GACCTGAGCGCGGTGCTGACAGACTCTGCGCC 795
```

```
RESULT 6
US-09-245-281-27
; Sequence 27, Application US/09245281
; Patent No. 6369196
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/09/245,281
; EARLIER FILING DATE: 1998-02-05
; EARLIER APPLICATION NUMBER: US 09/207,359
; EARLIER FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: US 09/099,041
; EARLIER FILING DATE: 1998-06-17
; EARLIER APPLICATION NUMBER: US 09/019,942
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 1470
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-245-281-27

Alignment Scores:
Pred. No.: 3.98e-05 Length: 1470
Score: 107.00 Matches: 35
Percent Similarity: 42.34% Conservative: 12
Best Local Similarity: 31.53% Mismatches: 40
Query Match: 12.91% Indels: 24
Gaps: 4

US-09-697-089-2_COPY_161_323 (1-163) x US-09-245-281-27 (1-1470)
QY 7 lileglugluserglylysglylysserthrlleuenglartglealmetleutrp 26
Db 481 ATCTGGTGATGCTGGGCGTGGCAAGTCATGCTGACAGCGGCTGACAGCCTCTGG 540
QY 27 glyserglylyscyslysalaleuthrllyspheleuValpheleuArgleuser 46
Db 541 GCCACGGGCGCGTAGACGAGGGGCAATTCCTCCACTTCCGCTGCCGATGTC 600
QY 47 Argala-----glnglylyleuphegluThrleucys 57
Db 601 AGCTGCTCAAGAAAGTACAGCGCTGCTGTCGACGACCTCTTCAAGCAGCTACTGC 660
QY 58 AsplnleuAspIleProglYThrleArglysglnThrPheMetAlaMetleu 77
Db 661 -----TACCCAGAGCGGAGCCCGAGAGAGGTGTTT---GCCTTCCTGCTG 702
QY 78 LysleuArglnArgValleuPheleuAspIlyTyransgluPhe----- 93
Db 703 CGCTTCCCGCCACGTCGGCCCTTTCACCTTCGATGCGCTGAGACGACTGCGACTTG 762
QY 94 -----LysProGlnAsnCysPro 99
Db 763 GACCTGAGCCGCGTGCCTGACAGCTCCTGCCCC 795

RESULT 7
US-09-207-359B-27
; Sequence 27, Application US/09207359B
; Patent No. 6469140
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/207,359B
; CURRENT FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
```

```
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 1470
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-207-359B-27

Alignment Scores:
Pred. No.: 3.98e-05 Length: 1470
Score: 107.00 Matches: 35
Percent Similarity: 42.34% Conservative: 12
Best Local Similarity: 31.53% Mismatches: 40
Query Match: 12.91% Indels: 24
Gaps: 4

US-09-697-089-2_COPY_161_323 (1-163) x US-09-207-359B-27 (1-1470)
QY 7 lileglugluserglylysglylysserthrlleuenglartglealmetleutrp 26
Db 481 ATCTGGTGATGCTGGGCGTGGCAAGTCATGCTGACAGCGGCTGACAGCCTCTGG 540
QY 27 glyserglylyscyslysalaleuthrllyspheleuValpheleuArgleuser 46
Db 541 GCCACGGGCGCGTAGACGAGGGGCAATTCCTCCACTTCCGCTGCCGATGTC 600
QY 47 Argala-----glnglylyleuphegluThrleucys 57
Db 601 AGCTGCTCAAGAAAGTACAGCGCTGCTGTCGACGACCTCTTCAAGCAGCTACTGC 660
QY 58 AsplnleuAspIleProglYThrleArglysglnThrPheMetAlaMetleu 77
Db 661 -----TACCCAGAGCGGAGCCCGAGAGAGGTGTTT---GCCTTCCTGCTG 702
QY 78 LysleuArglnArgValleuPheleuAspIlyTyransgluPhe----- 93
Db 703 CGCTTCCCGCCACGTCGGCCCTTTCACCTTCGATGCGCTGAGACGACTGCGACTTG 762
QY 94 -----LysProGlnAsnCysPro 99
Db 763 GACCTGAGCCGCGTGCCTGACAGCTCCTGCCCC 795

RESULT 8
US-09-099-041A-9
; Sequence 9, Application US/09099041A
; Patent No. 6340576
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/09/099,041A
; CURRENT FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2859
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-099-041A-9

Alignment Scores:
Pred. No.: 0.000108 Length: 2859
Score: 107.00 Matches: 35
Percent Similarity: 42.34% Conservative: 12
Best Local Similarity: 31.53% Mismatches: 40
Query Match: 12.91% Indels: 24
Gaps: 4
```

US-09-697-089-2_COPY_161_323 (1-163) x US-09-099-041A-9 (1-2859)

Oy	7	IIeGIuGIyGusereGIyGIyGIySseThrlneuenuInrGlelaamleuTrip	26
Db	598	ATTCGGGTATnGTCTGGGGGGGCAATGCTATGCTACAGGGCTGCAGACCTCTGG	657
Oy	27	GIySerGIyScySLysAlaLeuThrlLysPheLysPheValPhePheLeuArgLeuSer	46
Db	658	GCCACGGGCCGGCTAGACGCGAGGGGTCAAATTCCTTCCTCCATCTCCCTCCGATGTC	717
Oy	47	ArgAla	57
Db	718	AGCTGCTTCAAGAAAGTGCAGGCTGTCTGTGCAGGACCTGCTTTCACAGCACTACTGC	777
Oy	58	AspGlnLeuLeuAspIleProGIyThrlLeaArgLysGlnThrPheMetAlaLeuLeu	77
Db	778	-----TACCAGACGCGGAGCCCGGAGGAGGGTGTTT---GCCTTCGTGCTG	819
Oy	78	LysLeuArgGlnArgValLeuPheLeuLeuAspGIyTyrrAsnGluPhe	93
Db	820	CGCTTCCTCCCGACGTGGGCCCTTTCACCTTGATGATGGCTGTGACGACGTGCACACTGGGACTTG	879
Oy	94	-----LysProGlnAsnCysPro	99
Db	880	GACCTGAGCCGCGTGCCTGCAGCAGCTCTCCGCCCC	912

[illegible]

```

OY      58 AspGlnLeuLeuAspIleProGlyThrIleArgLysGlnIntrPhenMetAlaMetLeuLeu 77
Db      778 -----TACCAGAGCGGGAGCCCGAGGAGGTGT--GCCTCTCTGCTG 819
OY      78 LysLeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPhe----- 93
Db      820 GCGTTCCTCCACGTGGCCCTCTCACTTCCTGATGGCTGGAGAGACTGCACTCGGACTTG 875
OY      94 -----LysProGlnAsnCysPro 99
Db      880 GACCTGAGCGCGGTGCTCGACAGAGCTCTGCGCC 912

RESULT 10
US-09-207-359B-9
; Sequence 9, Application US/09207359B
; Patent No. 6469140
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/207,359B
; CURRENT FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2659
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-207-359B-9

```

[illegible]

```
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/09/099,041A
; PRIOR FILING DATE: 1998-06-17
; PRIOR FILING DATE: 09/019,942
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 3080
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1470)
US-09-099-041A-25

Alignment Scores:
Pred. No.: 0.000121 Length: 3080
Score: 107.00 Matches: 35
Percent Similarity: 42.34% Conservative: 12
Best Local Similarity: 31.53% Mismatches: 40
Query Match: 12.91% Indels: 24
Gaps: 4

US-09-697-089-2_COPY_161_323 (1-163) x US-09-099-041A-25 (1-3080)
QY 7 lIeGlUgIuSeRgLySgLySgThrLeuGlnArgIleAlaMetLeuTrp 26
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 481 ATCTGGGTGATGCTGGGGGCGGAGCCATGCTGTACAGCGGCGACAGCCTCGG 540
QY 27 gLySeRgLyScYsLySAlaLeuThrLySpheLySphValPhePheLeuArgLeuSer 46
    ::|||:||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 GCCACGGGCGGCTAGACGAGGGGCAAAATTCCTTCACCTTCGCTGCCGATGTC 600
QY 47 ArgAla-----GlnGlyLeuPheGlnuThrLeuCyS 57
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 601 AGCTGCTTCAAGAAAGTACAGAGCTGTGTCTGACGAGACCGCTCTTCAAGCACTACTGC 660
QY 58 AspGlnLeuLeuAspIleProGlyThrIleArgLySgInThrPheMetAlaMetLeuLeu 77
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 661 -----TACCCAGACGGGAGCCCGAGAGAGGTGT---GCCTTCCTGCTG 702
QY 78 LysLeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPhe----- 93
    ::|||:||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 703 CGCTTCCCGCCAGCGCCCTCTTACCTTGATGCGCTGCGACGAGCTGCACCTCGGACTTG 762
QY 94 -----LysProGlnAsnCysPro 99
    ::|||:||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 763 GACCTGAGCGCGCTGCTGACAGCTCCTGCCGCC 795

RESULT 12
US-09-245-281-25
; Sequence 25, Application US/09245281
; Patent No. 6369196
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/09/245,281
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: US 09/207,359
; EARLIER FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: US 09/099,041
; EARLIER FILING DATE: 1998-06-17
; EARLIER APPLICATION NUMBER: US 09/019,942
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 25
; LENGTH: 3080
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-245-281-25

Alignment Scores:
Pred. No.: 0.000121 Length: 3080
Score: 107.00 Matches: 35
Percent Similarity: 42.34% Conservative: 12
Best Local Similarity: 31.53% Mismatches: 40
Query Match: 12.91% Indels: 24
Gaps: 4

US-09-697-089-2_COPY_161_323 (1-163) x US-09-245-281-25 (1-3080)
QY 7 lIeGlUgIuSeRgLySgLySgThrLeuGlnArgIleAlaMetLeuTrp 26
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 481 ATCTGGGTGATGCTGGGGGCGGAGCCATGCTGTACAGCGGCGACAGCCTCGG 540
QY 27 gLySeRgLyScYsLySAlaLeuThrLySpheLySphValPhePheLeuArgLeuSer 46
    ::|||:||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 GCCACGGGCGGCTAGACGAGGGGCAAAATTCCTTCACCTTCGCTGCCGATGTC 600
QY 47 ArgAla-----GlnGlyLeuPheGlnuThrLeuCyS 57
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 601 AGCTGCTTCAAGAAAGTACAGAGCTGTGTCTGACGAGACCGCTCTTCAAGCACTACTGC 660
QY 58 AspGlnLeuLeuAspIleProGlyThrIleArgLySgInThrPheMetAlaMetLeuLeu 77
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 661 -----TACCCAGACGGGAGCCCGAGAGAGGTGT---GCCTTCCTGCTG 702
QY 78 LysLeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPhe----- 93
    ::|||:||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 703 CGCTTCCCGCCAGCGCCCTCTTACCTTGATGCGCTGCGACGAGCTGCACCTCGGACTTG 762
QY 94 -----LysProGlnAsnCysPro 99
    ::|||:||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 763 GACCTGAGCGCGCTGCTGACAGCTCCTGCCGCC 795

RESULT 13
US-09-207-359B-25
; Sequence 25, Application US/09207359B
; Patent No. 6469140
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/207,359B
; CURRENT FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 3080
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1470)
US-09-207-359B-25

Alignment Scores:
Pred. No.: 0.000121 Length: 3080
Score: 107.00 Matches: 35
Percent Similarity: 42.34% Conservative: 12
Best Local Similarity: 31.53% Mismatches: 40
Query Match: 12.91% Indels: 24
Gaps: 4
```

US-09-697-089-2_copy_161_323 (1-163) x US-09-207-359B-25 (1-3080)

QY 7 lIeGlUGlYgIuSerGlyLySgIyLysSerThrIleuLeuGlnArgIleAlaMetLeuTrp 26
Db 481 ATCTGGGTGATGCTGGGGGTGGCAAGTCATGCTGACAGCGGCTGACAGAGCTCTGG 540

QY 27 GlySerGlyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSer 46
Db 541 GCCACGGGCGGCTAGACGACGGGCTCAATCTCTTCACCTTCGCTGCGCTGCTGTC 600

QY 47 ArgAla-----GlnGlyGlyLeuPheGluThrLeuCys 57
Db 601 AGCTGCTTCAAGAAAGTACAGGCTGTGTCTGACAGACCTGCTCTTCAACACACTGTC 660

QY 58 AspGlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeu 77
Db 661 -----TACCCAGACGGGACCCGAGGAGGTGTTT---GCCCTCTGCTG 702

QY 78 LysLeuArgGlnArgValIleuPheLeuLeuAspGlyTyrAnsluPhe----- 93
Db 703 CGCTTCCCGCCACGTCGGCCCTTTCACCTTCGATGCGCTGACGAGCTGACTCGACTTG 762

QY 94 -----LysProGlnAsnCysPro 99
Db 763 GACCTGAGCCGCGTGCCTGACAGCTCCTGCCCC 795

RESULT 14
US-09-099-041A-7
; Sequence 7, Application US/09099041A
; Patent No. 6340576
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/09/099,041A
; PRIORITY FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIORITY FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 3382
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (245)...(3103)
US-09-099-041A-7

Alignment Scores:
Pred. No.: 0.000139 Length: 3382
Score: 107.00 Matches: 35
Percent Similarity: 42.34% Conservative: 12
Best Local Similarity: 31.53% Mismatches: 40
Query Match: 12.91% Indels: 24
DB: 4 Gaps: 4

US-09-697-089-2_copy_161_323 (1-163) x US-09-099-041A-7 (1-3382)

QY 7 lIeGlUGlYgIuSerGlyLySgIyLysSerThrIleuLeuGlnArgIleAlaMetLeuTrp 26
Db 842 ATCTGGGTGATGCTGGGGGTGGCAAGTCATGCTGACAGCGGCTGACAGAGCTCTGG 901

QY 27 GlySerGlyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSer 46
Db 902 GCCACGGGCGGCTAGACGACGGGCTCAATCTCTTCACCTTCGCTGCGGCTGTC 961

QY 47 ArgAla-----GlnGlyGlyLeuPheGluThrLeuCys 57
Db 962 AGCTGCTTCAAGAAAGTACAGGCTGTGTCTGACAGACCTGCTTCAACACACTGTC 1021

QY 58 AspGlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeu 77
Db 1022 -----TACCCAGACGGGACCCGAGGAGGTGTTT---GCCCTCTGCTG 1063

QY 78 LysLeuArgGlnArgValIleuPheLeuLeuAspGlyTyrAnsluPhe----- 93
Db 1064 CGCTTCCCGCCACGTCGGCCCTTTCACCTTCGATGCGCTGACGAGCTGACTCGACTTG 1123

QY 94 -----LysProGlnAsnCysPro 99
Db 1124 GACCTGAGCCGCGTGCCTGACAGCTCCTGCCCC 1156

RESULT 15
US-09-245-281-7
; Sequence 7, Application US/09245281
; Patent No. 6369196
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/09/245,281
; PRIORITY FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: US 09/207,359
; EARLIER FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: US 09/099,041
; EARLIER FILING DATE: 1998-06-17
; EARLIER APPLICATION NUMBER: US 09/019,942
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 3382
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-245-281-7

Alignment Scores:
Pred. No.: 0.000139 Length: 3382
Score: 107.00 Matches: 35
Percent Similarity: 42.34% Conservative: 12
Best Local Similarity: 31.53% Mismatches: 40
Query Match: 12.91% Indels: 24
DB: 4 Gaps: 4

US-09-697-089-2_copy_161_323 (1-163) x US-09-245-281-7 (1-3382)

QY 7 lIeGlUGlYgIuSerGlyLySgIyLysSerThrIleuLeuGlnArgIleAlaMetLeuTrp 26
Db 842 ATCTGGGTGATGCTGGGGGTGGCAAGTCATGCTGACAGCGGCTGACAGAGCTCTGG 901

QY 27 GlySerGlyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSer 46
Db 902 GCCACGGGCGGCTAGACGACGGGCTCAATCTCTTCACCTTCGCTGCGGCTGTC 961

QY 47 ArgAla-----GlnGlyGlyLeuPheGluThrLeuCys 57
Db 962 AGCTGCTTCAAGAAAGTACAGGCTGTGTCTGACAGACCTGCTTCAACACACTGTC 1021

QY 58 AspGlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeu 77
Db 1022 -----TACCCAGACGGGACCCGAGGAGGTGTTT---GCCCTCTGCTG 1063

QY 78 LysLeuArgGlnArgValIleuPheLeuLeuAspGlyTyrAnsluPhe----- 93
Db 1064 CGCTTCCCGCCACGTCGGCCCTTTCACCTTCGATGCGCTGACGAGCTGACTCGACTTG 1123

QY 94 -----LysProGlnAsnCysPro 99
Db 1124 GACCTGAGCCGCGTGCCTGACAGCTCCTGCCCC 1156

Mon Feb 3 14:11:39 2003

us-09-697-089-2_copy_161_323.p2n.rml

Page 8

Job time : 43.8989 secs


```

; LENGTH: 891
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(891)
; US-09-864-921-179

```

Alignment Scores:	
Pred. No.:	9.63e-106
Score:	829.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	9
Length:	891
Matches:	16
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-697-089-2_COPY_161_323 (1-163) x US-09-864-921-179 (1-891)

```

OY      1 LeuGlnSerProCysIleIleGluIleGlyIleuSerGlyIleGlySerThrIleuLeuGln 20
        |||||||
Db      1 CTTGAGACCCCCCTGCATATTGAAAGGGAATCTGGCAAAAGCAATCCACTCTGCTGCAG 60

OY      21 ArgIleAlaMetLeuTyrPglySerGlyCysLysAlaLeuThrLysPheLysPheVal 40
        |||||||
Db      61 CGCATTTGCATATGCTGTGGGGCTCCGAAAGTCCAAAGGCTCTGACCAAGTTCAAAATTCGTC 120

OY      41 PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGlnThrLeuGlyAspGlnLeu 60
        |||||||
Db      121 TTCTTCCTCCGCTCAGACAGGGCCAGGGGTGGACTTTTGGAAACCTCTGTATCAACTC 180

OY      61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80
        |||||||
Db      181 CTGGAATATACCTGGGACACATCGAAGACAGACATTCATATGCCATCTGCTGAAGCTGGCG 240

OY      81 GlnArgValIleuPheLeuLeuAspGlyTyrAsnGlnPheLysProGlnAsnCysProGlu 100
        |||||||
Db      241 CAGAGGGTCTTCTTCTCTCTGATGTGCTACATGAAATTCAGCCCCACAGAACTGCCAGAA 300

OY      101 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr 120
        |||||||
Db      301 ATCGAAGCCCTGATTAAGAAAGAAACCAACCGCTTCAAGAAACATGTGATATCTACCCACTAC 360

OY      121 ThrGlyCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGlnValGlyAspMet 140
        |||||||
Db      361 ACTGATGCTCCAGAGCACAATACGCGCAGATTGGTGGCCCTGACTGCTGAGGTGGGGATATG 420

OY      141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGlnLeuAlaGluGly 160
        |||||||
Db      421 ACAGAAAGACAGCGCCCAAGGCTCTCATCCGAGAAGGTGATCAAGAGAGCTTCTGAAAGC 480

OY      161 LeuLeuLeu 163
        |||||||
Db      481 TTGTTGCTC 489

RESULT 2
US-09-841-739-3
: Sequence 3, Application US/09841739
: Patent No. US20020034784A1
: GENERAL INFORMATION:
: APPLICANT: Berlin, John
: TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
: FILE REFERENCE: 07334-329001
: CURRENT APPLICATION NUMBER: US/09/841,739
: CURRENT FILING DATE: 2001-08-29
: PRIOR APPLICATION NUMBER: US 09/697,089
: PRIOR FILING DATE: 2000-10-26
: PRIOR APPLICATION NUMBER: US 60/161,822
: PRIOR FILING DATE: 1999-10-27
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 3072
: TYPE: DNA

```

ORGANISM: Homo sapiens
US-09-841-739-3

Alignment Scores:	
Pred. No.:	6, 11e-105
Score:	829.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	10
	Gaps: 0
	Matches: 163
	Conservative: 0
	Mismatches: 0
	Indels: 0
	Gaps: 0

US-09-697-089-2_COPY_161_323 (1-163) x US-09-841-739-3 (1-3072)

```

OY      1 LeuInSerProGyIleIleIleGluGlyIuSerGlyIySglYySserThrLeuLeuGln 20
Db      481 CTTCAAGACCCCTCGATCATTTGAAGGGGAATCTGGCAAAAGGCAAGTCACCTCTCTCGAG 540
OY      21 ArgIleAlaMetLeuIrrpGlySerGlyScySlySaIaleuThrIyPhelYpPheVal 40
Db      541 CGCATTTGCCATGCTCTGGGGGCTCCGGAAAGTCAAGAGCTCTGACCAATTCAATTGCTC 600
OY      41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 60
Db      601 TTCTTCCTCCGCTCCAGAGGGCCAGGGGTGGACTTTTGAACCCCTCTGTGATCACTC 660
OY      61 LeuAspIleProGlyIThrIleArgIySgIInThrPheMetAlaMetLeuLeuIyLeuArg 80
Db      661 CTGGATTAATACCTGGCCACATCAGAGACAGACATTCAATGCCCATGCTCTTAAGCTGGG 720
OY      81 GlnArgValLeuPheLeuLeuAspGlyTyTrAsnGluPheIyProGlnAsnCysProGlu 100
Db      721 CAGAGGGTTCTTTCTCTTGATGGCTACATGAAATTCAAGCCCAAGACTGCCCAAGAA 780
OY      101 IleguIalaleuIleIyGluAsnHisArgPheIySasMetValIleValIThrThrThr 120
Db      781 ATCGAAGCCCTGATTAAGAAACCAACCGCTCAAGAACATGATCTGTACCACTACC 840
OY      121 ThrGluCysLeuArgHisIleArgIInPheGlyAlaLeuThrAlaGluValGlyAspMet 140
Db      841 ACTGATGCTCCTGAGGCACATACGGCAGTTGGTGGCCCTGACTGCTGAGAGTGGGGATATG 900
OY      141 ThrGluAspSerAlaGlnAlaLeuIleArgIuValLeuIleIySgIuLeuAlaGluGly 160
Db      901 ACAGAAAGACAGAGCCCAAGGCTCTCATCCAGAAAGTGTGATCAAGAGACTTGTGAAGGC 960
OY      161 LeuLeuLeu 163
Db      961 TTGTGTCTC 969

RESULT 3
US-09-841-739-1
; Sequence 1, Application US/09841739
; Patent No. US20020034784A1
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/09/841,739
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3133
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36) ... (3107)
US-09-841-739-1

```


Alignment Scores:

Pred. No.:	6.3e-105	Length:	3133
Score:	829.00	Matches:	163
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-697-089-2_COPY_161_323 (1-163) x US-09-841-739-1 (1-3133)

```
QY 1 LeuGlnSerProCysIleIleGlnGlyGluSerGlyLysSerThrLeuGln 20
    |||||||
DB 516 CTTGAGAGCCCTGCATCATTTGAAGGGGAATCTGGCAAGCAAGCTCCTGCTCAG 575
QY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheVal 40
    |||||||
DB 576 CGCATTCGCATGCTCTGGGCTCCGGAAAGTGCAGAGCTGTGACCAAGTTCAATTGCTC 635
QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu 60
    |||||||
DB 636 TTCTTCTCCGCTCTCAGCAGAGGCCAGGGTGAGCTTTTGAACCTCTGTGATCAACTC 695
QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80
    |||||||
DB 696 CTGGATATACCTGGCAACATCAGGAAGCAGACATTCATGGCCATGCTGTGAAGCTCGG 755
QY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 100
    |||||||
DB 756 CAGAGGTTCTTTCTCTTCTTGTGCTGATGCTACAAATTCAGCCCCAGAACTGCCAGAA 815
QY 101 IleGluAlaLeuLeuIleLysGluAsnHisArgPheLysAsnMetValIleValIleThrThr 120
    |||||||
DB 816 ATCGAAGCCCTGATTAAGGAACACACCGCTTCAAGAACATGGCATCGTACCACACTAC 875
QY 121 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValIleGlyAspMet 140
    |||||||
DB 876 ACTGAGTGCTTGAGGACATACGAGGAGTTTGTCCTGTGAGTGAGGGGAGATAG 935
QY 141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 160
    |||||||
DB 936 ACAGAAAGACAGCCGCCAGGCTCTCATCCGAGAAAGTGCTGATCAAGAGGCTTGCGAAGGC 995
QY 161 LeuLeuLeu 163
    |||||||
DB 996 TTGTGTGCTC 1004
```

RESULT 4

```
US-09-864-921-96
; Sequence 96, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Plo, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sung-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: NO. US20020176853A1el Card Domain Containing
; FILE REFERENCE: P-1J 4752
; CURRENT APPLICATION NUMBER: US/09/864, 921
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579, 240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
```

; SOFTWARE: FastSeq for Windows Version 4.0

```
; SEQ ID NO 96
; LENGTH: 3396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (277)...(3348)
US-09-864-921-96
```

Alignment Scores:

Pred. No.:	7.1e-105	Length:	3396
Score:	829.00	Matches:	163
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-697-089-2_COPY_161_323 (1-163) x US-09-864-921-96 (1-3396)

```
QY 1 LeuGlnSerProCysIleIleGlnGlyGluSerGlyLysSerThrLeuGln 20
    |||||||
DB 757 CTTGAGAGCCCTGCATCATTTGAAGGGGAATCTGGCAAGCAAGCTCCTGCTCAG 816
QY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheVal 40
    |||||||
DB 817 CGCATTCGCATGCTCTGGGCTCCGGAAAGTGCAGAGCTGTGACCAAGTTCAATTGCTC 876
QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu 60
    |||||||
DB 877 TTCTTCTCCGCTCTCAGCAGAGGCCAGGGTGAGCTTTTGAACCTCTGTGATCAACTC 936
QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80
    |||||||
DB 937 CTGGATATACCTGGCAACATCAGGAAGCAGACATTCATGGCCATGCTGTGAAGCTCGG 996
QY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 100
    |||||||
DB 997 CAGAGGTTCTTTCTCTTCTTGTAGTGCTTACATATTCAGGCCCCAGAACTGCCAGAA 1056
QY 101 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValIleThrThr 120
    |||||||
DB 1057 ATCGAAGCCCTGATTAAGGAACACACCGCTTCAAGAACATGTCATCGTACCACACTAC 1116
QY 121 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValIleGlyAspMet 140
    |||||||
DB 1117 ACTGAGTGCTTGAGGACATACGAGGAGTTTGTCCTGTGAGTGAGGGGAGATAG 1176
QY 141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 160
    |||||||
DB 1177 ACAGAAAGACAGCCGCCAGGCTCTCATCCGAGAAAGTGCTGATCAAGAGGCTTGCGAAGGC 1236
QY 161 LeuLeuLeu 163
    |||||||
DB 1237 TTGTGTGCTC 1245
```

RESULT 5

```
US-09-841-739-6
; Sequence 6, Application US/09841739
; Patent No. US20020034784A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH
; FILE REFERENCE: 07334-339001
; CURRENT APPLICATION NUMBER: US/09/841, 739
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
```

LENGTH: 3612
TYPE: DNA
ORGANISM: Homo sapiens
US-09-841-739-6

Alignment Scores:

Pred. No.:	7.79e-105	Length:	3612
Score:	829.00	Matches:	163
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-697-089-2_COPY_161_323 (1-163) x US-09-841-739-6 (1-3612)

QY 1 LeuGlnSerProCysIleIleGlnGlyGlnSerGlyGlySerThrLeuGln 20
DB 952 CTTCAAGCCCTGCTATCTTGAAGGGATCTGGCAAGGCCACTGCTGCAG 1011
QY 21 ArgIleAlaMetLeuTrpGlySerGlyCysLysAlaLeuThrLysPheVal 40
DB 1012 CGAATTGCCATGCTCTGGGGCTCCGAAAGTGCAGGCTGTGCAAGTTCAATTGCTC 1071
QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu 60
DB 1072 TTCTTCTCCGCTCTCAGCAGGGCCAGGGTGGACTTTTGAACCTCTGTGATCAACTC 1131
QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 80
DB 1132 CTGGATATACCTGGCAATCAGGAAGCAGACATTCATGCGCCCTGCTGAAAGCTGGCG 1191
QY 81 GlnArgValLeuPheLeuLysAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 100
DB 1192 CAGAGGCTTCTTTCTTCTGTGATGCTCAATGATTCAGGCCCAAGTCCAGAG 1251
QY 101 IleGluAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThr 120
DB 1252 ATCGAAGCCCTGATTAAGAAACACCCCTTCAMAGAACATGCTCATCCACTAC 1311
QY 121 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140
DB 1312 ACTGATGCTCTGAGCAGCATACGCGAGTTGGTCCCTGACTGCTAGGGGGGATATG 1371
QY 141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGly 160
DB 1372 ACAGAAGACAGCGCCCGAGCTCTCATCCGAAAGTCTGTGATCAAGAGCTTGTGAAGC 1431
QY 161 LeuLeuLeu 163
DB 1432 TTGTTGCTC 1440

RESULT 6

US-09-841-739-4
Sequence 4, Application US/09841739
Patent No. US20020034784A1
GENERAL INFORMATION:
APPLICANT: Berlin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
FILE REFERENCE: 07334-329001
CURRENT APPLICATION NUMBER: US/09/841,739
PRIOR FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 09/697,089
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 3615
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS

LOCATION: (1)...(3612)
US-09-841-739-4

Alignment Scores:

Pred. No.:	7.8e-105	Length:	3615
Score:	829.00	Matches:	163
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-697-089-2_COPY_161_323 (1-163) x US-09-841-739-4 (1-3615)

QY 1 LeuGlnSerProCysIleIleGlnGlyGlnSerGlyGlySerThrLeuGln 20
DB 952 CTTCAAGCCCTGCTATCTTGAAGGGATCTGGCAAGGCCACTGCTGCAG 1011
QY 21 ArgIleAlaMetLeuTrpGlySerGlyCysLysAlaLeuThrLysPheVal 40
DB 1012 CGAATTGCCATGCTCTGGGGCTCCGAAAGTGCAGGCTGTGCAAGTTCAATTGCTC 1071
QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu 60
DB 1072 TTCTTCTCCGCTCTCAGCAGGGCCAGGGTGGACTTTTGAACCTCTGTGATCAACTC 1131
QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 80
DB 1132 CTGGATATACCTGGCAATCAGGAAGCAGACATTCATGCGCCCTGCTGAAAGCTGGCG 1191
QY 81 GlnArgValLeuPheLeuLysAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 100
DB 1192 CAGAGGCTTCTTTCTTCTGTGATGCTCAATGATTCAGGCCCAAGTCCAGAG 1251
QY 101 IleGluAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThr 120
DB 1252 ATCGAAGCCCTGATTAAGAAACACCCCTTCAMAGAACATGCTCATCCACTAC 1311
QY 121 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140
DB 1312 ACTGATGCTCTGAGCAGCATACGCGAGTTGGTCCCTGACTGCTAGGGGGGATATG 1371
QY 141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGly 160
DB 1372 ACAGAAGACAGCGCCCGAGCTCTCATCCGAAAGTCTGTGATCAAGAGCTTGTGAAGC 1431
QY 161 LeuLeuLeu 163
DB 1432 TTGTTGCTC 1440

RESULT 7

US-09-841-739-12/C
Sequence 12, Application US/09841739
Patent No. US20020034784A1
GENERAL INFORMATION:
APPLICANT: Berlin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH
FILE REFERENCE: 07334-329001
CURRENT APPLICATION NUMBER: US/09/841,739
PRIOR FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 09/697,089
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 3615
TYPE: DNA
ORGANISM: Homo sapiens
US-09-841-739-12
Alignment Scores:
Pred. No.: 7.8e-105 Length: 3615

Score: 829.00 Matches: 163
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-697-089-2_COPY_161_323 (1-163) x US-09-841-739-12 (1-3615)

```
OY 1 LeuGlnSerProCysIleIleGlnGlyIuSerGlyLysGlyLysSerThrLeuGln 20
DB 2664 CTTCAGAGCCCTGCATCTTAAGAGGATGCGCAAGGCAAGTCCACTGCTGCAG 2605
OY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
DB 2604 CGAATTGCATGCTCTGGGGCTCCGGAAGTCCAGAGGCTGTGACCAAGTCAATTGCGC 2545
OY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 60
DB 2544 TTCTTCCCTCCGTCAGCAGGCGCCAGGGGTGACTTTTGAACCCCTGTGATCAACTC 2485
OY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80
DB 2484 CTGGAATACCTGCGACATCAAGAAAGCAGACATTGATGCGCATGCTGAAGCTGGCG 2425
OY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnGlyProGlu 100
DB 2424 CAGAGGGTTCTTTCCTTCTTATGCTGATGATGATTAAGCCCAAGAACTGCCAGAA 2365
OY 101 IleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThrThr 120
DB 2364 ATCGAAGCCCTGATTAAGAAACCAACCCCTCAAGAAACATGTCATCGTCAACCTAC 2305
OY 121 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValLysPmet 140
DB 2304 ACTGATGCTGAGGACATCAAGCAATTTGGTCCCTGACGCTGAGGTGGGGATTAG 2245
OY 141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGlnLeuAlaGlnGly 160
DB 2244 ACAGAAAGAGGGCCAGGCTCTCATCGAAGAAAGTGTGATCAAGAGAGCTTCTGAAGC 2185
OY 161 LeuLeuLeu 163
DB 2184 TTGTGTCTC 2176
```

RESULT 8

US-09-764-864-754
Sequence 754, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P7223
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 754
LENGTH: 522
TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: SITE
LOCATION: (360)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (468)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (499)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (505)

OTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-754

Alignment Scores: 2.82e-29
Pred. No.: 276.00 Length: 522
Score: 276.00 Matches: 69
Percent Similarity: 81.11% Conservative: 4
Best Local Similarity: 76.67% Mismatches: 13
Query Match: 33.29% Indels: 6
DB: 10 Gaps: 1

US-09-697-089-2_COPY_161_323 (1-163) x US-09-764-864-754 (1-522)

```
OY 1 LeuGlnSerProCysIleIleGlnGlyIuSerGlyLysGlyLysSerThrLeuGln 20
DB 246 CTTCAGAGCCCTGCATCTTAAGAGGATGCGCAAGGCAAGTCCACTGCTGCAG 305
OY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLys-PheVal 40
DB 306 CGCATTTGCCATGCTCTGGGGCTCCGGAAGTCCAGAGGCTGTGACCAAGTTCANNTGCT 365
OY 40 Ihe-PheLeuArgLeuSerArgAlaGlnGly-GlyLeuPheGluThrLeuCysAspGln 59
DB 366 CTCTTCTCCTGTTCAACAGGCGCCAGGGGTGACTTTTGAACCCCTGTGATCA 425
OY 60 LeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeu 79
DB 426 TTCCG-GGTATACGGGACA-TTCAAGAGGCGACATTCAGGCCNGT---GCTGAGGTG 480
OY 80 ArgGlnArgValLeuPheLeuLeu 87
DB 481 CGGCAAGGGCTCTTTCNTCTTG 504
```

RESULT 9

US-08-913-322-1
Sequence 1, Application US/08913322
Patent No. US20020137028A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Roy, Natalie
APPLICANT: Robertson, George
APPLICANT: Tamal, Katsu
TITLE OF INVENTION: USER OF NEURONAL APOPTOSIS INHIBITOR
FILE REFERENCE: 07891/013001
CURRENT APPLICATION NUMBER: US/08/913,322
CURRENT FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: PCT/JP97/00142
EARLIER FILING DATE: 1997-01-17
EARLIER APPLICATION NUMBER: GB 9601108.5
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 5504
TYPE: DNA
ORGANISM: Homo sapiens
US-08-913-322-1

Alignment Scores: 2.91e-22
Pred. No.: 236.50 Length: 5504
Score: 236.50 Matches: 53
Percent Similarity: 58.96% Conservative: 26
Best Local Similarity: 39.55% Mismatches: 48
Query Match: 28.53% Indels: 7
DB: 8 Gaps: 3

US-09-697-089-2_COPY_161_323 (1-163) x US-08-913-322-1 (1-5504)

```
OY 1 LeuGlnSerProCysIleIleGlnGlyIuSerGlyLysGlyLysSerThrLeuGln 20
DB 1779 TTGAACCTGTCATGTCGTGAGGGGTGAACCTGGAAGTGAAGAAAGCGTCTCTGAAG 1838
```

QY	21	Arg1Leu1aMetLeuThrPrgLysSerGlyCysLysAlaLeuThrLysPheLysPheVal	40			
Db	1839	AAATACCTTTCTGTGGGCGATCGGATGCTCCCTGGTTAAACAGGTTCCACTGCTT	1898			
QY	41	PhePheLeuArgLeuSer-----ArgAlaGInGlyGlyLeuPheGluThrLeuCysAsp	58			
Db	1869	TTCTACTCTCCCTTAGTTCCACACAGACAGAGGGGCTGGCCAGTATCATTTGTGAC	1958			
QY	59	GlnLeuAspLlePrgGlyThrLleArgLysGlnThrPheMetAlaMetLeuLeuLys	78			
Db	1959	CAGCTCCCTAGAGAAAGAGGATCTGTTACTGAAAGTGATGAGGACATTAATCCACAG	2018			
QY	79	LeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPhe-----LysPrgGln	96			
Db	2019	TTTAAAGATAGGCTTATTCCTTTAGATGACTCAAAAGAAATATGTTCAATCCCTCAA	2078			
QY	97	AsnCysPrgGluLleGluAlaLeuLleLysGluAsnHisArgPheLysAsnMetValIle	116			
Db	2079	-----GTCAATAGGAAACGATTTCAAAAAACCATTAATCCGGAGCTGCTATG	2129			
QY	117	ValThrThrThrThrGlyCysLeuArgHisLleArgGlnPhe	130			
Db	2130	ATTGCTGTCCGTACAAACAGGGCCAGGACATCCGCCGATAC	2171			
RESULT 10						
US-08-913-322-21						
Sequence 21, Application US/08913322						
Patent No. US20020137028a1						
GENERAL INFORMATION:						
APPLICANT: Korneljuk, Robert G.						
APPLICANT: Mackenzie, Alexander E.						
APPLICANT: Roy, Natalie						
APPLICANT: Robertson, George						
APPLICANT: Tamai, Katsu						
TITLE OF INVENTION: USER OF NEURONAL APOPTOSIS INHIBITOR						
TITLE OF INVENTION: (NAIP)						
FILE REFERENCE: 07891/013001						
CURRENT APPLICATION NUMBER: US/08/913,322						
CURRENT FILING DATE: 1997-09-12						
EARLIER APPLICATION NUMBER: PCT/JP97/00142						
EARLIER FILING DATE: 1997-01-17						
EARLIER APPLICATION NUMBER: GB 9601108.5						
EARLIER FILING DATE: 1996-01-19						
NUMBER OF SEQ. ID NOS: 27						
SOFTWARE: FastSeq for Windows Version 3.0						
SEQ ID NO 21						
LENGTH: 6124						
TYPE: DNA						
ORGANISM: Homo sapiens						
US-08-913-322-21						
Alignment Scores:						
Pred. No.: 3,42e-22 Length: 6124						
Score: 236.50 Matches: 53						
Percent Similarity: 58.96% Conservative: 26						
Best Local Similarity: 39.55% Mismatches: 48						
Query Match: 28.53% Indels: 7						
DB: 8 Gaps: 3						
US-09-697-089-2_COPY_161_323 (1-163) x US-08-913-322-21 (1-6124)						
QY	1	LeuGlnSerPrgCysLleLeuGlnGlyGlnSerGlyLysGlyLysSerThrLeuLeuGln	20			
Db	1675	TTGAACCTGTGCATGTGTGTGGAGGGTGAAGCTGGAAAGTGAAGAGCGTCTCTGGAAG	1734			
QY	21	Arg1Leu1aMetLeuThrPrgLysSerGlyLysCysLysAlaLeuThrLysPheLysPheVal	40			
Db	1735	AAAATAGCTTTCTGTGGGCGATCTGGAATGCTCCCTGTTAAACAGCTTCAAGCTGTT	1794			
QY	41	PhePheLeuArgLeuSer-----ArgAlaGInGlyGlyLeuPheGluThrLeuCysAsp	58			
Db	1795	TTTCACTCTCCCTTAGTTCACACAGACAGAGAGGGCTGGCCAGTATCATTTGTGAC	1854			

QY	59	glnleuaspilleglualeuileuileysglnshnshtasrghelysasmetvalile	78
Db	1855	CAGCTCTAGAGAAAGAAAGAGATCTGTACTGAATGTGCATGAGACCAATTATTCACAG	1914
QY	79	leuarglnarvalleupheleuleuaspilytyrasnglupe-----lysprogl	96
Db	1915	TTAAGATCAGGTCTTATTCCTTTAGATGACTCAAAAGAAATATGTCAATCCCTCAA	1974
QY	97	asnrcysprogluileglualaleuileysglnshnshtasrghelysasmetvalile	116
Db	1975	-----GTCAATGAGAAATGATTCACAAAACCACTTATCCCGGACCTGCTATFG	2025
QY	117	valthrthrthrthrglucysleuarghisilearglnphe	130
Db	2026	ATTGCTGCTGCCTACAAACAGGCGCAGGACATCCGCCGATAC	2067
RESULT	11		
US-09-967-768A-184			
Sequence 184, Application US/09967768A			
Patent No. US20020150877A1			
GENERAL INFORMATION:			
APPLICANT: Augustus, Meena			
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign			
TITLE OF INVENTION: Sets			
FILE REFERENCE: 689290-72			
CURRENT APPLICATION NUMBER: US/09/967,768A			
CURRENT FILING DATE: 2001-09-28			
PRIOR APPLICATION NUMBER: US/60/236,109			
PRIOR FILING DATE: 2000-09-28			
PRIOR APPLICATION NUMBER: US/60/236,034			
PRIOR FILING DATE: 2000-09-28			
PRIOR APPLICATION NUMBER: US/60/236,111			
PRIOR FILING DATE: 2000-09-28			
NUMBER OF SEQ ID NOS: 325			
SOFTWARE: PatentIn version 3.0			
SEQ ID NO 184			
LENGTH: 6124			
TYPE: DNA			
ORGANISM: Homo sapiens			
US-09-967-768A-184			
Alignment Scores:			
Pred. No.:	3.42e-22	Length:	6124
Score:	236.50	Matches:	53
Percent Similarity:	58.96%	Conservative:	26
Best Local Similarity:	39.55%	Mismatches:	48
Query Match:	28.53%	Indels:	7
DB:	10	Gaps:	3
US-09-697-089-2_COPY_161_323 (1-163) x US-09-967-768A-184 (1-6124)			
QY	1	leuqinsrprocylllellleuglucylusergilylsgilylserthleuengl	20
Db	1675	TTGAACCTGTCATGTGTGTGGAGGTGAAGCTGGAATGGAAAGACGCTCTCTGAG	1734
QY	21	argllealametleuarglysergilylscylsyalaleuthrlylspheleysbheval	40
Db	1735	AAATAGCTTTCTGTGGGCATCTGATGCGTGTCCCGTGTAAACAGAGTTCACAGTGT	1794
QY	41	phepheleuargleuser-----argalaglnglylgleuphegluthleucysasp	58
Db	1795	TTCTACTCTCCCTTATGTCACACAGACGAGGAGGCGCGCCAGTATCATCTGTGAC	1854
QY	59	glnleuaspilleglualeuileuileysglnshnshtasrghelysasmetvalile	78
Db	1855	CAGCTCTAGAGAAAGAAAGATCTGTACTGAATGTGCATGAGACCAATTATTCACAG	1914
QY	79	leuarglnarvalleupheleuleuaspilytyrasnglupe-----lysprogl	96
Db	1915	TTAAGATCAGGTCTTATTCCTTTAGATGACTCAAAAGAAATATGTCAATCCCTCAA	1974
QY	97	asnrcysprogluileglualaleuileysglnshnshtasrghelysasmetvalile	116


```

: APPLICANT: Damiano, Jason S.
: APPLICANT: Lee, Sug-Hyung
: APPLICANT: Oliveira, Vasco A.
: APPLICANT: Hayashi, Hideki
: APPLICANT: Pavlovskii, Krzysztof
: TITLE OF INVENTION: No. US2002017683A1e1 Card Domain Containing
: FILE REFERENCE: P-LJ 4752
: CURRENT APPLICATION NUMBER: US/09/864,921
: PRIOR FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 09/579,240
: PRIOR FILING DATE: 2000-05-24
: PRIOR APPLICATION NUMBER: US 09/666,347
: PRIOR FILING DATE: 2000-10-10
: PRIOR APPLICATION NUMBER: US 60/275,980
: PRIOR FILING DATE: 2001-03-14
: NUMBER OF SEQ ID NOS: 195
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 173
: LENGTH: 888
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1) ... (888)
: US-09-864-921-173

Alignment Scores:
Pred. No.: 2.48e-07 Length: 888
Score: 120.50 Matches: 33
Percent Similarity: 48.98% Conservative: 15
Best local Similarity: 33.67% Mismatches: 33
Query Match: 14.54% Indels: 17
DB: Gaps: 3

US-09-697-089-2_COPY_161_323 (1-163) x US-09-864-921-173 (1-888)

Oy 6 llellegluglyugserglylysglylysserthrienuenlmglylealewleu 25
Db 19 cttgggtgggttgaggggggagtgccaaagcagctcttgagggcctgacgttgacg 78
Oy 26 trpelyserglylyscyslysalaleuthrllyspheylsphenaleupheleuargleu 45
Db 79 tggcgctgaggg-----caagacttccagagatttctcttcttccattcacctgc 132
Oy 46 serargalagln-----glylyleuphegluhtrleu 56
Db 133 cggagagctgcagtcagtcagccaaacacactctctgcgagcttactcttggagcactgc 192
Oy 57 cysaspglnleuleuaspilpiefroglythrillearglyslgnlphrhemetalwleu 76
Db 193 tggttggcct-----gatgttgtrcamaaacaacatttccagattacttc 234
Oy 77 leuylsleuarglnargvalleupheleuleuaspilgytrnsnltupheyls 94
Db 235 cttgaccacccctgaccgctgctcgtgttAACCTTGATGAGGCTTGACGAGATTCAAG 288

RESULT 15
US-09-833-381-1214
: Sequence 1214, Application US/09833381
: Patent No. US20020132090A1
: GENERAL INFORMATION:
: APPLICANT: Robison, Keith E.
: TITLE OF INVENTION: No. US20020132090A1e1 Nucleic Acid and Protein Homologs
: FILE REFERENCE: 5800-119
: CURRENT APPLICATION NUMBER: US/09/833,381
: CURRENT FILING DATE: 2001-04-11
: PRIOR APPLICATION NUMBER: 09/516,448
: PRIOR FILING DATE: 2000-02-29
: NUMBER OF SEQ ID NOS: 2050
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 1214
: LENGTH: 2724

```

[illegible]

Search completed: January 31, 2003, 18:05:15
Job time : 51.1385 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 31, 2003, 13:16:47 : Search time 2073.15 Seconds

(without alignments)
1976.816 Million cell updates/sec

Title: US-09-697-089-2_COPY_161_323

Perfect score: 829

Sequence: 1

BL0SDM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+g2n.model -DEV=x1h
-Q=/cgn2_1/USPTO.spool/US09697089/runat_29012003_092754_19749/app_query.fasta.1.981
-DB=Pending_Patents_NA_Main -QFWT=fastap -SUFFIX=p2n.rmpm -MINMATCH=0.1
-LOOCL=0 -LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=Bl0sdm62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09697089 -ECN_L1_3083 -runat_29012003_092754_19749
-NCP=6 -ICU=3 -NO_XLPHY -NO_MAP -LARGQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV.TIMEOUT=130 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Pending_Patents_NA_Main:*
1: /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US081_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US082_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US083_COMB.seq:*
8: /cgn2_6/ptodata/2/pna/US084_COMB.seq:*
9: /cgn2_6/ptodata/2/pna/US085_COMB.seq:*
10: /cgn2_6/ptodata/2/pna/US086_COMB.seq:*
11: /cgn2_6/ptodata/2/pna/US087_COMB.seq:*
12: /cgn2_6/ptodata/2/pna/US088_COMB.seq:*
13: /cgn2_6/ptodata/2/pna/US089_COMB.seq:*
14: /cgn2_6/ptodata/2/pna/US090_COMB.seq:*
15: /cgn2_6/ptodata/2/pna/US091_COMB.seq:*
16: /cgn2_6/ptodata/2/pna/US092_COMB.seq:*
17: /cgn2_6/ptodata/2/pna/US093_COMB.seq:*
18: /cgn2_6/ptodata/2/pna/US094_COMB.seq:*
19: /cgn2_6/ptodata/2/pna/US095A_COMB.seq:*
20: /cgn2_6/ptodata/2/pna/US095B_COMB.seq:*
21: /cgn2_6/ptodata/2/pna/US095C_COMB.seq:*
22: /cgn2_6/ptodata/2/pna/US095D_COMB.seq:*
23: /cgn2_6/ptodata/2/pna/US096A_COMB.seq:*
24: /cgn2_6/ptodata/2/pna/US096B_COMB.seq:*
25: /cgn2_6/ptodata/2/pna/US096C_COMB.seq:*
26: /cgn2_6/ptodata/2/pna/US096E_COMB.seq:*
27: /cgn2_6/ptodata/2/pna/US096F_COMB.seq:*
28: /cgn2_6/ptodata/2/pna/US097A_COMB.seq:*

29: /cgn2_6/ptodata/2/pna/US097B_COMB.seq:*
30: /cgn2_6/ptodata/2/pna/US097C_COMB.seq:*
31: /cgn2_6/ptodata/2/pna/US098A_COMB.seq:*
32: /cgn2_6/ptodata/2/pna/US098B_COMB.seq:*
33: /cgn2_6/ptodata/2/pna/US098C_COMB.seq:*
34: /cgn2_6/ptodata/2/pna/US099A_COMB.seq:*
35: /cgn2_6/ptodata/2/pna/US099B_COMB.seq:*
36: /cgn2_6/ptodata/2/pna/US099C_COMB.seq:*
37: /cgn2_6/ptodata/2/pna/US099D_COMB.seq:*
38: /cgn2_6/ptodata/2/pna/US100A_COMB.seq:*
39: /cgn2_6/ptodata/2/pna/US100B_COMB.seq:*
40: /cgn2_6/ptodata/2/pna/US101A_COMB.seq:*
41: /cgn2_6/ptodata/2/pna/US101B_COMB.seq:*
42: /cgn2_6/ptodata/2/pna/US102A_COMB.seq:*
43: /cgn2_6/ptodata/2/pna/US102B_COMB.seq:*
44: /cgn2_6/ptodata/2/pna/US6000_COMB.seq:*
45: /cgn2_6/ptodata/2/pna/US6001_COMB.seq:*
46: /cgn2_6/ptodata/2/pna/US6002_COMB.seq:*
47: /cgn2_6/ptodata/2/pna/US6003_COMB.seq:*
48: /cgn2_6/ptodata/2/pna/US6004_COMB.seq:*
49: /cgn2_6/ptodata/2/pna/US6005_COMB.seq:*
50: /cgn2_6/ptodata/2/pna/US6006_COMB.seq:*
51: /cgn2_6/ptodata/2/pna/US6007_COMB.seq:*
52: /cgn2_6/ptodata/2/pna/US6008_COMB.seq:*
53: /cgn2_6/ptodata/2/pna/US6009_COMB.seq:*
54: /cgn2_6/ptodata/2/pna/US6010_COMB.seq:*
55: /cgn2_6/ptodata/2/pna/US6011_COMB.seq:*
56: /cgn2_6/ptodata/2/pna/US6012_COMB.seq:*
57: /cgn2_6/ptodata/2/pna/US6013_COMB.seq:*
58: /cgn2_6/ptodata/2/pna/US6014_COMB.seq:*
59: /cgn2_6/ptodata/2/pna/US6015_COMB.seq:*
60: /cgn2_6/ptodata/2/pna/US6016_COMB.seq:*
61: /cgn2_6/ptodata/2/pna/US6017_COMB.seq:*
62: /cgn2_6/ptodata/2/pna/US6018_COMB.seq:*
63: /cgn2_6/ptodata/2/pna/US6019_COMB.seq:*
64: /cgn2_6/ptodata/2/pna/US6020_COMB.seq:*
65: /cgn2_6/ptodata/2/pna/US6021_COMB.seq:*
66: /cgn2_6/ptodata/2/pna/US6022_COMB.seq:*
67: /cgn2_6/ptodata/2/pna/US6023_COMB.seq:*
68: /cgn2_6/ptodata/2/pna/US6024_COMB.seq:*
69: /cgn2_6/ptodata/2/pna/US6025_COMB.seq:*
70: /cgn2_6/ptodata/2/pna/US6026_COMB.seq:*
71: /cgn2_6/ptodata/2/pna/US6027_COMB.seq:*
72: /cgn2_6/ptodata/2/pna/US6028_COMB.seq:*
73: /cgn2_6/ptodata/2/pna/US6029_COMB.seq:*
74: /cgn2_6/ptodata/2/pna/US6030_COMB.seq:*
75: /cgn2_6/ptodata/2/pna/US6031_COMB.seq:*
76: /cgn2_6/ptodata/2/pna/US6032_COMB.seq:*
77: /cgn2_6/ptodata/2/pna/US6033_COMB.seq:*
78: /cgn2_6/ptodata/2/pna/US6034_COMB.seq:*
79: /cgn2_6/ptodata/2/pna/US6035_COMB.seq:*
80: /cgn2_6/ptodata/2/pna/US6036_COMB.seq:*
81: /cgn2_6/ptodata/2/pna/US6037_COMB.seq:*
82: /cgn2_6/ptodata/2/pna/US6038_COMB.seq:*
83: /cgn2_6/ptodata/2/pna/US6039_COMB.seq:*
84: /cgn2_6/ptodata/2/pna/US6040_COMB.seq:*
85: /cgn2_6/ptodata/2/pna/US6041_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	ID	Description
1	829	100.0	891	33	US-09-864-921-179	Sequence 179, App
2	829	100.0	1976	38	US-10-029-386-22860	Sequence 22860, A
3	829	100.0	2002	38	US-10-029-386-25135	Sequence 25135, A
4	829	100.0	2215	1	PCT-0501-07143-22	Sequence 22, Appl
5	829	100.0	2215	42	US-10-221-097-22	Sequence 22, Appl
6	829	100.0	2343	22	US-09-578-789-15	Sequence 15, Appl


```

; OTHER INFORMATION: SWISSPROT HIT: Q9JTB6, EVALUE 2.00e+40
; OTHER INFORMATION: NT HIT: g115296339, EVALUE 0.00e+00
; OTHER INFORMATION: EST_HUMAN HIT: AV656315.1, EVALUE 0.00e+00
US-10-029-386-22860

```

Alignment Scores:	
Pred. No.:	1.77e-94
Score:	829.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	38
Length:	1976
Matches:	163
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-697-089-2_COPY_161_323 (1-163) x US-10-029-386-22860 (1-1976)

Qy	1	LeuLeuSerProCysIleIleGluGlyLeuSerGlyLysGlyLysSerThrLeuLeuGln	20
Db	1758	CTTAGAGCCCCCTCATTCATTGAAGGGGAATCTGGCAAAAGCAAGTCCACTCTGGTGGAG	1699
Qy	21	ArgIleAlaMetLeuIleTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal	40
Db	1698	CGAATTGGCATGCTCTGGGGGCTCCGGAAAGTCGAAGGCTGTGACCACAAATTCAAAATTCGTC	1639
Qy	41	PhePheLeuAlaGlyLeuSerArgAlaGlnGlyLysLeuPheGluThrLeuCysAspGlnLeu	60
Db	1638	TTTCTTCCTCCCTCTCAGCAGGGCCACAGGGTGGACTTTTGGAAACCTCTGTGATCAATCTC	1579
Qy	61	LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg	80
Db	1578	CTGGATTAACCTGGGCACACATCAGGAAGCAGACATTCAATGGCCATCTCTGTAAAGTGGGG	1519
Qy	81	GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu	100
Db	1518	CAGAGGGTCTTTTCTCTTGTGATGGCTACAAATGAAATTCAGCCCCACAGAACTGGCCCAAA	1459
Qy	101	IleLeuAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr	120
Db	1458	ATCGAAGCCCTGATTAAGAAAGAAACCCGCTTCAAGAACATAGTGTATGTCACCACTACCC	1399
Qy	121	ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet	140
Db	1398	ACTAGAGTCCGAGAGGCACATACGGCAGCTTGTGTCCTCCCTGACTGCTGAAGTGGGGGATATYG	1339
Qy	141	ThrGluAspSerAlaGlnAlaLeuIleArgLysValLeuIleLysGluLeuAlaGluGly	160
Db	1338	ACAAAGACACAGCCGCCAGGCTCTCATCCGAAAGTGCATCAAGAGACCTTGCTGAAGCC	1279
Qy	161	LeuLeuLeu 163	
Db	1278	TTTGTTCCTC 1270	

```

RESULT 3
US-10-029-386-25135/C
; Sequence 25135, Application US/10029386
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ. ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 25135
; LENGTH: 2002
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL121653.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.36
; OTHER INFORMATION: EST_HUMAN HIT: AV656315.1, EVALUATE 0.00e+00

```

```

; OTHER INFORMATION: SWISSPROT HIT: Q9JIB6, EVALUE 2.00e-40
; OTHER INFORMATION: NT HIT: g115296399, EVALUE 0.00e+00
US-10-029-386-25135

```

Pred. No.:	1.8e-94	2002
Score:	829.00	163
Percent Similarity:	100.00%	Matches:
Best Local Similarity:	100.00%	Conservative:
Query Match:	100.00%	Mismatches:
DB:	38	Indels:
		Gaps:

US-09-697-089-2_COPY_161_323 (1-163) x US-10-029-386-25135 (1-2002)

Qy	1	LeuGlnSerProCysIleIleGlnIlyGlnSerGlyIlyGlySerThrLeuLeuGln	20
Db	1782	CTTAGAGGCCCTGCATCATTTGAAGGGAAATCTGGCAAAAGGCAAGTCCACTCTGCTGGAG	1723
Qy	21	ArgIleAlaMetLeuThrPglySerGlyLysCysLysAlaLeuThrLysPheLysPheVal	40
Db	1722	CGAATTGCCATGCTCTGGGGCTCCGGAAAGTGCAAGCGCTGACCAAGTTCMAATTTCGTC	1653
Qy	41	PhePheLeuArgLeuSerArgAlaGlnGlyIleuPheGluThrLeuCysAspGlnLeu	60
Db	1662	TTCCTCTCCGTCACGACAGGCCACGGGTGACCTTTTGAACCTCTGTGATCAACTC	1603
Qy	61	LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg	80
Db	1602	CTGGATTACTCTGGCAACATACAGAAAGCAGACATTCATGGCCATGCTGTAAGCTGGCG	1543
Qy	81	GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu	100
Db	1542	CAGAGGGTTTCTTCTCTCTGATGGCTCAATGAAATTCACCCCAACATGGCCCAAA	1483
Qy	101	IleGluValaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValaThrThrThr	120
Db	1482	ATCGAACCCCTGATTAAAGGAAACCAACGCCCTTCAGAAACATGTGATGTGCACACATCC	1423
Qy	121	ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet	140
Db	1422	ACTGATAGCCCTGAGGGACACATACGGCAGTTGGTGTGCCCTGACATGCTAGAGCTGGGGGATATYG	1363
Qy	141	ThrGlnuSpSerIaGlnAlaLeuIleArgGluValaLeuIleLysGluLeuAlaGluGly	160
Db	1362	ACGAAACACAGCGCCCGACGCTCATCCGACGAAGAGTCTGATCAAGAGACTTGTCTGAAGC	1303
Qy	161	LeuLeuLeu 163	
Db	1302	TTGTGTGCTC 1294	

```

PCRT-0501-07143-22
: Sequence 22. Application PC/TUS0107143
: GENERAL INFORMATION:
: APPLICANT: SMITHLINE BEECHAM CORPORATION
: APPLICANT: SMITHLINE BEECHAM P.L.C.
: TITLE OF INVENTION: NOVEL COMPOUNDS
: FILE REFERENCE: GP50016
: CURRENT APPLICATION NUMBER: PC/TUS01/07143
: CURRENT FILING DATE: 2001-03-08
: PRIOR APPLICATION NUMBER: 60/187,107
: PRIOR FILING DATE: 2000-03-06
: PRIOR APPLICATION NUMBER: 60/236,874
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/188,916
: PRIOR FILING DATE: 2000-03-13
: PRIOR APPLICATION NUMBER: 60/237,846
: PRIOR FILING DATE: 2000-10-03
: NUMBER OF SEQ. ID NOS.: 52
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 22
: LENGTH: 2215
: TYPE: DNA

```

```
; ORGANISM: Homo sapiens
PCT-US01-07143-22

Alignment Scores:
Pred. No.: 2,07e-94      Length: 2215
Score: 829.00           Matches: 163
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%    Mismatches: 0
Query Match: 100.00%             Indels: 0
DB: 1                         Gaps: 0

US-09-697-089-2_COPY_161_323 (1-163) x PCT-US01-07143-22 (1-2215)

QY 1 LeuGlnSerProCysIleIleGlnGlyuSerGlySgIySserThrLeuLeuGln 20
Db CTTGAGAGCCCTGCATCATTTGAAGGGAAATCTGGCAAGGCAAGTCCACTCTGTCGAG 498

QY 21 ArgIleAlaMetLeuTrpGlySerGlyScySlySAlaLeuThrLysPheLysPheVal 40
Db CGAATTGCCATGCTCTGGGGCTCCGAAAGTGCAGAGGCTGTGACCAAGTCAAAATTCGTC 558

QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGlnThrLeuCysAspGlnLeu 60
Db TTCTTCCTCCGCTCAGCAGAGGCCAGGGTGGACTTTTGAACCTCTGTGATCAACTC 618

QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 80
Db CTGGAATATACCTGGCACAATCAGAGACGACATTCATGGCCATCTCTGAGAGCTGGCG 678

QY 81 GlnArgValLeuPheLeuLeuAspGlyTyraSngIuPheLysProGlnAsnCysProGlu 100
Db CAGAGGGTCTTCTTCCTTCTTGATGGCTACATGAAATTCAGCCCAAGCTGCCAGAA 738

QY 101 IleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThrThr 120
Db ATCGAAGCCCTGATTAAGAAACACCGCTTCAAGAACATGATGATGACCACTACCC 798

QY 121 ThrGlnCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGlnValGlyAspMet 140
Db ACTGAGTCCCTGAGGACACATACGGCAGTTTGTCCTGACGCTGAGAGTGGGGATATG 858

QY 141 ThrGlnAspSerAlaGlnAlaLeuIleArgGlnValLeuIleLysGlnLeuAlaGlnGly 160
Db ACAGAAAGACAGCGCCAGGCTCTCATCCGAAAGTGTGATCAAGAGACTGTGTAAGGC 918

QY 161 LeuLeuLeu 163
Db TTGTTGCTC 927

RESULT 5
US-10-221-097-22
; Sequence 22, Application US/10221097
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdock, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50016
; CURRENT APPLICATION NUMBER: US/10/221,097
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: PCT/US01/07143
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 32
```

```
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 2215
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-221-097-22

Alignment Scores:
Pred. No.: 2,07e-94      Length: 2215
Score: 829.00           Matches: 163
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%    Mismatches: 0
Query Match: 100.00%             Indels: 0
DB: 42                         Gaps: 0

US-09-697-089-2_COPY_161_323 (1-163) x US-10-221-097-22 (1-2215)

QY 1 LeuGlnSerProCysIleIleGlnGlyuSerGlySgIySserThrLeuLeuGln 20
Db CTTGAGAGCCCTGCATCATTTGAAGGGAAATCTGGCAAGGCAAGTCCACTCTGTCGAG 498

QY 21 ArgIleAlaMetLeuTrpGlySerGlyScySlySAlaLeuThrLysPheLysPheVal 40
Db CGAATTGCCATGCTCTGGGGCTCCGAAAGTGCAGAGGCTGTGACCAAGTCAAAATTCGTC 558

QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGlnThrLeuCysAspGlnLeu 60
Db TTCTTCCTCCGCTCAGCAGAGGCCAGGGTGGACTTTTGAACCTCTGTGATCAACTC 618

QY 599 TTCTTCCTCCGCTCAGCAGAGGCCAGGGTGGACTTTTGAACCTCTGTGATCAACTC 618
Db 559 TTCTTCCTCCGCTCAGCAGAGGCCAGGGTGGACTTTTGAACCTCTGTGATCAACTC 618

QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 80
Db CTGGAATATACCTGGCACAATCAGAGACGACATTCATGGCCATCTCTGAGAGCTGGCG 678

QY 81 GlnArgValLeuPheLeuLeuAspGlyTyraSngIuPheLysProGlnAsnCysProGlu 100
Db CAGAGGGTCTTCTTCCTTCTTGATGGCTACATGAAATTCAGCCCAAGCTGCCAGAA 738

QY 101 IleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThrThr 120
Db ATCGAAGCCCTGATTAAGAAACACCGCTTCAAGAACATGATGATGACCACTACCC 798

QY 121 ThrGlnCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGlnValGlyAspMet 140
Db ACTGAGTCCCTGAGGACACATACGGCAGTTTGTCCTGACGCTGAGAGTGGGGATATG 858

QY 141 ThrGlnAspSerAlaGlnAlaLeuIleArgGlnValLeuIleLysGlnLeuAlaGlnGly 160
Db ACAGAAAGACAGCGCCAGGCTCTCATCCGAAAGTGTGATCAAGAGACTGTGTAAGGC 918

QY 161 LeuLeuLeu 163
Db TTGTTGCTC 927

RESULT 6
US-09-578-789-15
; Sequence 15, Application US/09578789
; GENERAL INFORMATION:
; APPLICANT: John C. Reed
; APPLICANT: Frederick P. Rio
; APPLICANT: Adam Godzik
; TITLE OF INVENTION: Novel Card Polypeptides
; FILE REFERENCE: P-LJ 4141
; CURRENT APPLICATION NUMBER: US/09/578,789
; CURRENT FILING DATE: 2000-05-23
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2343
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2340)
```

US-09-578-789-15

Alignment Scores:

Pred. No.: 2,23e-94 Length: 2343
Score: 829.00 Matches: 163
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-697-089-2_COPY_161_323 (1-163) x US-09-578-789-15 (1-2343)

QY 1 LeuGlnSerProCysIleIleGlnGlyGlnSerGlyLysGlyLysSerThrLeuLeuGln 20
DB 508 CTTGAGAGCCCTGATCATTTGAAGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAG 567
QY 21 ArgIleAlaMetLeuThrPheGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
DB 568 CGCATTTGCCATGCTCTGGGGGCTCCGGAAGTGCAGAGGCTGTGACCAAGTTCAAATTCGTC 627
QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 60
DB 628 TTCTTCTCTCCGTCCTCAGAGGGCCAGGTGGACTTTTGAAGCCCTGTGATCAACTC 687
QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80
DB 688 CTGGATATACCTGGCACATCAGAGAGCAGACATTCATGGCCATGCTGTGAAGCTGCAG 747
QY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 100
DB 748 CAGAGGGTCTTTCTTCTTCTGATGCTACATGATTCACACCCAGAGAGTCCAGAGAA 807
QY 101 IlegAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThrThr 120
DB 808 ATCGAAGCCCTGATTAAGGAAACACCGCTTCAAGACATGCTCACCCTACCTACC 867
QY 121 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140
DB 868 ACTGAGTGCCTGAGCACATACGAGAGTTGGTCCCTGACATGCTGAGAGTGGGGATAG 927
QY 141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 160
DB 928 ACAGAGAGACAGGCCAGGCTCTCATCCGAGAGATGCTGATCAAGAGAGCTTGTGAAGC 987
QY 161 LeuLeuLeu 163
DB 988 TTGTTGCTC 996

RESULT 7

US-09-579-240-15

; Sequence 15, Application US/09579240
; GENERAL INFORMATION:
; APPLICANT: John C. Reed
; APPLICANT: Frederick Pio
; APPLICANT: Adam Godzik
; TITLE OF INVENTION: Novel Card-Domain Containing
; TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use
; FILE REFERENCE: P-LJ 4211
; CURRENT APPLICATION NUMBER: US/09/579, 240
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2343
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2340)
US-09-579-240-15

Alignment Scores:

Pred. No.: 2,23e-94 Length: 2343

Score:

829.00 Matches: 163
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-697-089-2_COPY_161_323 (1-163) x US-09-579-240-15 (1-2343)

QY 1 LeuGlnSerProCysIleIleGlnGlyGlnSerGlyLysGlyLysSerThrLeuLeuGln 20
DB 508 CTTGAGAGCCCTGATCATTTGAAGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAG 567
QY 21 ArgIleAlaMetLeuThrPheGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
DB 568 CGCATTTGCCATGCTCTGGGGGCTCCGGAAGTGCAGAGGCTGTGACCAAGTTCAAATTCGTC 627
QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 60
DB 628 TTCTTCTCTCCGTCCTCAGAGGGCCAGGTGGACTTTTGAAGCCCTGTGATCAACTC 687
QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80
DB 688 CTGGATATACCTGGCACATCAGAGAGCAGACATTCATGGCCATGCTGTGAAGCTGCAG 747
QY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 100
DB 748 CAGAGGGTCTTTCTTCTTCTGATGCTACATGATTAAGCCCAAGAGTCCAGAGAA 807
QY 101 IlegAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThrThr 120
DB 808 ATCGAAGCCCTGATTAAGGAAACACCGCTTCAAGACATGCTCACCCTACCTACC 867
QY 121 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140
DB 868 ACTGAGTGCCTGAGCACATACGAGAGTTGGTCCCTGACATGCTGAGAGTGGGGATAG 927
QY 141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 160
DB 928 ACAGAGAGACAGGCCAGGCTCTCATCCGAGAGATGCTGATCAAGAGAGCTTGTGAAGC 987
QY 161 LeuLeuLeu 163
DB 988 TTGTTGCTC 996

RESULT 8

US-09-578-789-17

; Sequence 17, Application US/09578789
; GENERAL INFORMATION:
; APPLICANT: John C. Reed
; APPLICANT: Frederick Pio
; APPLICANT: Adam Godzik
; TITLE OF INVENTION: Novel Card Polypeptides
; FILE REFERENCE: P-LJ 4141
; CURRENT APPLICATION NUMBER: US/09/578, 789
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 2415
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2412)
US-09-578-789-17

Alignment Scores:

Pred. No.: 2,33e-94 Length: 2415
Score: 829.00 Matches: 163
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-697-089-2_COPY_161_323 (1-163) x US-09-578-789-17 (1-2415)

```
OY 1 LeuGlnSerProCysIleIleGlnGlyGlnSerGlyLysGlyLysSerThrLeuLeuGln 20
DB 508 CTGAGAGCCCTCGATCATGTAAGGGGAATCTGGCAAGGCAAGTCACCTGCTGCAG
OY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
DB 568 CGCATTTGCATGCTCTGGGGCTCCGGAAAGTGCAGAGCTTGACCAATTCAATTCGTC
OY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLysLeuPheGlnThrLeuCysAspGlnLeu 60
DB 628 TTCTTCCCTCCGTCACAGAGGCCAGGGTGGACTTTTGAACCCCTGTGATCACTC
OY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80
DB 688 CTGATATACCTGGACACATCAGGAAGCAGACATTCAATGCGCATGCTGAAAGCTGGG
OY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGlnPheLysProGlnAsnCysProGln 100
DB 748 CAGAGGGTCTTTTCCCTTCTTGATGCGTACATGATTCAGCCCAACTGCCACAA
OY 101 IleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThrThr 120
DB 808 ATCGAAGCCCTGATTAAGAAACACCGCTTCAAGACATGTCATGTCACACCTACC
OY 121 ThrGlnCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGlnValGlyAspMet 140
DB 868 ACTAGTCTCTGAGGACACATAGCGAGTTTGTCCTGACTGCTGAGAGTGGGGATATG
OY 141 ThrGlnAspSerAlaGlnAlaLeuIleArgGlnValLeuIleLysGlnLeuAlaGlnGly 160
DB 928 ACAGAAGACAGCGCCAGAGCTCTCATCCGAGAAGTGTGATCAAGAGACTTGTCAAGGC
OY 161 LeuLeuLeu 163
DB 988 TTGTTCCTC 996
```

RESULT 9

US-09-579-240-17
: Sequence 17, Application US/09579240
: GENERAL INFORMATION:
: APPLICANT: John C. Reed
: APPLICANT: Frederick Pio
: APPLICANT: Adam Godzik
: TITLE OF INVENTION: Novel Card-Domain Containing
: FILE REFERENCE: P-LJ 4211
: CURRENT APPLICATION NUMBER: US/09/579, 240
: CURRENT FILING DATE: 2000-05-24
: NUMBER OF SEQ ID NOS: 79
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 17
: LENGTH: 2415
: TYPE: DNA
: ORGANISM: Homo Sapien
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)...(2412)
US-09-579-240-17

Alignment Scores:

Pred. No.:	2,33e-94	Length:	2415
Score:	829.00	Matches:	163
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09-697-089-2_COPY_161_323 (1-163) x US-09-579-240-17 (1-2415)

OY 1 LeuGlnSerProCysIleIleGlnGlyGlnSerGlyLysGlyLysSerThrLeuLeuGln 20

```
DB 508 CTGAGAGCCCTCGATCATGTAAGGGGAATCTGGCAAGGCAAGTCACCTGCTGCAG 567
OY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
DB 568 CGCATTTGCATGCTCTGGGGCTCCGGAAAGTGCAGAGCTTGACCAATTCAATTCGTC 627
OY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLysLeuPheGlnThrLeuCysAspGlnLeu 60
DB 628 TTCTTCCCTCCGTCACAGAGGCCAGGGTGGACTTTTGAACCCCTGTGATCACTC 687
OY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80
DB 688 CTGATATACCTGGACACATCAGGAAGCAGACATTCAATGCGCATGCTGAAAGCTGGG 747
OY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGlnPheLysProGlnAsnCysProGln 100
DB 748 CAGAGGGTCTTTTCCCTTCTTGATGCGTACATGATTCAGCCCAACTGCCACAA 807
OY 101 IleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThrThr 120
DB 808 ATCGAAGCCCTGATTAAGAAACACCGCTTCAAGACATGTCATGTCACACCTACC 867
OY 121 ThrGlnCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGlnValGlyAspMet 140
DB 868 ACTAGTCTCTGAGGACACATAGCGAGTTTGTCCTGACTGCTGAGAGTGGGGATATG 927
OY 141 ThrGlnAspSerAlaGlnAlaLeuIleArgGlnValLeuIleLysGlnLeuAlaGlnGly 160
DB 928 ACAGAAGACAGCGCCAGAGCTCTCATCCGAGAAGTGTGATCAAGAGACTTGTCAAGGC 987
OY 161 LeuLeuLeu 163
DB 988 TTGTTCCTC 996
```

RESULT 10

US-09-577-408-3077
: Sequence 3077, Application US/09577408
: GENERAL INFORMATION:
: APPLICANT: Tang, Y. Tom
: APPLICANT: Tillinghast, John
: APPLICANT: Slinku, Ankura
: APPLICANT: Liu, Chenghua
: APPLICANT: Drmanac, Radoje T.
: TITLE OF INVENTION: Novel Nucleic Acids and
: FILE REFERENCE: 792
: CURRENT APPLICATION NUMBER: US/09/577, 408
: CURRENT FILING DATE: 2000-05-18
: NUMBER OF SEQ ID NOS: 8502
: SOFTWARE: PL_GCT_genes Version 1.0
: SEQ ID NO 3077
: LENGTH: 3018
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: (682)...(2040)
: OTHER INFORMATION: similar to g13688110 in the genepept database release 115,
: OTHER INFORMATION: Run with FASTX 3.3f00, default parameters
US-09-577-408-3077

Alignment Scores:

Pred. No.:	3.15e-94	Length:	3018
Score:	829.00	Matches:	163
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09-697-089-2_COPY_161_323 (1-163) x US-09-577-408-3077 (1-3018)

OY 1 LeuGlnSerProCysIleIleGlnGlyGlnSerGlyLysGlyLysSerThrLeuLeuGln 20

|||||
Db 715 CTTGAGAGCCCTGCATCATTTGAAGGGAATCTGCGAAGCAAGCAATCCACTGCTGCGAG 774
Qy 21 Arg1leAlaMetLeuThrGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
Db 775 CGCATTTGCCATGCTCTGGGGCTCGGAAAGTGCAGAGGCTGTGACCAAGTTCAAAATTCGTC 834
Qy 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 60
Db 835 TTCTTCCCTCCGCTCAGAGAGGCGCCAGGGTGACTTTTGAACCCCTCTGTATCACTC 894
Qy 61 LeuAsp1leProGlyThr1leArgLysGlnThrPheMetAlaMetLeuLysLeuArg 80
Db 895 CTGGATATACCTGGCACAATCAGAGAACGACATTCATGCGCATGCTGCTGAAGCTGCGG 954
Qy 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnGlyProGlu 100
Db 955 CAGAGGGTCTTTCTCTTGTATGCTACAAATGAATTCAGCCCAAGAACCTGCCAGAA 1014
Qy 101 l1eg1ua1leu1leLysGluAsnHisArgPheLysAsnMetVal1leValThrThrThr 120
Db 1015 ATCGAAGCCCTGATTAAGAAACCAACCGCTTCAGAAACATGTGTCATGCTCACCCTACC 1074
Qy 121 ThrGluCysLeuArgHis1leArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140
Db 1075 ACTGAGTGCCTGAGGACATACGCGAGTTTGGTCCCTGACTGCTGAGGTGGGGGATATG 1134
Qy 141 ThrGluAspSerAlaGlnAlaLeu1leArgGluValLeu1leLysGluLeuAlaGluGly 160
Db 1135 ACAGAAAGACAGCGCCAGGCTCTCATCCGAGAAATGCTGATCAAGAGAGCTTGTGAAGGC 1194
Qy 161 LeuLeuLeu 163
Db 1195 TTGTTGCTC 1203

RESULT 11
PCT-US00-29643-3
: Sequence 3, Application PC/TUS0029643
: GENERAL INFORMATION:
: APPLICANT: Millennium Pharmaceuticals, Inc.
: TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
: FILE REFERENCE: 07334-136MO1
: CURRENT APPLICATION NUMBER: PCT/US00/29643
: PRIOR FILING DATE: 2000-10-26
: PRIOR APPLICATION NUMBER: US 60/161,822
: PRIOR FILING DATE: 1999-10-27
: NUMBER OF SEQ ID NOS: 11
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 3072
: TYPE: DNA
: ORGANISM: Homo sapiens
PCT-US00-29643-3

Alignment Scores:
Pred. No.: 3,23e-94 Length: 3072
Score: 829.00 Matches: 163
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-697-089-2_COPY_161_323 (1-163) x PCT-US00-29643-3 (1-3072)

Qy 1 LeuGlnSerProCys1le1leGlnGlyLysSerGlyLysSerThrLeuLeuGln 20
Db 481 CTTGAGAGCCCTGCATCATTTGAAGGGAATCTGCGAAGCAAGCAATCCACTGCTGCGAG 540
Qy 21 Arg1leAlaMetLeuThrGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
Db 541 CGCATTTGCCATGCTCTGGGGCTCGGAAAGTGCAGAGGCTGTGACCAAGTTCAAAATTCGTC 600

Qy 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 60
Db 601 TTCTTCCCTCCGCTCAGAGAGGCGCCAGGGTGACTTTTGAACCCCTCTGTATCACTC 660
Qy 61 LeuAsp1leProGlyThr1leArgLysGlnThrPheMetAlaMetLeuLysLeuArg 80
Db 661 CTGGATATACCTGGCACAATCAGAGAACGACATTCATGCGCATGCTGCTGAAGCTGCGG 720
Qy 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnGlyProGlu 100
Db 721 CAGAGGGTCTTTCTCTTGTATGCTACAAATGAATTCAGCCCAAGAACCTGCCAGAA 780
Qy 101 l1eg1ua1leu1leLysGluAsnHisArgPheLysAsnMetVal1leValThrThrThr 120
Db 781 ATCGAAGCCCTGATTAAGAAACCAACCGCTTCAGAAACATGTGTCATGCTCACCCTACC 840
Qy 121 ThrGluCysLeuArgHis1leArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140
Db 841 ACTGAGTGCCTGAGGACATACGCGAGTTTGGTCCCTGACTGCTGAGGTGGGGGATATG 900
Qy 141 ThrGluAspSerAlaGlnAlaLeu1leArgGluValLeu1leLysGluLeuAlaGluGly 160
Db 901 ACAGAAAGACAGCGCCAGGCTCTCATCCGAGAAATGCTGATCAAGAGAGCTTGTGAAGGC 960
Qy 161 LeuLeuLeu 163
Db 961 TTGTTGCTC 969

RESULT 12
US-09-697-089-3
: Sequence 3, Application US/09697089
: GENERAL INFORMATION:
: APPLICANT: Bertin, John
: TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
: FILE REFERENCE: 07334-136001
: CURRENT APPLICATION NUMBER: US/09/697,089
: PRIOR FILING DATE: 2000-10-26
: PRIOR APPLICATION NUMBER: US 60/161,822
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 3072
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-697-089-3

Alignment Scores:
Pred. No.: 3,23e-94 Length: 3072
Score: 829.00 Matches: 163
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-697-089-2_COPY_161_323 (1-163) x US-09-697-089-3 (1-3072)

Qy 1 LeuGlnSerProCys1le1leGlnGlyLysSerGlyLysSerThrLeuLeuGln 20
Db 481 CTTGAGAGCCCTGCATCATTTGAAGGGAATCTGCGAAGCAAGCAATCCACTGCTGCGAG 540
Qy 21 Arg1leAlaMetLeuThrGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
Db 541 CGCATTTGCCATGCTCTGGGGCTCGGAAAGTGCAGAGGCTGTGACCAAGTTCAAAATTCGTC 600
Qy 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 60
Db 601 TTCTTCCCTCCGCTCAGAGAGGCGCCAGGGTGACTTTTGAACCCCTCTGTATCACTC 660
Qy 61 LeuAsp1leProGlyThr1leArgLysGlnThrPheMetAlaMetLeuLysLeuArg 80

Db	661	CTGCATTAACCTGGCACAATCGAAGACGACGACATTCAATGCCCATCTGTAACTGGG	720
OY	81	GlnArgValLeuPheLeuIleuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu	100
Db	721	CAGAGGGTTCTTTTCCTCTTGATGGCTACAAATGAATTCAGCCCAACTGGCCCAAA	780
OY	101	IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr	120
Db	781	ATCGAAGCCCTGTATAAGAAAACCACCGCTTCAAGAACAATGGTCATGCTCACCACTACC	840
OY	121	ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet	140
Db	841	ACTGATGCTCCCTGAGGCACATACGGCAGTTGGTGGCTCGACTGCTGAGGTGGGGATATG	900
OY	141	ThrgluAspSerAlaGluAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly	160
Db	901	ACGAGAGACAGCGCCCAACGCTCTCATCCGAGAAGTGTGATCAAGAGAACCTGTGTAAAGC	960
OY	161	LeuLeuLeu 163	
Db	961	TTCGTGCTC 969	

```

RESULT 13
US-09-841-739-3
; Sequence 3, Application US/09841739
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-328001
; CURRENT APPLICATION NUMBER: US/09/841,739
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3072
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-841-739-3

```

Alignment Scores:	
Pred. No.:	3, 23e-94
Score:	829.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	32
Length:	3072
Matches:	163
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-697-089-2_COPY_161_323 (1-163) X US-09-841-739-3 (1-3072)

QY	1	LeuGlnSerProCysIleIleGlnGlybSerGlyIysSgIySsSerThrIleuGln	20
QY	1	LeuGlnSerProCysIleIleGlnGlybSerGlyIysSgIySsSerThrIleuGln	20
Db	481	CTTCCAGAGCCCTGCATATTGAAGGGAAATCTGGCAAGGCAAGTCACCTCTGCTCAG	54.0%
QY	21	ArgIleAlaMetIleuTrpGlySerGlyIysCysIysAlaIeuThrIlyPheIysPheVal	40
Db	541	CCCATTTGCATCTCTGGGGGCTCCGGAAGTACCAAGGCTGTGACCACAGTTCAATTTCCTC	60.0%
QY	41	PhePheIleuArgIleSerArgAlaGlnGlyIleuPheGluThrIleuCysAspGlnIleu	60
Db	601	TTCTTCTCTCCGCTCTCAGAGGGCCCAAGGGTGGACTTTTGAACCCCTCTGTGATCAATCTC	66.0%
QY	61	IleuAspIleProGlyThrIleArgIysGlnThrPheMetAlaMetIleuIlySleuArg	80
Db	661	CTGGATTATACCTGGGACAAATCAGGAAGCAGACATTCATGCGCCATGCTGCTGAAGCTGGG	72.0%
QY	81	GlnArgValIleuPheIleuIleuAspGlyIlyrAsnGluPheIlyProGlnAsnCysProGlu	100
Db	721	CAGAGGGTCTTTCTCTCTGTGATGGCTACATGATTAATTCAGGCCCAAGAACTGCCCGAGAA	78.0%

QY	101	IleGluAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThrThr	120
Db	761	ATCGAAGCCCTGGATTAAGAGAAACACCACCGCTCTCAAGAACATGGTCATCGTCACCACTACC	840
QY	121	ThrGlnCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGlnValGlyAspMet	140
Db	841	ACTGATGCTCCCTGAGGACCATATCGGCAAGTTGGTCCCTGACTCTGAGGTGGGGGATATG	900
QY	141	ThrGlnAspSerAlaGlnAlaLeuIleArgGlnValLeuIleLysGlnLeuAlaGlnGly	160
Db	901	ACAGAGACACAGCGGCCAGCGCTCATCTCCGAGAAATGCTGATCAAGAGAGCTTGGTGAAGCC	960
QY	161	LeuLeuLeu 163	
Db	961	TTGTGTCTC 969	
RESULT 14			
US-10-156-733-1			
; Sequence 1. Application US/10156733			
; Comment. INFORMATION			

```

1  APPLICANT: Altemtli, Emao S
2  TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING
3  TITLE OF INVENTION: FACTOR
4  FILE REFERENCE: 480140, 477
5  CURRENT APPLICATION NUMBER: US/10/156,733
6  CURRENT FILING DATE: 2002-05-24
7  NUMBER OF SEQ. ID NOS: 14
8  SOFTWARE: FastSeq for Windows Version 4.0
9  SEQ ID NO 1
10 LENGTH: 3075
11 TYPE: DNA
12 ORGANISM: Homo sapiens
13 FEATURE:
14 NAME/KEY: CDS
15 LOCATION: (1)...(3075)
16 US-10-156-733-1

```

Alignment Scores:	
Pred. No.:	3.24e-94
Length:	3075
Score:	829.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	41
Length:	3075
Matches:	163
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-697-089-2_COPY_161_323 (1-163) X US-10-156-733-1 (1-3075)

OY	1	IleugInserProcyllIlelIngInyIsuerglysglylsysertlrHeuIn	20
Db	481	CITTCAGAGCCCTGATATTGAAGGGAAATGTGGCAAGAAGCATCCTGCTGCAG	540
OY	21	ArgIleAlaMetLeuTrpGlySerGlyScySylsalaleuthrLysPheVal	40
Db	541	CGAATTGCCATGCTGTGGGGCTCCGGAANAAGCAAGGCTTGACCAAGTCCAATTGCTC	600
OY	41	PhePheLeuArgLeuSerArgAlaInclLygLeuPhegluThrLeucysAspGlnLeu	60
Db	601	TTCCTTCCTCCGCTCTCAGAGGGCCAGGGGTGGACTTTTGAACCCTCTGTGATCAATC	660
OY	61	IeuAspIleProglTythrIleaArgLysGlnThrPheMeIaMetLeuLeuLysLeuArg	80
Db	661	CTGGATATACCTGGCACATCAGNAGACAGACATTCATGAGCGCAATGCTGAACCTGCGG	720
OY	81	GlnArgValLeuPheLeuLeuAspLtyrAsnGlunPheLysProGlnAsnCysProGlu	100
Db	721	CAGAGGGCTTCTTTCCTCTTATGTCATCAATCAATTCAGCCCCAGAACCTGCCCGAA	780
OY	101	IleGluAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThrThr	120
Db	781	ATCGAAGCCCTGATTAAGAAAAACACCGCTTCAAGAACATGATCTGATCCACATACC	840
OY	121	ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet	140

Db 841 ACTGATGCTCGAGGCACATACGCGAGTTTGGTCCCTGACTGCTGAGGTGGGGATATG 900
QY 141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValIleLysGluLeuAlaGluGly 160
|||||
Db 901 ACAGAGACAGCGCCAGGCTCTCATCCGAGAGTGTGATCAAGAGCTTGTGAAGGC 960
QY 161 LeuLeuLeu 163
|||||
Db 961 TTGTTGCTC 969

RESULT 15

PCT-US00-29643-1
; Sequence 1, Application PC/TUS0029643
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 0734-136WO1
; CURRENT APPLICATION NUMBER: PCT/US00/29643
; CURRENT FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3133
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36) ... (3107)
PCT-US00-29643-1

Alignment Scores:

Pred. No.: 3.32e-94 Length: 3133
Score: 829.00 Matches: 163
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-697-089-2_copy_161_323 (1-163) x PCT-US00-29643-1 (1-3133)

QY 1 LeuGlnSerProCysIleIleGluGlyLysSerThrLeuLeuGln 20
|||||
Db 516 CTTGAGACCCCTGCATCATTTGAAGGGAATCTGGCANAAGCAATCCACTTGTCTGCG 575
QY 21 ArgIleAlaMetLeuTyrGlySerGlyLysCysIleAlaLeuThrLysPheLysPheVal 40
|||||
Db 576 CGCATGCGCATGCTCTGGGGCTCCGGAAGTGCAAGGCTGTGACCAAGTCAATTGCTG 635
QY 41 PhePheLeuAlaGlyLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 60
|||||
Db 636 TTTCTTCCCTCCGCTCAGAGGAGGCGGAGTCTTTTGAAACCTCTGTGATCAACTC 695
QY 61 LeuAspIleProGlyThrIleArgGlyGlnThrPheMetAlaMetLeuLeuLysLeuArg 80
|||||
Db 696 CTGGATTAACCTGGACACAATCAGAGCAGACATTCAATGCCATGCTGCTGAAGCTGCGG 755
QY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 100
|||||
Db 756 CAGAGGGTTCTTTCCCTCTTGATGGCTACATGAATTCAGGCCAGACACTGCCAGAA 815
QY 101 IleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThrThr 120
|||||
Db 816 ATCGAAGCCCTGATTAAGGAAACACCGCTTCAGAACATGGTCAATGCTCACCACTAC 875
QY 121 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140
|||||
Db 876 ACTGATGCTCGAGGCACATACGCGAGTTTGGTGGCTGACTGCTGAGGTGGGGATATG 935
QY 141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValIleLysGluLeuAlaGluGly 160
|||||

Db 936 ACAGAGACAGCGCCAGGCTCTCATCCGAGAGTGTGATCAAGAGCTTGTGAAGGC 995
QY 161 LeuLeuLeu 163
|||||
Db 996 TTGTTGCTC 1004

Search completed: January 31, 2003, 17:55:31
Job time : 2076.15 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 31, 2003, 13:24:32 : Search time 153.327 Seconds
(without alignments)
1295.994 Million cell updates/sec

Title: US-09-697-089-2_COPY_161_323
Perfect score: 829
Sequence: 1 LQSPCIEGSGKSKSLD.....SAQALIREVLKEALAEULL 163

Scoring table:
BLOSUM62
Xgapop 10.0, Ygapext 0.5
Xgapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2500250 segs, 609544256 residues

Total number of hits satisfying chosen parameters: 5000500

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame_plus_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09697089/runat_29012003_092755_19775/app_query.fasta.1.981
-DB=Pending_Patents_NA_New -QFMT=fastap -SUFFIX=p2n.rnpn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HAPPSTZP=500 -MILEN=0
-MAXLEN=2000000000 -USER=US09697089.ecgn_1_1_91.etrnat.29012003_092755_19775
-NCPU=6 -ICPU=3 -NO_XLPTX -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/2/pna/PCF_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	829	100.0	3075	1 PCT-US02-21946A-1
2	829	100.0	3219	1 PCT-US02-21946A-14
3	829	100.0	3543	6 US-10-276-781-111
4	236.5	28.5	5984	6 US-10-285-408-2
5	236.5	28.5	6133	5 US-09-949-002-84
6	236.5	28.5	6133	5 US-09-949-002-125
7	236.5	28.5	60194	5 US-09-949-002-656
8	236.5	28.5	60195	5 US-09-949-002-697
9	235.5	28.4	3210	5 US-09-724-676-6819
10	235.5	28.4	3210	5 US-09-724-676A-6819
11	235.5	28.4	3597	5 US-09-724-676-6801

12	235.5	28.4	3597	5	US-09-724-676A-6801	Sequence 6801, Ap
13	235.5	28.4	4143	5	US-09-724-676-6810	Sequence 6810, Ap
14	235.5	28.4	4143	5	US-09-724-676A-6810	Sequence 6810, Ap
15	235.5	28.4	4259	5	US-09-724-676-6816	Sequence 6816, Ap
16	235.5	28.4	4259	5	US-09-724-676A-6816	Sequence 6816, Ap
17	235.5	28.4	4268	5	US-09-724-676-6824	Sequence 6824, Ap
18	235.5	28.4	4268	5	US-09-724-676A-6824	Sequence 6824, Ap
19	235.5	28.4	4280	5	US-09-724-676-6818	Sequence 6818, Ap
20	235.5	28.4	4280	5	US-09-724-676A-6818	Sequence 6818, Ap
21	235.5	28.4	4646	5	US-09-724-676-6798	Sequence 6798, Ap
22	235.5	28.4	4646	5	US-09-724-676A-6798	Sequence 6798, Ap
23	235.5	28.4	4667	5	US-09-724-676-6800	Sequence 6800, Ap
24	235.5	28.4	4667	5	US-09-724-676A-6800	Sequence 6800, Ap
25	235.5	28.4	5189	5	US-09-724-676-6815	Sequence 6815, Ap
26	235.5	28.4	5189	5	US-09-724-676A-6815	Sequence 6815, Ap
27	235.5	28.4	5192	5	US-09-724-676-6807	Sequence 6807, Ap
28	235.5	28.4	5192	5	US-09-724-676A-6807	Sequence 6807, Ap
29	235.5	28.4	5210	5	US-09-724-676-6817	Sequence 6817, Ap
30	235.5	28.4	5210	5	US-09-724-676A-6817	Sequence 6817, Ap
31	235.5	28.4	5213	5	US-09-724-676-6809	Sequence 6809, Ap
32	235.5	28.4	5213	5	US-09-724-676A-6809	Sequence 6809, Ap
33	235.5	28.4	5576	5	US-09-724-676-6797	Sequence 6797, Ap
34	235.5	28.4	5576	5	US-09-724-676A-6797	Sequence 6797, Ap
35	235.5	28.4	5597	5	US-09-724-676-6799	Sequence 6799, Ap
36	235.5	28.4	5597	5	US-09-724-676A-6799	Sequence 6799, Ap
37	235.5	28.4	6122	5	US-09-724-676-6806	Sequence 6806, Ap
38	235.5	28.4	6122	5	US-09-724-676A-6806	Sequence 6806, Ap
39	235.5	28.4	6143	5	US-09-724-676-6808	Sequence 6808, Ap
40	235.5	28.4	6143	5	US-09-724-676A-6808	Sequence 6808, Ap
41	111	13.4	4141	6	US-10-295-981-42	Sequence 42, Ap1
42	107	12.9	1470	6	US-10-295-981-27	Sequence 27, Ap1
43	107	12.9	2859	6	US-10-295-981-9	Sequence 9, Ap1
44	107	12.9	3080	1	PCT-US02-38606-94	Sequence 94, Ap1
45	107	12.9	3080	6	US-10-295-981-25	Sequence 25, Ap1

ALIGNMENTS

RESULT 1
PCT-US02-21946A-1
: Sequence 1, Application PC/TUS0221946A
: GENERAL INFORMATION:
: APPLICANT: Thomas Jefferson University
: APPLICANT: Alnemir, Emdad S.
: TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING
: FILE REFERENCE: 480140.477PC
: CURRENT APPLICATION NUMBER: PCT/US02/21946A
: CURRENT FILING DATE: 2002-05-24
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 3075
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)...(3075)
PCT-US02-21946A-1

Alignment Scores:

Pred. No.: 5.62e-96 Length: 3075
Score: 829.00 Matches: 163
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-697-089-2_COPY_161_323 (1-163) x PCT-US02-21946A-1 (1-3075)

Qy 1 LeuGlnSerProCysIleIleGlnGlySerGlyGlySerThrLeuGln 20
DB 481 CTTGAGCCCTGATCATGAGGGAATCTGCAAGGCAAGTCACACTGCTGAG 540

QY	21	ArglllelametleuTrpGlySerGlyLysCysLysAlaIeuthrLysPheLysPheVal	40
Db	541	CGAATTCGCCATGCCTCTGGGGCTCCGGAATGCAAGGCTTGACCAAGTTCAATTCTGC	600
QY	41	PhePheLeuArgLeuSerArgAlaGlnGlyIleuPheGluThrLeuCysAspGlnLeu	60
Db	601	TTCTTCCTCCGCTCTCACACAGGGCCCAAGGGGAGCATTTTTCAAAACCCCTCTGTATCAACTC	660
QY	61	LeuAspIleProGlyThrIleArgLysGlnThrPheMetIaMetLeuLysIleuArg	80
Db	661	CTGATATACCTGGCCACAAATCAGGAACACAGACATTCATTGGCCATGCTGCTGAAGCTCGG	720
QY	81	GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu	100
Db	721	CAGAGGGTCTTTTTCCTCTTGATGGCTACAAATGATTAAGGCCCACTGGACCTGCCAGAA	780
QY	101	IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValIThrThrThr	120
Db	781	ATCGAAGCCCGAATAAGGAAACACACCGCTCTCAAGAACATGTGCATCGTCACACATACC	840
QY	121	ThrGluCysLeuArgHisIleArgGlnPheGlyAlaIeuthrAlaGluValGlyAspMet	140
Db	841	ACTGATGCTCCGAGGACACATACGCGCACTTGTGTCTCCCTGACTGCTGAGGTGGGGGATATG	900
QY	141	ThrGluAspSerAlaGlnAlaIleuIleArgGluValLeuIleLysGluLeuAlaGlnGly	160
Db	901	ACAGAGACACAGCCGCAAGGCTCTCATCTCGAGAACTGCTGATCAAGAGAGCTTGCGAAGGC	960
QY	161	LeuLeuLeu 163	
Db	961	TTGTGTCTC 969	

RESULT 2

```

: Sequence 14, Application PCT/US0221946A
: GENERAL INFORMATION:
: APPLICANT: Thomas Jefferson University
: APPLICANT: Alnemrl, Emd S.
: TITLE OF INVENTION: IPAF, AN ICE-PROTEASE A
: TITLE OF INVENTION: FACTOR
: FILE REFERENCE: 480140.477PC
: CURRENT APPLICATION NUMBER: PCT/US02/21946A
: CURRENT FILING DATE: 2002-05-24
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 14
: LENGTH: 3219
: TYPE: DNA
: ORGANISM: Homo sapiens
PCT-US02-21946A-14

```

Alignment Scores:

Pred. No.:	5	98e-96	length:	3219
Score:	829.00		Matches:	163
Percent Similarity:	100.00%		Conservative:	0
Best Local Similarity:	100.00%		Mismatches:	0
Query Match:	100.00%		Indels:	0
DB:	1		Gaps:	0

US-09-697-089-2_COPY_161_323 (1-163) x PCT-US02-21946A-14 (1-3219)

Qy	1	LeuGlnSerProGysIleIleGluGlyYglSerGlyLysSerThrLeuGln	20
Qy	625	CTTGAGACCCCTGGATCATTTGAAGGGGAATCTGGCAAGGCAAGTCACCTCGCTCAG	684
Db	21	ArgIleIaMetLeuTrpGlySerGlyLysGlySalaLeuThrLysPheVal	40
Qy	685	CGAATGGCCATGCTCTGGGGGCTCCGGAAAGTCAAGGCTCGACCAAGTTCAAAATTCGTC	744
Db	41	PhePheLeuArgLeuSerArgAlaGlnIlyGlyLeuPheGluTrpThrLeuCysAspGlnLeu	60
Qy	745	TTCTTCCTCCGCTCTAGCAGGGGCCAGGGTGACCTTTTGAAGCCCTCTGTGATCAACTC	804
Db			

QY	61	LeuAspIleProGlyThrIleArgGlyGlnThrPheMetAlaMetLeuLeuIleuAsnArg	80
Db	805	CTGATrTACTTGCCACAAATCAGAGAAGCAGACTTCATCGCCATGCTCTGAAGTGGG	864
QY	81	GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnGysProGlu	100
Db	865	CAGAGGCTTCTTTCCTTCTTGATGGCTCAATGAAATTCAGCCCAACATGGCCCAAA	924
QY	101	IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr	120
Db	925	ATCCAAACCCCTGATAAAGGAAAACCAACCCCTTCAGAAACATGGTATGCTACCACTAC	984
QY	121	ThrGluGlyLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet	140
Db	985	ACTAGAGCTCTGAGGCCATACAGGCGAGTTGGTGGCTTACTAGCTGAGAGTGGGGCATATG	1044
QY	141	ThrGluAspSerIleGlnAlaLeuIleArgGluValLeuIleLysGluIleuAlaGluGly	160
Db	1045	ACAAAGACACAGCCCGCCAGGCTTCTATTCGAGAAAGTCTGATCAAGSAGCTTCTCAAGC	1104
QY	161	LeuLeuLeu 163	
Db	1105	TTGTGTGCTC 1113	

RESULT 3

; Sequence 111, Application US/10276781

; GENERAL INFORMATION:

```

? APPLICANT: Hyseq, Inc.
? APPLICANT: Tang et al.
? TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
? FILE REFERENCE: 21272-018 (785 config)
? CURRENT APPLICATION NUMBER: US/10/276,781
? CURRENT FILING DATE: 2002-11-18
? PRIOR APPLICATION NUMBER: 09/491,404
? PRIOR FILING DATE: 2000-01-25
? NUMBER OF SEQ ID NOS: 2018
? SOFTWARE: fastseq for windows version 3.0
? SEQ ID NO 111
? LENGTH: 3545
? TYPE: DNA
? ORGANISM: Homo sapiens
? US-10-276-781-111

```

Alignment Scores:

Pred. No.:	6.83e-96	Length:	3545
Score:	829.00	Matches:	163
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-697-089-2_COPY_161_323 (1-163) x US-10-276-781-111 (1-3545)

QY 1 LeuGlnSerProCysIleIleISGLuGlyIuSerdLysIySGLysSerThrIleuGln 20
 Db 712 CTTCGAGCCCCGTCATATTGAAGGGGAATCTGGCAAGGCAAGTCACCTCTGCTCAG 77111
 QY 21 ArgIlealaMetLeuTrrPglySerCylLysCysLysalaLeuThrLysPheVal 40
 Db 772 CGCATTTGCCAATGCTCTGGGGGCTCCGGAAAGCAAGGCTCTGACCAACGTTCAAAATTTGTC 83111
 QY 41 PhePheLeuArgLeuSerArgAlaGlnIyGlyLeuPheGluThrLeuCysAspGlnLeu 60
 Db 832 TTCTCTCCCTCCGCTCTCAGCAGGGCCAGAGGTGGACTTTTGTGAACCCCTCTGTGATCAACTC 89111
 QY 61 LeuAspIleProGlyIThrIleAlaTrpSgInThrPheMetIalaMetLeuLeuLysLeuArg 80
 Db 892 CTGGATTATTCCTGGCACAATCAGGAAGCAGACATTCAAGCGCAATGCTGTAAACTCGGG 95111
 QY 81 GlnArgValLeuPheLeuLeuAspGlyITyrTrsngIuPheLysProGlnAsnCysProGlu 100111

```
Db 952 CAGAGGCTTTTCCTTCCTGATGGCTACAAATGATTCAGCCCGAGAACTGCCAGAA 1011
QY 101 IIEGLUALaleuilelysgluasnhsargphelysasmetValIleValhrrhr 120
Db 1012 ATCGAAGCCCTGATAAAGAAACACCGCTTCAGAAACATGTCATCTCCACCTACC 1071
QY 121 ThrGlucYsLeuAArgHisIleAArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140
Db 1072 ACTGATGCTGCTGAGCAGACATGAGCAGTTGGTGGCCCTGACCTGCTAGAGGTGGGATATG 1131
QY 141 ThrGluAspSerAlaGlnAlaLeuIleAArgGluValleuilelysglualeuIleagluGly 160
Db 1132 ACAGAAAGCAGCGCCAGGCTCTCATCCGAGAAAGTGCTGATCAAGAGAGCTGCTGAAAGC 1191
QY 161 LeuLeuLeu 163
Db 1192 TTGTTGCTC 1200

RESULT 4
US-10-285-408-2
; Sequence 2, Application US/10285408
; GENERAL INFORMATION:
; APPLICANT: IKEDA, Johe
; TITLE OF INVENTION: Monoclonal Antibodies Against Human Apoptosis Inhibitory Protein
; FILE REFERENCE: 2002-1440/MMC/00653
; CURRENT APPLICATION NUMBER: US/10/285,408
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 09/830,338
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: PCT/JP99/05841
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 5984
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDC
; LOCATION: (292)..(4500)
US-10-285-408-2

Alignment Scores:
Pred. No.: 2,17e-19 Length: 5984
Score: 236.50 Matches: 53
Percent Similarity: 58.96% Conservative: 26
Best Local Similarity: 39.55% Mismatches: 48
Query Match: 28.53% Indels: 7
DB: 6 Gaps: 3

US-09-697-089-2_COPY_161_323 (1-163) x US-10-285-408-2 (1-5984)
QY 1 LeuGlnSerProCysIleIleGlnGlyGluSerGlyLysGlyLysSerThrLeuLeuGln 20
Db 1675 TTGAACCTGTCATGTGATGGAGGTGAAGCTGGAAGGAAAGCGGTCTCTCGAAG 1734
QY 21 ArgIleAlaMetLeuThrPglYserGlyLysCysLysAlaLeuThrLysPheVal 40
Db 1735 AAAAATGACTTCTGTGGCATCTGATGCTGCCCTGTTAAACAGGTTCACGCTGGTT 1794
QY 41 PhePheLeuArgLeuSer-----ArgAlaGlnGlyGlyLeuPheGlnThrLeuLeuCysAsp 58
Db 1795 TTCTACCTCTCCCTTAGTTCACACACAGACACAGAGGGGCTGCCAGATATCATCTGTGAC 1854
QY 59 GlnLeuLeuAspIleProGlyThrIleAArgGlyGlnThrPheMetAlaMetLeuLeuLys 78
Db 1855 CAGCTCCCTAGAGAAAGAGATCTGTACTGAATGTGATGAGAACATTTATCCAGCAG 1914
QY 79 LeuAArgGlnAArgValleuPheLeuLeuAspGlyTyrAsnGlnPhe-----LysProGln 96
Db 1915 TTAAAGATACAGTCTTATCTCTTTAGATGACTACAAAGAAATATGTTCATCCCTCAA 1974
```

```
QY 97 AsnCysProGluIleGlnAlaLeuilelysgluasnhsargphelysasmetValIle 116
Db 1975 -----GTCATAGGAAGAAACTGATTCATAAAAAACCATTTATCCCGAGACCTGCGATTG 2025
QY 117 ValThrThrThrThrGlnCysLeuAArgHisIleAArgGlnPhe 130
Db 2026 ATTGCTGTCCGTACAAACAGGCGCAGGACATCCGCGCATAC 2067

RESULT 5
US-09-949-002-84
; Sequence 84, Application US/09949002
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CLO00790
; CURRENT APPLICATION NUMBER: US/09/949,002
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: fastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 6133
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-84

Alignment Scores:
Pred. No.: 2,24e-19 Length: 6133
Score: 236.50 Matches: 53
Percent Similarity: 58.96% Conservative: 26
Best Local Similarity: 39.55% Mismatches: 48
Query Match: 28.53% Indels: 7
DB: 5 Gaps: 3

US-09-697-089-2_COPY_161_323 (1-163) x US-09-949-002-84 (1-6133)
QY 1 LeuGlnSerProCysIleIleGlnGlyGluSerGlyLysGlyLysSerThrLeuLeuGln 20
Db 1684 TTGAACCTGTCATGTGATGGAGGTGAAGCTGGAAGGAAAGCGGTCTCTCGAAG 1743
QY 21 ArgIleAlaMetLeuThrPglYserGlyLysCysLysAlaLeuThrLysPheVal 40
Db 1744 AAAAATGACTTCTGTGGCATCTGATGCTGCCCTGTTAAACAGGTTCACAGCTGGTT 1803
QY 41 PhePheLeuArgLeuSer-----ArgAlaGlnGlyGlyLeuPheGlnThrLeuLeuCysAsp 58
Db 1804 TTCTACCTCTCCCTTAGTTCACACACAGACACAGAGGGGCTGCCAGATATCATCTGTGAC 1863
QY 59 GlnLeuLeuAspIleProGlyThrIleAArgGlyGlnThrPheMetAlaMetLeuLeuLys 78
Db 1864 CAGCTCCCTAGAGAAAGAGATCTGTACTGAATGTGATGAGAACATTTATCCAGCAG 1923
QY 79 LeuAArgGlnAArgValleuPheLeuLeuAspGlyTyrAsnGlnPhe-----LysProGln 96
Db 1924 TTAAAGATCAGGCTCTTATCTCTTTAGATGACTCAAAAGAAATATGTTCATCCCTCAA 1983
QY 97 AsnCysProGluIleGlnAlaLeuilelysgluasnhsargphelysasmetValIle 116
Db 1984 -----GTCATAGGAAGAAACTGATTCATAAAAAACCATTTATCCCGAGACCTGCGATTG 2034
QY 117 ValThrThrThrThrGlnCysLeuAArgHisIleAArgGlnPhe 130
Db 2035 ATTGCTGTCCGTACAAACAGGCGCAGGACATCCGCGCATAC 2076

RESULT 6
US-09-949-002-125
; Sequence 125, Application US/09949002
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
```

```
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 6133
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-125

Alignment Scores:
Pred. No.: 2,24e-19 Length: 6133
Score: 236.50 Matches: 53
Percent Similarity: 58.96% Conservative: 26
Best Local Similarity: 39.55% Mismatches: 48
Query Match: 28.53% Indels: 7
Gaps: 3

US-09-697-089-2_COPY_161_323 (1-163) x US-09-949-002-125 (1-6133)
QY 1 LeuGlnSerProCysIleIleGluGlySerGlyLysSerThrLeuGln 20
    ||| ||| :|||:|||||:|||||:|||||:|||||:
Db 1684 TTGAACCTGTCATGTCGTGGAGGTCGAACTGGAAGAGCGTCCTCTGAG 1743
QY 21 ArgIleAlaMetLeuThrPglYSerGlyLysGlyLysAlaLeuThrLysPheVal 40
    :|||:|||||:|||||:|||||:|||||:|||||:
Db 1744 AAAATAGCTTTTCTGTGGCATCTGAGTCCTCCCTGTTAAACAGGTCCTCAGCTT 1803
QY 41 PhePheLeuArgValSer-----ArgAlaGlnGlyLeuPheGluThrLeuCysasp 58
    |||:|||||:|||||:|||||:|||||:|||||:
Db 1804 TTCTACTCTCTCCTTAGTTCACACAGACAGAGGGGCTGGCCAGTATCTGTAC 1863
QY 59 GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLys 78
    |||:|||||:|||||:|||||:|||||:|||||:
Db 1864 CAGCTCCTAGAGAAAGAGGATCTGTACTGAAATGTGCATGAGAACATATATCCAGCAG 1923
QY 79 LeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGlnPhe-----LysProGln 96
    |||:|||||:|||||:|||||:|||||:|||||:
Db 1924 TTAAAGAAATCAGGCTTATCTTTTATGATGACTACAAAGAAATATGTTCATCTCTCA 1983
QY 97 AsnCysProGluIleGluAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIle 116
    |||:|||||:|||||:|||||:|||||:|||||:
Db 1984 -----GTCATAGGAAACTGATTCAAAAAACCACTATATCCGAGCTGCTATGT 2034
QY 117 ValThrThrThrThrGluCysLeuArgHisIleArgGlnPhe 130
    :|||:|||||:|||||:|||||:|||||:
Db 2035 ATTGCTGTCCGTACAAACAGGCGCAGGACATCCGCCGATAC 2076

RESULT 7
US-09-949-002-656
; Sequence 656, Application US/09949002
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 656
; LENGTH: 60194
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-656
```

```
Alignment Scores:
Pred. No.: 5.1e-18 Length: 60194
Score: 236.50 Matches: 53
Percent Similarity: 58.96% Conservative: 26
Best Local Similarity: 39.55% Mismatches: 48
Query Match: 28.53% Indels: 7
Gaps: 3

US-09-697-089-2_COPY_161_323 (1-163) x US-09-949-002-656 (1-60194)
QY 1 LeuGlnSerProCysIleIleGluGlySerGlyLysSerThrLeuGln 20
    ||| ||| :|||:|||||:|||||:|||||:|||||:
Db 41011 TTGAACCTGTCATGTCGTGGAGGTCGAACTGGAAGAGCGTCCTCTGAG 41070
QY 21 ArgIleAlaMetLeuThrPglYSerGlyLysGlyLysAlaLeuThrLysPheVal 40
    :|||:|||||:|||||:|||||:|||||:|||||:
Db 41071 AAAATAGCTTTTCTGTGGCATCTGAGTCTGCTCCCTGTTAAACAGGTCCTCAGCTGTT 41130
QY 41 PhePheLeuArgValSer-----ArgAlaGlnGlyLeuPheGluThrLeuCysasp 58
    |||:|||||:|||||:|||||:|||||:|||||:
Db 41131 TTCTACTCTCTCCTTAGTTCACACAGACAGAGGGGCTGGCCAGTATCTGTGAC 41190
QY 59 GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLys 78
    |||:|||||:|||||:|||||:|||||:|||||:
Db 41191 CAGCTCCTAGAGAAAGAGGATCTGTACTGAAATGTGCATGAGAACATATATCCAGCAG 41250
QY 79 LeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGlnPhe-----LysProGln 96
    |||:|||||:|||||:|||||:|||||:|||||:
Db 41251 TTAAAGAAATCAGGCTTATCTTTTATGATGACTACAAAGAAATATGTTCATCTCTCA 41310
QY 97 AsnCysProGluIleGluAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIle 116
    |||:|||||:|||||:|||||:|||||:|||||:
Db 41311 -----GTCATAGGAAACTGATTCAAAAAACCACTATATCCGAGCTGCTATGT 41361
QY 117 ValThrThrThrThrGluCysLeuArgHisIleArgGlnPhe 130
    :|||:|||||:|||||:|||||:|||||:
Db 41362 ATTGCTGTCCGTACAAACAGGCGCAGGACATCCGCCGATAC 41403

RESULT 8
US-09-949-002-697
; Sequence 697, Application US/09949002
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 697
; LENGTH: 60195
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-697

Alignment Scores:
Pred. No.: 5.1e-18 Length: 60195
Score: 236.50 Matches: 53
Percent Similarity: 58.96% Conservative: 26
Best Local Similarity: 39.55% Mismatches: 48
Query Match: 28.53% Indels: 7
Gaps: 3

US-09-697-089-2_COPY_161_323 (1-163) x US-09-949-002-697 (1-60195)
QY 1 LeuGlnSerProCysIleIleGluGlySerGlyLysSerThrLeuGln 20
    ||| ||| :|||:|||||:|||||:|||||:|||||:
Db 41011 TTGAACCTGTCATGTCGTGGAGGTCGAACTGGAAGAGCGTCCTCTGAG 41070
```

QY	21	ArglieAmelLeuTrpGlySerGlyCysLysAlaLeuThrLysPheVal	40
Db	41071	AAATAGCTTTTCTGTGGCATCTGGAGCTCTCCCTGTTAAACAGGTTCCAGCTGGTT	41130
QY	41	PhePheLeuArgLeuSer-----ArgAlaGlnGlyGlyLeuPheGluThrLeuCysAsp	58
Db	41131	TTCTACCTCTCCCTTAGTTCCACGACGACGAGGGGCTGGCCAGTATCATCTGTGAC	41190
QY	59	GlnLeuLeuAspLleProGlyThrLleArgLysGlnThrPheMetAlaMetLeuLys	78
Db	41191	CAGCTCCAGAGAAAGAGATCTGTACTGAAATGTGCATGAGGACATTTATCCAGCAG	41250
QY	79	LeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPhe-----LysProGln	96
Db	41251	TTAAGGATTCAGGCTTATTTCTCTTTAGATGACTACAAAGAAATATGTTCATTCCTCA	41310
QY	97	AsnCysProGluLleGluAlaLeuLleLysGlnAsnHisArgPheLysAsnMetValIle	116
Db	41311	-----GTCAATGAGAAACTGATTCAAAAAACCCATTATCCCGACCTGCTATG	41361
QY	117	ValThrThrThrThrGluCysLeuArgHisLleArgGlnPhe	130
Db	41362	ATTGCTGTCCGTACAACAGGGCCAGGACATCCGCCGATAC	41403
RESULT 9			
US-09-724-676-6819			
: Sequence 6819, Application US/09724676			
: GENERAL INFORMATION:			
: APPLICANT: CompuGen LTD			
: TITLE OF INVENTION: Variants of alternative splicing			
: FILE REFERENCE: 129181.4 CompuGen			
: CURRENT APPLICATION NUMBER: US/09/724,676			
: CURRENT FILING DATE: 2000-11-28			
: NUMBER OF SEQ ID NOS: 97222			
: SOFTWARE: PatentIn version 3.2			
: SEQ ID NO 6819			
: LENGTH: 3210			
: TYPE: DNA			
: ORGANISM: Homo sapiens			
US-09-724-676-6819			
Alignment Scores:			
Pred. No.:	1,24e-19	Length:	3210
Score:	235.50	Matches:	53
Percent Similarity:	58.96%	Conservative:	26
Best Local Similarity:	39.55%	Mismatches:	48
Query Match:	28.41%	Indels:	7
DB:	5	Gaps:	3
US-09-697-089-2_COPY_161_323 (1-163) x US-09-724-676-6819 (1-3210)			
QY	1	LeuGlnSerProCysLleLleGlnGlyLysSerGlyLysSerThrLeuLeuGln	20
Db	726	TTGAACCTGTGCATGCTGTGGAGGTTAACTGGAACTGGAAAGACGCTCTCTGAAG	785
QY	21	ArglieAmelLeuTrpGlySerGlyCysLysAlaLeuThrLysPheVal	40
Db	786	AAATAGCTTTTCTGTGGCATCTGGAGCTCTCCCTGTTAAACAGGTTCCAGCTGGTT	845
QY	41	PhePheLeuArgLeuSer-----ArgAlaGlnGlyGlyLeuPheGluThrLeuCysAsp	58
Db	846	TTTCACTCCCTCTAGTTCCACGACGACGAGGGGCTGGCCAGTATCATCTGTGAC	905
QY	59	GlnLeuLeuAspLleProGlyThrLleArgLysGlnThrPheMetAlaMetLeuLys	78
Db	906	CAGCTCCAGAGAAAGAGATCTGTACTGAAATGTGCATGAGGACATTTATCCAGCAG	965
QY	79	LeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPhe-----LysProGln	96
Db	966	TTAAGGATTCAGGCTTATTTCTCTTTAGATGACTACAAAGAAATATGTTCATTCCTCA	1025
QY	97	AsnCysProGluLleGluAlaLeuLleLysGlnAsnHisArgPheLysAsnMetValIle	116

```

Db      1026 -----GHCATAGGAACACTGATTCATAAAAAAACCACTATTCCCGACCTGCCTATTG 1076
Qy      117 ValThrThrThrTrgUcYsLeuAArgHnHisIleArgGlnPhe 130
       :::: ||| ||| ||||| ::::
Db      1077 ATTGCTGTCCGTACAAACAGGAGGCCAGGAGCATCCGCCGATAC 1118

RESULT 10
US-09-724-676A-6819
; Sequence 6819, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6819
; LENGTH: 3210
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-6819

Alignment Scores:
Pred. No.:          1,24e-19           Length:        3210
Score:             235.50              Matches:         53
Percent Similarity: 58.96%              Conservative:    26
Best Local Similarity: 39.55%            Mismatches:     48
Query Match:       28.41%               Indels:          7
                                   Gaps:                3

US-09-697-089-2_COPY_161_323 (1-163) x US-09-724-676A-6819 (1-3210)
Qy      1 LeucInsErProCysIleIleGGluIngUylGUsErGlyLysGlyLysSerThrLeuEngLn 20
       ||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      726 TTGAACCTCTGCAAGCTGTGTGGAGGGTGAAAGCTGGAAAGTGGAAAACAGGCTCTCTGAAG 785
Qy      21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      786 AAAATACCTTTCTGTGGGATCTGGATGGTGCTGCCCTGTTAACAGGTCACAGCTGTT 845
Qy      41 PhePheLeuArgLeuSer-----ArgAlaGlnGlyGlyLeuPheGlnIuThrLeuCysAsp 58
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      846 TTCACCTCTCCCTTACTTCCACCACAGCACAGACGAGGGGCTGGCAGATCATCTGTGCAC 905
Qy      59 GlnLeuLeuAspIlePrrGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLys 78
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      906 CAGCTCTCCTAGAAAAGAAGAGATGCTTTACTGAAATGTGCTTAGAGACAATATTCACAGAG 965
Qy      79 LeuArgGlnArgValLeuPheLeuLeuAspGlyTYrAsnGluPhe-----LysProGln 96
       ||||| :::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      966 TTAAGAAGTACAGGCTTATTCCTTTAGATGACTACAAAGAATATGTTCATATCCCTCAA 10255
Qy      97 AsnCysProGUllegUalalaueIlleLysGluAsnHnHisArgPheLysHsnMetValIle 116
       ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1026 -----GTCAATAGGAACAACTGATTCACAAAACCAACTTATCCCGAGCTGCCTATTG 1076
Qy      117 ValThrThrThrThrTrgUcYsLeuAArgHnHisIleArgGlnPhe 130
       :::: ||| ||| ||||| ::::
Db      1077 ATTGCTGTCCGTACAAACAGGAGGCCAGGAGCATCCGCCGATAC 1118

RESULT 11
US-09-724-676-6801
; Sequence 6801, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
```

SEQ ID NO 6801
LENGTH: 3597
TYPE: DNA
ORGANISM: Homo sapiens
US-09-724-676-6801

Alignment Scores:
Pred. No.: 1,45e-19
Score: 235.50
Percent Similarity: 58.96%
Best Local Similarity: 39.55%
Query Match: 28.41%
Matches: 53
Conservative: 26
Mismatches: 48
Indels: 7
Gaps: 3

US-09-697-089-2_COPY_161_323 (1-163) x US-09-724-676-6801 (1-3597)

Oy 1 LeuGlnSerProCysIleIleGlnGlyLysSerGlyLysSerThrLeuGln 20
Db 1113 TTGAACCTGTCATGTCGTGGAGGTCGACCTGGAAGACGCTCCTCGTAG 1172
Oy 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysAlaLeuThrLysPheLysPheVal 40
Db 1173 AAAATAGCTTTCTGCTGGGCACTGATGCTGCCCTGTTAAACAGGTTCCAGCTGGTT 1232
Oy 41 PhePheLeuArgLeuSer-----ArgAlaGlnGlyLysLeuPheGlnThrLeuCysAsp 58
Db 1233 TTCTACCTCTCCCTTAGTTCACACGACGAGGCGGCTGGCCAGTATCATCTGTGAC 1292
Oy 59 GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLys 78
Db 1293 CAGCTCCCTAGAGAAAGAGATCTTACTGAAATGTCGTCGAGGAGAACATTATCCAGCAG 1352
Oy 79 LeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGlnPhe-----LysProGln 96
Db 1353 TTAAAGATCAGGCTCTTATCTTTCCTTTAGATGACTCAAAAGAAATATGTTCAATCCCTCAA 1412
Oy 97 AsnCysProGluIleGlnAlaLeuLysGlnAsnHisArgPheLysAsnMetValIle 116
Db 1413 -----GTCATAGGAAACTGATTCACAAAACACCTTATCCGACCTGCTATTG 1463
Oy 117 ValThrThrThrThrGlnCysLeuArgHisIleArgGlnPhe 130
Db 1464 ATTGCTGTCCGTACAAACAGGCGCCAGGACATCCGCCCATAC 1505

RESULT 12
US-09-724-676A-6801
Sequence 6801, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724.676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6801
LENGTH: 3597
TYPE: DNA
ORGANISM: Homo sapiens
US-09-724-676A-6801

Alignment Scores:
Pred. No.: 1,45e-19
Score: 235.50
Percent Similarity: 58.96%
Best Local Similarity: 39.55%
Query Match: 28.41%
Matches: 53
Conservative: 26
Mismatches: 48
Indels: 7
Gaps: 3

US-09-697-089-2_COPY_161_323 (1-163) x US-09-724-676A-6801 (1-3597)

Oy 1 LeuGlnSerProCysIleIleGlnGlyLysSerGlyLysSerThrLeuGln 20
Db 1113 TTGAACCTGTCATGTCGTGGAGGTCGACCTGGAAGACGCTCCTCGTAG 1172

Db 1113 TTGAACCTGTCATGTCGTGGAGGTCGACCTGGAAGACGCTCCTCGTAG 1172
Oy 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysAlaLeuThrLysPheLysPheVal 40
Db 1173 AAAATAGCTTTCTGCTGGGCACTGATGCTGCCCTGTTAAACAGGTTCCAGCTGGTT 1232

Oy 41 PhePheLeuArgLeuSer-----ArgAlaGlnGlyLysLeuPheGlnThrLeuCysAsp 58
Db 1233 TTCTACCTCTCCCTTAGTTCACACGACGAGGCGGCTGGCCAGTATCATCTGTGAC 1292
Oy 59 GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLys 78
Db 1293 CAGCTCCCTAGAGAAAGAGATCTTACTGAAATGTCGTCGAGGAGAACATTATCCAGCAG 1352

Oy 79 LeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGlnPhe-----LysProGln 96
Db 1353 TTAAAGATCAGGCTCTTATCTTTCCTTTAGATGACTCAAAAGAAATATGTTCAATCCCTCAA 1412
Oy 97 AsnCysProGluIleGlnAlaLeuLysGlnAsnHisArgPheLysAsnMetValIle 116
Db 1413 -----GTCATAGGAAACTGATTCACAAAACACCTTATCCGACCTGCTATTG 1463
Oy 117 ValThrThrThrThrGlnCysLeuArgHisIleArgGlnPhe 130
Db 1464 ATTGCTGTCCGTACAAACAGGCGCCAGGACATCCGCCCATAC 1505

RESULT 13
US-09-724-676-6810
Sequence 6810, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724.676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6810
LENGTH: 4143
TYPE: DNA
ORGANISM: Homo sapiens
US-09-724-676-6810

Alignment Scores:
Pred. No.: 1,76e-19
Score: 235.50
Percent Similarity: 58.96%
Best Local Similarity: 39.55%
Query Match: 28.41%
Matches: 53
Conservative: 26
Mismatches: 48
Indels: 7
Gaps: 3

US-09-697-089-2_COPY_161_323 (1-163) x US-09-724-676-6810 (1-4143)

Oy 1 LeuGlnSerProCysIleIleGlnGlyLysSerGlyLysSerThrLeuGln 20
Db 1659 TTGAACCTGTCATGTCGTGGAGGTCGACCTGGAAGACGCTCCTCGTAG 1718
Oy 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysAlaLeuThrLysPheLysPheVal 40
Db 1719 AAAATAGCTTTCTGCTGGGCACTGATGCTGCCCTGTTAAACAGGTTCCAGCTGGTT 1778
Oy 41 PhePheLeuArgLeuSer-----ArgAlaGlnGlyLysLeuPheGlnThrLeuCysAsp 58
Db 1779 TTCTACCTCTCCCTTAGTTCACACGACGAGGCGGCTGGCCAGTATCATCTGTGAC 1838
Oy 59 GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLys 78
Db 1839 CAGCTCCCTAGAGAAAGAGATCTTACTGAAATGTCGTCGAGGAGAACATTATCCAGCAG 1898
Oy 79 LeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGlnPhe-----LysProGln 96
Db 1899 TTAAAGATCAGGCTCTTATCTTTCCTTTAGATGACTCAAAAGAAATATGTTCAATCCCTCAA 1958

```

Oy 97 AsnGysProGluIleGluAlaLeuIleLysGluAsnHisArgPheLysAsmMetValIle 116
Db 1959 -----GTCATGAGAAACAGTATCAAAAAACCACTATTCCCGGACSTGGCTATTG 2009
Oy 117 ValThrThrThrGlyLeuLysLeuAsnHisIleArgGlnPhe 130
Db 2010 ATTGCTGTCCGTACAAACAGCGCCACGAGCAATCCGCCCATAC 2051

RESULT 14
US-09-724-676A-6810
: Sequence 6810, Application US/09724676A
: GENERAL INFORMATION:
: APPLICANT: Compugen LTD
: TITLE OF INVENTION: Variants of alternative splicing
: FILE REFERENCE: 129181.4 Compugen
: CURRENT APPLICATION NUMBER: US/09/724,676A
: CURRENT FILING DATE: 2000-11-28
: NUMBER OF SEQ ID NOS: 97222
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 6810
: LENGTH: 4143
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-724-676A-6810

Alignment Scores:
Pred. No.: 1,76e-19 Length: 4143
Score: 235.50 Matches: 53
Percent Similarity: 58.96% Conservative: 26
Best Local Similarity: 39.55% Mismatches: 48
Query Match: 28.41% Indels: 7
DB: 5 Gaps: 3

US-09-697-089-2_COPY_161_323 (1-163) x US-09-724-676A-6810 (1-4143)
Oy 1 LeuGlnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeuGln 20
Db 1659 TTGAACTCTCTCATGCTGTGGAGGGGTGAAGCTGGAAAGTGAAGAACGGTCTCTGTAG 1718
Oy 21 ArgIleIleMetLeuThrPrgLysSerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
Db 1719 AAAATACCTTTTCTGTGGGATGTGATGCTGTGCTCCCTTTAAACAGGTTCCAGCTGGTT 1778
Oy 41 PhePheLeuArgLeuSer-----ArgAlaGlnGlyGlyLeuPheGlnThrLeuGlyAsp 58
Db 1779 TTCTACCTCTCCCTTAGTTAGTTCACACAGACAGACGAGGGCTGGCAGTATCATCTGTGAC 1838
Oy 59 GlnLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLys 78
Db 1839 CAGCTCTCAAGAAAGAGAGATCTGTACTGAAAGTGCCTGAGAGACATATATCCAGCAG 1898
Oy 79 LeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGlnPhe-----LysProGln 96
Db 1899 TTAAAGATCAGGCTTATTATCTCTTTAGATGACTCAAAAGAAATATGTTCATATCCCTCAA 1958
Oy 97 AsnGysProGluIleGluAlaLeuIleLysGluAsnHisArgPheLysAsmMetValIle 116
Db 1959 -----GTCATGAGAAACAGTATCAAAAAACCACTATTCCCGGACSTGGCTATTG 2009
Oy 117 ValThrThrThrThrGlyLysLeuArgHisIleArgGlnPhe 130
Db 2010 ATTGCTGTCCGTACAAACAGCGCCACGAGCAATCCGCCCATAC 2051

RESULT 15
US-09-724-676-6816
: Sequence 6816, Application US/09724676
: GENERAL INFORMATION:
: APPLICANT: Compugen LTD
: TITLE OF INVENTION: Variants of alternative splicing
: FILE REFERENCE: 129181.4 Compugen
: CURRENT APPLICATION NUMBER: US/09/724,676
: CURRENT FILING DATE: 2000-11-28
: NUMBER OF SEQ ID NOS: 97222

```

```

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6816
; LENGTH: 4259
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-6816

Alignment Scores:
Pred. No.: 1.83e-19 Length: 4259
Score: 235.50 Matches: 53
Percent Similarity: 58.96% Conservative: 26
Best Local Similarity: 39.55% Mismatches: 48
Query Match: 28.41% Indels: 7
DB: Gaps: 3

US-09-697-089-2_COPY_161_323 (1-163) x US-09-724-676-6816 (1-4259)

OY 1 LeuGlnSerProCysIleIleGlnGlyGluSerGlyGlySerThrLeuGln 20
      ||| ||| :|||:|||||:||||| |||||: |||||:
DB 726 TTGAACCTGTGATCTGTGTGGAGGGAAGCTGGAAACAGGCTCTCTGTAG 785

OY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheAl 40
      :|||:||||| ||||| ||||| ||| ||| :|||: |||
DB 786 AAAATACCTTTTCTGTGTGGCATCTGCATGCTGCTCCCTTTAAACAGGTTCCAGCTGGTT 845

OY 41 PhePheLeuArgLeuSer-----ArgAlaGlnGlyLysLeuPheGlnThrLeuCysAsp 58
      |||:||||| ||||| ||| ||||| :|||:|||||
DB 846 TTTCACCTCTCCCTTACTTCCACACAGACAGAGAGGGCTGCCAGTATCATCTGTAC 905

OY 59 GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLys 78
      |||:||||| :|||:||||| ||||| ||||| :|||:|||||
DB 906 CAGCTCTACAGAAAGAAAGATCTGTACTGGAATGTGCGTAGGAACATTATCCACAG 965

OY 79 LeuArgGlnArgValIlePheLeuLeuAspGlyTyrAsnGluPhe-----LysProGln 96
      |||:||||| :|||:||||| ||| ||| ||||| |||||
DB 966 TTAAAGATCAAGCTCTTATCTTTTAGTAGTACTACAAAGAAATATGTTCATATCCCTCA 1025

OY 97 AsnCysProGluIleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIle 116
      ||| ||||| ||||| ||||| :|||:|||||
DB 1026 -----GNCATAGGAAGAAATGATTTCAAAAAAACCATTTATCCCGGACCTGCTATTG 1076

OY 117 ValThrThrThrThrGlnGlyLysLeuArgHisIleArgGlnPhe 130
      ||| ||| ||| |||||:|||||
DB 1077 ATTGCTGTCCGATCAACAGAGCCACGAGACATCCGCGATAC 1118

```

Search completed: January 31, 2003, 18:03:05
Job time : 168.327 secs

THIS PAGE BLANK (uspto)

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 31, 2003, 11:41:11 : Search time 2961.36 seconds
(without alignments)
2004.811 Million cell updates/sec

Title: US-09-697-089-2_COPY_762_965

Perfect score: 1046
Sequence: 1 LKNLTKLIMDKMNEEDAI.....GNRVSSDGMFMGVFENLK 204

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame_p2n.model -DEV=xlh
-O=/cgn2_1/uspro_pool/us09697089/runat_29012003_092753_19716/app_query.fasta.1.981
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blsum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09697089.ecgn.1.1.3568_etunat_29012003_092753_19716 -NCFPU=6 -ICPU=3
-NO_XUPXY -NO_MMAP -LARGEQUERY -NEG.SCORES=0 -WAIT -LONGLOG -DEV.TIMECUT=120
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:*
1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_ov:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rtd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1046	100.0	618	6 AX318176	AX318176 Sequence
2	1046	100.0	1355	6 IR2005417	AL389934 Homo sapi
3	1046	100.0	1395	6 AX318093	AX318093 Sequence
4	1046	100.0	1395	9 AY027788	AY027788 Homo sapi
5	1046	100.0	3133	9 AY032589	AY032589 Homo sapi
6	1046	100.0	3219	9 AY035391	AY035391 Homo sapi
7	1046	100.0	3360	9 BC031555	BC031555 Homo sapi
8	1046	100.0	3396	6 AX318091	AX318091 Sequence
9	1046	100.0	3396	9 AY027787	AY027787 Homo sapi
10	1046	100.0	3581	9 AF376061	AF376061 Homo sapi
11	1042	99.6	3335	9 AK095467	AK095467 Homo sapi
12	331	31.6	138909	9 CNS01DS3	AL121653 BAC sequ
13	331	31.6	185281	2 AC011232	AC011232 Homo sapi
14	336	31.2	160583	2 AC010968	AC010968 Homo sapi
15	298	28.5	553	11 G55568	G55568 SHGC-100923
16	238	22.8	185469	2 AC0101793	AC101793 Mus muscu
17	202	19.3	162692	2 CNS01DS8	AL11658 BAC sequ
18	176	16.8	8366	2 AC131423	AC131423 Rattus no
19	147.5	14.1	3447	6 AX427592	AX427592 Sequence
20	147.5	14.1	3447	10 AF074018	AF074018 Mus muscu
21	124.5	11.9	3162	3 AY113398	AY113398 Drosophill
22	124	11.9	202431	2 AC116395	AC116395 Mus muscu
23	122.5	11.7	61107	2 AC017941	AC017941 Drosophill
24	122.5	11.7	191466	3 AC008348	AC008348 Drosophill
25	122.5	11.7	307363	3 AE003457	AE003457 Drosophill
26	121.5	11.6	3069	6 AX459879	AX459879 Sequence
27	121	11.6	4550	2 AY128499	AY128499 Drosophill
28	121	11.6	67738	2 AC019571	AC019571 Drosophill
29	121	11.6	175440	3 AC007804	AC007804 Drosophill
30	121	11.6	217756	3 AE003717	AE003717 Drosophill
31	120.5	11.5	132179	9 AL672142	AL672142 Human DNA
32	120	11.5	2470	9 AK000338	AK000338 Homo sapi
33	120	11.5	2754	9 BC003407	BC003407 Homo sapi
34	120	11.5	2826	6 AX405866	AX405866 Sequence
35	120	11.5	2846	9 BC008586	BC008586 Homo sapi
36	120	11.5	2847	9 AK022951	AK022951 Homo sapi
37	120	11.5	76170	25 ATAC2329	AC002329 Arabidops
38	118.5	11.3	2400	9 AC098833	AC098833 Oryza sat
39	118.5	11.3	1573	9 BC011186	BC011186 Homo sapi
40	118	11.3	1514	6 E62970	E62970 Recombinant
41	118	11.3	1682	9 H0M1HRP	M22414 Human place
42	118	11.3	1682	11 G28528	G28528 human STR S
43	118	11.3	1697	9 BC011500	BC011500 Homo sapi
44	118	11.3	1698	6 I08072	I08072 Sequence 4
45	118	11.3	1698	6 I08072	I08072 Sequence 4

RESULT 1

ALIGNMENTS

TDTEIRILGAFGKPNPLKNFOOLNLAGNRSSDGMIAFMGVENLKOIYFPDFSTKEE
LPDPALVRKLSQVLSKLFLEQEARLVGMQGFDDDLVSTGAFKLVTA"

BASE COUNT 416 a 265 c 312 g 362 t

ORIGIN

Alignment Scores:

Pred. No.:	2,52e-95	Length:	1355
Score:	1046.00	Matches:	204
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
		Gaps:	0

US-09-697-089-2_COPY_762_965 (1-204) x IR2005417 (1-1355)

Qy 1 LeuLysAsnLeuThrLysLeuLleMetAspAsnLleLysMetAsnGluGluAspAlaIle 20
|||||
Db 530 TTGAAGAACCTTACAAACCTCATATGATAAACATAAAGATGAATGAAGAAGATGCTATA 589
Qy 21 LysLeuAlaGluGluLysLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40
|||||
Db 530 AAACAGCTGAAGGCGCTGAAAAACCTGAAGAGATGTGTTATTTTCATTGACCCACTTG 649
Qy 41 SerAspIleGluGluGluMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60
|||||
Db 650 TCTGCATTTGGAGAGGAGATGATACATAGTCAAGTCTCTGCAAGTGAACCTGTGAC 709
Qy 61 LeuGluGluIleGluLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80
|||||
Db 710 CTTGAAGAAATTCATTAAGTCTCCTGCTGCTGCTGCAAAAGCAGTGAATCCTAGCT 769
Qy 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100
|||||
Db 770 CAGAACTTTCACAAATTTGGTCAAACTGAGCATCTTGATTTATCGAAAAATTAACCTGGAA 829
Qy 101 LysAspGluAsnGluAlaLeuHisGluLeuLleAspArgMetAsnValLeuGluGluLeu 120
|||||
Db 830 AAAGATGAAATGAAGAGCTTCATGACTGATCGACAGAGATGAAGTGTGTAGAACAGCTC 889
Qy 121 ThrAlaLeuMetLeuProTribGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140
|||||
Db 890 ACCGACATGATGCTCCCTCGGGCGTGTGACGTGCAAGGACAGCTGACAGCCCTGTTGAAA 949
Qy 141 HisLeuGluGluValProGluLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160
|||||
Db 950 CATTTGGAGAGGTCGCCAACATGCTCAAGCTTGGGTTGAAAACTGGAGACTCACAAAT 1009
Qy 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln 180
|||||
Db 1010 ACAGAGATTAGAAATTTAGTGTCATTTTGTGAAAGAACCCCTGAAAAACTTCCAGCAG 1069
Qy 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPleuAlaPheMetGlyAlaPhe 200
|||||
Db 1070 TTGAATTTGGGGGGAATCGTGTGAGCAGTATGATGATGCTTGGCTTCATGGGTATATT 1129
Qy 201 GluAsnLeuLys 204
|||||
Db 1130 GAGATCTTAG 1141

RESULT 3
AX318093 1395 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 98 from Patent WO0190156.
ACCESSION AX318093
VERSION AX318093.1 GI:17900822

KEYWORDS

ORGANISM

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
1 Reed,J.C., Plo,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,
Oliveira,V.A., Hayashi,H. and Pawlowski,K.

TITLE Card domain containing polypeptides, encoding nucleic acids, and
methods of use
JOURNAL Patent: WO 0190156-A 98 29-NOV-2001;
The Burnham Institute (US)

FEATURES
source
1. .1395
/organism="Homo sapiens"
/db_xref="taxon:9606"
277. .1356
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD19341.1"
/db_xref="GI:17900823"

CDS

translation="MNRKNSRALLIRMGMTYIKOTIDLFYNNVLRREVNITICE
KVEDARGLTHMLTKGSESCNLELSKEMNYPLFODLNGSLDLSGNLNLTK
LIMONIKRNEEDALIKLEGLNKLKMKLFETHLSDIGEGADYIVKLSLSPCLEET
QLVSCCLSANAVKILIAONLHNLVKLSLIDISENLEKGNALHELIDRMVNLQJLA
LMLPMGCDVQGLSLSLKHLIEVPQLVKLGKLMRLIDTEIRILGAFGKPNPLKNFOO
LNLAGNRVSSDGMIAFMGVENLKOIYFPDFSTKEFLPDPALVRKLSQVLSKLFLEQ
EARLVGMQGFDDDLVSTGAFKLVTA"

BASE COUNT 436 a 248 c 327 g 364 t

ORIGIN

Alignment Scores:

Pred. No.:	2.61e-95	Length:	1395
Score:	1046.00	Matches:	204
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
		Gaps:	0

US-09-697-089-2_COPY_762_965 (1-204) x AX318093 (1-1395)

Qy 1 LeuLysAsnLeuThrLysLeuLleMetAspAsnLleLysMetAsnGluGluAspAlaIle 20
|||||
Db 565 TTGAAGAACCTTACAAACCTCATATGATAAACATAAAGATGAATGAAGAAGATGCTATA 624
Qy 21 LysLeuAlaGluGluLysLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40
|||||
Db 635 AAACAGCTGAAGGCGCTGAAAAACCTGAAGAGATGTGTTATTTTCATTGACCCACTTG 684
Qy 41 SerAspIleGluGluGluMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60
|||||
Db 685 TCTGCATTTGGAGAGGAGATGATACATAGTCAAGTCTCTGCAAGTGAACCTGTGAC 744
Qy 61 LeuGluGluIleGluLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80
|||||
Db 745 CTTGAAGAAATTCATTAAGTCTCCTGCTGCTGCTGCAAAAGCAGTGAATCCTAGCT 804
Qy 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100
|||||
Db 805 CAGAACTTTCACAAATTTGGTCAAACTGAGCATCTTGATTTATCGAAAAATTAACCTGGAA 864
Qy 101 LysAspGluAsnGluAlaLeuHisGluLeuLleAspArgMetAsnValLeuGluGluLeu 120
|||||
Db 865 AAAGATGAAATGAAGAGCTTCATGACTGATCGACAGAGATGAAGTGTGTAGAACAGCTC 924
Qy 121 ThrAlaLeuMetLeuProTribGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140
|||||
Db 925 ACCGACATGATGCTCCCTCGGGCGTGTGACGTGCAAGGACAGCTGACAGCCCTGTTGAAA 984
Qy 141 HisLeuGluGluValProGluLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160
|||||
Db 985 CATTTGGAGAGGTCGCCAACATGCTCAAGCTTGGGTTGAAAACTGGAGACTCACAAAT 1044
Qy 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln 180
|||||
Db 1045 ACAGAGATTAGAAATTTAGTGTCATTTTGTGAAAGAACCCCTGAAAAACTTCCAGCAG 1104
Qy 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPleuAlaPheMetGlyAlaPhe 200
|||||
Db 1105 TTGAATTTGGGGGGAATCGTGTGAGCAGTATGATGATGCTTGGCTTCATGGGTATATT 1164

QY 201 GluAsnLeuLys 204
|||||
Db 1165 GAGAACTCTTAAG 1176

RESULT 4
AY027788

LOCUS AY027788 1395 bp mRNA linear PRI 20-JUL-2001
DEFINITION Homo sapiens CIANB (CIAN1) mRNA, complete cds.
ACCESSION AY027788
VERSION AY027788.1 GI:14324114
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Damiano,J.S., Stehlik,C., Plo,F., Godzik,A. and Reed,J.C.
TITLE Cian, a novel human ced-4-like gene
JOURNAL Genomics 75 (1-3), 77-83 (2001)
MEDLINE 21365712
PUBMED 11472070
REFERENCE 2 (bases 1 to 1395)
AUTHORS Stehlik,C., Damiano,J.S., Plo,F., Godzik,A. and Reed,J.C.
TITLE Direct Submission
JOURNAL Submitted (21-FEB-2001) Program on Apoptosis and Cell Death
Research, The Burnham Institute, 10901 North Torrey Pines Road, La
Jolla, CA 92037, USA

FEATURES
source
1..1395
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/map="2p22-p21"
/tissue-type="lung"
1..1395
/gene="CIAN1"
277..1356
/gene="CIAN1"
/note="alternatively spliced; similar to Ced-4"
/codon_start=1
/product="CIANB"
/protein_id="AAK14777.1"
/db_xref="GI:14324115"
/translation="MNFIKDNRSLIORMGTVIKOITDDLFWNVNLNREVNIIICE
KYQDADARGIHIMLIKKSSECNLFKLSKEMVPLFDGNGSGSLDSGNKLNTRK
LIMDKIMNEDAIKLAEGKLNKMKLFHLSDGEMDYIVKSLSEPDLEET
OLVSCISAAVVIIONLHNLYKLTSTIDISEVYLEDGMEALHEIDRNVEQLTA
LMLPMGCDVQSGSLSLKLEEVYPOLYKCLKKWRLLDTDIRILGAFETGKNPLKNFQ
LNLAGNVSDDGLAEFGVENLKQVFFDFSTKEFLPDALVKKLSQVLSKLTFLQE
ARLVGMQFDDDDLSVITGAFKLVTA"

BASE COUNT 436 a 248 c 327 g 384 t
ORIGIN

Alignment Scores:
Pred. No.: 2.61e-95 Length: 1395
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-697-089-2_COPY_762_965 (1-204) x AY027788 (1-1395)

QY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluAspAlaIle 20
|||||
Db 565 TTGAAGAACCCTTAACAAAGCTATATAGATACATAAAGATGATGAAGAAGATGCTATA 624

QY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40
|||||
Db 625 AACTAGCTGAAGGCGCTGAAGAAACCTGAAGAAGATGTATTATTCAATTGACCCACTTG 684

QY 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60
|||||

Db 685 TCTCACATTGGAGAGCGAATGAGATTACATAGTACTCTGTCAAGTGAACCTGTGAC 744

QY 61 LeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80
|||||
Db 745 CTTGAGAAATTTCAATTAGTCTCCTGCTGCTGCTGCTGCTCAATGACGAGAAATCTGAGT 804

QY 81 GluAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100
|||||
Db 805 CAGAACTTCACAAATTTGGTCAAACTGACATCTTGTATTATTCAGAAATATCTGGA 864

QY 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValIleGluGlnLeu 120
|||||
Db 865 AAAGATGGAATGAAGCTCTTTCATGAACCTGATGCACAGATGAACCTGATGAACAGCTC 924

QY 121 ThrAlaLeuMetLeuPheProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLys 140
|||||
Db 925 ACCGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 984

QY 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrPargLeuThrAsp 160
|||||
Db 985 CATTTGGAGAGAGCTCCACAACTGTCAGAGCTTGGTGAAGAACTGAGACTCACAGAT 1044

QY 161 ThrGluLeuArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln 180
|||||
Db 1045 ACAGAGATTGAATTTAGTGCAATTTTGGAAAGAACCTCTGAAAACTTCACACAG 1104

QY 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPheAlaPheMetGlyValPhe 200
|||||
Db 1105 TTGAATTTGGCGGGAATCGTGTGACGATGATGATGATGCTTGCCTTCATGCGTATTT 1164

QY 201 GluAsnLeuLys 204
|||||
Db 1165 GAGAACTCTTAAG 1176

RESULT 5
AY032589

LOCUS AY032589 3133 bp mRNA linear PRI 25-MAY-2001
DEFINITION Homo sapiens caspase recruitment domain protein 12 mRNA, complete
cds.
ACCESSION AY032589
VERSION AY032589.1 GI:13899172
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Geddes,B.J., Wang,L., Huang,W.-J., Lavellee,M., Manji,G.A.,
Brown,M., Jurman,M., Morganstern,J., Merriam,S., Glucksmann,A.,
Distefano,P.S. and Berlin,J.
TITLE Human CARD12 is a novel CED4/Apaf-1 family member that induces
apoptosis
JOURNAL Biochem. Biophys. Res. Commun. 284 (1), 77-82 (2001)
MEDLINE 21268963
PUBMED 11374873
REFERENCE 2 (bases 1 to 3133)
AUTHORS Berlin,J.
TITLE Direct Submission
JOURNAL Submitted (15-APR-2001) Neurobiology, Millennium Pharmaceuticals
Inc., 640 Memorial Drive, Cambridge, MA 02139, USA

FEATURES
source
1..3133
/organism="Homo sapiens"
/db_xref="taxon:9606"
35..3110
/note="CARD12; CED4/Apaf-1 family member"
/codon_start=1
/product="caspase recruitment domain protein 12"
/protein_id="AAK38730.1"
/db_xref="GI:13899173"
/translation="MNFIKDNRSLIORMGTVIKOITDDLFWNVNLNREVNIIICE
KYQDADARGIHIMLIKKSSECNLFKLSKEMVPLFDGNGSGSLDSGNKLNTRK
LIMDKIMNEDAIKLAEGKLNKMKLFHLSDGEMDYIVKSLSEPDLEET
OLVSCISAAVVIIONLHNLYKLTSTIDISEVYLEDGMEALHEIDRNVEQLTA
LMLPMGCDVQSGSLSLKLEEVYPOLYKCLKKWRLLDTDIRILGAFETGKNPLKNFQ
LNLAGNVSDDGLAEFGVENLKQVFFDFSTKEFLPDALVKKLSQVLSKLTFLQE
ARLVGMQFDDDDLSVITGAFKLVTA"

```

LSPCIIIGESGKSTLLRIAMLMGSGKCALTKFEVFLRLSRNGGLFETLCD
OLDIPGIRKQOTRAMLKLRORVLELDDYNKRPONCEPIELIKENRFRKMYI
VTTECLRHQRQFALRAEYGDHEDSAQALIRVLAKEIABGLLQIQSRCLRL
MKTPLFVYITCAIQMGSEFHSHTQTLFEHFYDLILQKNHKKHGVASDFEIRSLD
CGDLALBGEVSHKDFELOYVSYNEDVLTGLCKTAQRFKRYKFFKRSQEXT
AGRLSLLTSHHEBEVYKNGYLQKMSIDISTSYSLRYTCGSSVEATRAVMKH
LAAVYOHGCLGLSIAKRPILROESLOSVKMTTBOELIKANINSFVCGIHLQEST
SKASLOEFAFPQCKSLYINSGNIPDLPFPEHLPKASALDPFKIDPYGAMASW
EKAAEDTGGIHEMERAPETIYPSRAVSLEFFNKKOERTLEVTLRDSKLKODITYLGK
IFSSATSLRLQIKRCAGVAGSLVLSCTKNYISLMEASPLTIEDERTITSVNLKT
LSIHDLOQRRLPGGLTDSLGMLKNITKLIMONIKMNEADAIKLEGLNLMKMFHL
THLSDIGEMDYIVKSLSEPCDEEIOVSCCSANAVKILIAONLHNLVLSLIDS
ENYLEKDGNEALHELIDRMNVLEQTLALMLPMGCDVQGLSLKLKHEEYQVLVGL
KNWRITDEIRILGAFPGKNPLKNPQOINLAGNRYSSDGMALAFMGVEFNKOLVFPDF
STKEFLPDPAVRRLSOVLSKLTFLQERLRYGMPDDDDLSVITGARFLVYA"

misc_feature
/note="CARD; Region: caspase recruitment domain"
522..1406
/note="NBS; Region: nucleotide-binding site"
2001..3107
misc_feature
/note="LRR; Region: leucine-rich repeats"
BASE COUNT 903 a 691 c 729 g 810 t
ORIGIN

Alignment Scores:
Pred. No.: 6,62e-95 Length: 3133
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-697-089-2_COPY_762_965 (1-204) x AY032589 (1-3133)

QY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluLysAlaIle 20
DB 2319 TTGAAGAAGACCTTACAAAGCTCATATGATACATAAAGATGAATGAGAAGAGATGCTATA 2378
QY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40
DB 2379 AAACTAGCTGAAGGCCCTGAAAAAAGATGATGTTTATTCATTGACCCACCTTG 2438
QY 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60
DB 2439 TCTGCATTTGGAGAGAGATGATACATGCAAGTCTCTGTCAAGTGAACCTGTGAC 2498
QY 61 LeuGluGluIleGlnLeuValSerCysLeuSerAlaAsnAlaValLysIleLeuAla 80
DB 2499 CTTGAAGAATTCATTTAGTCTCCTGCTGCTGCAAAATGACAGTGAATCCTAGCT 2558
QY 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100
DB 2559 CAGAAATCTTCAAAATTTGGTCAAACTGAGCATTTGATTATTCAGAAAAATTAACCTGGAA 2618
QY 101 LysAspGlyAsnGluAlaLeuHisGlnLeuIleAspArgMetAsnValLeuGluGlnLeu 120
DB 2619 AAAAGATGAGAAAGAGCTCTTATGACTGATCGACAGATGAACGTGCTAACAACAGCTC 2678
QY 121 ThrAlaLeuMetLeuProTyrPylCysAspValGlnGlySerLeuSerSerLeuLeuLys 140
DB 2679 ACCGACATGATGCTCCCTGGGGCTGTGACGTCAAGGACAGCTGAGCCTGTGAAA 2738
QY 141 HisLeuGluGluValAlaProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160
DB 2739 CATTTGGAGAGAGTCCCAACACTGCTCAAGCTTGGGTGAAAAAATGAGACTCAAGAT 2798
QY 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPhgGlnGln 180
DB 2799 ACGAGATTTAGATTTTGGTGCATTTTGGGAAAGAACCTCTGTGAAGAACTTCCAGGCG 2858
QY 181 LeuAsnLeuAlaGlyLysAsnArgValSerSerAspGlyTyrPleuAlaPheMetCylValPhe 200
DB 2859 TTGAATTTGGCGGAAATCGTGTGAGCAGTATGATGCTGCTTCAATGGGTGATATT 2918
```

```

QY 201 GlnAsnLeuLys 204
DB 2919 GAGAAATCTTAAAG 2930

RESULT 6
AY035391
LOCUS
DEFINITION Homo sapiens ICE-protease activating factor mRNA, complete cds.
ACCESSION AY035391
VERSION AY035391.1 GI:14334214
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 3219)
Poyet,J.L., Srinivasula,S.M., Tnani,M., Raznara,M.,
Fernandes-Alnemri,T. and Alnemri,E.S.
Identification of Ipa1, a human caspase-1-activating protein
related to Ape1-1
JOURNAL U. Biol. Chem. 276 (30), 28309-28313 (2001)
MEDLINE 21359454
PUBMED 11390368
REFERENCE
2 (bases 1 to 3219)
Poyet,J.L., Srinivasula,S.M., Fernandes-Alnemri,T. and
Alnemri,E.S.
Direct Submission
Submitted (16-May-2001) Microbiology and Immunology, Thomas
Jefferson University, 233 S. 10th Street, Philadelphia, PA 19107,
USA

FEATURES
source
1..3219
location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/map="p21-22"
145..3219
/note="IPAF; CED4/Apaf-1 family member; caspase-associated
recruitment domain containing protein"
/codon_start=1
/product="ICE-protease activating factor"
/protein_id="AAK59843.1"
/db_xref="GI:14334215"
/translation="MNPFKDNRSLQIMGNTVYKQITDDLFYNNVNLREVNITCC
KVEDDAAGIITHMLIKGSESCNLFSLKEMWNPFLFDLNGQSLFHTSGDLDL
QDLDLVHTPSEFLNYPLEGEDIDITFNLKSPTEVLRKQDHNHREQLNLGLQ
LQSPCIIIGESGKSTLLRIAMLMGSGKCALTKFEVFLRLSRNGGLFETLCD
OLDIPGIRKQOTRAMLKLRORVLELDDYNKRPONCEPIELIKENRFRKMYI
VTTECLRHQRQFALRAEYGDHEDSAQALIRVLAKEIABGLLQIQSRCLRL
MKTPLFVYITCAIQMGSEFHSHTQTLFEHFYDLILQKNHKKHGVASDFEIRSLD
H
CGDLALBGEVSHKDFELOYVSYNEDVLTGLCKTAQRFKRYKFFKRSQEXT
AGRLSLLTSHHEBEVYKNGYLQKMSIDISTSYSLRYTCGSSVEATRAVMKH
LAAVYOHGCLGLSIAKRPILROESLOSVKMTTBOELIKANINSFVCGIHLQEST
SKASLOEFAFPQCKSLYINSGNIPDLPFPEHLPKASALDPFKIDPYGAMASW
EKAAEDTGGIHEMERAPETIYPSRAVSLEFFNKKOERTLEVTLRDSKLKODITYLGK
IFSSATSLRLQIKRCAGVAGSLVLSCTKNYISLMEASPLTIEDERTITSVNLKT
LSIHDLOQRRLPGGLTDSLGMLKNITKLIMONIKMNEADAIKLEGLNLMKMFHL
THLSDIGEMDYIVKSLSEPCDEEIOVSCCSANAVKILIAONLHNLVLSLIDS
ENYLEKDGNEALHELIDRMNVLEQTLALMLPMGCDVQGLSLKLKHEEYQVLVGL
KNWRITDEIRILGAFPGKNPLKNPQOINLAGNRYSSDGMALAFMGVEFNKOLVFPDF
STKEFLPDPAVRRLSOVLSKLTFLQERLRYGMPDDDDLSVITGARFLVYA"

BASE COUNT 934 a 696 c 748 g 841 t
ORIGIN

Alignment Scores:
Pred. No.: 6,83e-95 Length: 3219
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
```

US-09-697-089-2_COPY_762_965 (1-204) x AY035391 (1-3219)

QY 1 LeuysasleuThrlsleuilemetaspasniileysmetasngluaspalaile 20
|||||
Db 2428 TTGAAGAACCTTACAAAGCTCTATATGATATACATTAAGATCAATGAAGAAAGATCTATA 2487

QY 21 LysleualagluGlyLeuylsasnleuylslysmetCysleuphehisleuthrisleu 40
|||||
Db 2488 AAACAGCTGAAGGCCCTGAAAAAAGCTGAAGAAGATGTGTATTTTCATTGACCCACTTG 2547

QY 41 SeraspillegluGlymetaspryrllevalysSerleuserSerGluProcysasp 60
|||||
Db 2548 TCTGACATTGGAGAGGAGGATGATTACATGCTCTCTCAAGTCAAGAACCCCTGTGAC 2607

QY 61 LeuglugluileglnleuValserCysCysleuserAlaasnAlValylsileleuala 80
|||||
Db 2608 CTTGAAGAATTCATTATGTCCTCGCTGCTGTGCAAAAGCAGTGAATTCCTAGCT 2667

QY 81 GluasleuHsasnleuValylsleuSerlleuaspleuserGluasnTyrleuglu 100
|||||
Db 2668 CAGAACTTCCACAAATTTGGTCAAACTGAGACATTTGATTTATCAGAAAAATTACCTGGA 2727

QY 101 LysaspGlyasnGlualeuHsleuileasparGmetasnValleugluInleu 120
|||||
Db 2728 AAAGATGGAATGAAGCTCTTCATGACTGATGACAGAGATGAAGCTGTAGAACAGCTC 2787

QY 121 ThrAlaMetleuProTrrpGlyCysaspValGlnGlySerleuserSerleuLeuyls 140
|||||
Db 2788 ACCGACATGATGCTGCTGCTGGGGCTGTGACGTGCAAGGACAGCTGACGCTGTGAAA 2847

QY 141 HsleugluGluValProGlnleuValylsleuGlyleuylsAsnTrrpArgleuthrasp 160
|||||
Db 2848 CATTGGGAGAGGCTCCCACTCTCAAGCTTGAGGTTGAAAACTGAGAGACTCACAGAT 2907

QY 161 ThrGluileArgileleuGlyValaphhephegilyLysasnProleuylsAsnphelngln 180
|||||
Db 2908 ACAGAGATTAAGATTTTGGGTCATTTTGGAAAGAACCCCTGTAACAACTCCAGCAG 2967

QY 181 LeuasnleualaglyAsnArgValserSeraspGlyTrrpleualaPhemetGlyValphe 200
|||||
Db 2968 TTGAATTTGGGGGGAATCGTGTGAGCAGTGTGATGATGCGCTTCATGGGTATATT 3027

QY 201 Gluasleuyls 204
|||||
Db 3028 GAGAACTTTAAG 3039

RESULT 7
BC031555 3360 bp mRNA linear PRI 26-JUN-2002
LOCUS BC031555
DEFINITION Homo sapiens, caspase recruitment domain protein 12, clone
HMC:35330 IMAGE:5179909, mRNA, complete cds.
ACCESSION BC031555
VERSION BC031555.1 GI:21594975
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3360)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgaps-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center

Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amgdbcm.tmc.edu
Gunnar, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://Image.llnl.gov>
Series: IRAC Plate: 50 Row: a Column: 10
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis.

FEATURES
source
1..3360
/location=Qualifiers
/organism="Homo sapiens"
/db_xref="LocustID:58484"
/db_xref="taxon:9606"
/clone="MGC:35330 IMAGE:5179909"
/tissue_type="Brain, Lung, Testis, adult, pooled whole"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
/note="vector: pCMV-Sport6"
232..3306
/codon_start=1
/product="caspase recruitment domain protein 12"
/protein_id="AA031555.1"
/db_xref="GI:21594976"
/translation="MNRTRKNSRLIORMGTYIKOTDPLFYNNVNRREVNICE
KVEDDARKGITHMLKKGESCSNLELSLKBWNPPLPDJNGSLFPHOTSGDDDLA
QDNKDLHTPSGLNFPYLEDIDIFLMLKSTFEPVLMRDHHRHREQLTLGLDA
LOSPLIIEGSGKSTYLORIAMLMSGCKALTKRPVFFPLSLPAOGLEFLTD
OLDIDPIETIRKQFAMALIKROVLEFLDGYNEFRKQNEPEALIKENHRRKNVY
VTTTTECLRHROFGALTAEVGDMTESAALIREVILKEALGSLIOLIOKSCILRL
MKPLFVYITCALOMGSESRHSHTQTLFRTFDLIQKKHKKCYAASDFRISDH
CGDIALGVSPKFTDFELQDVSYNEDVALDTGLCTYTLQRRPKKFFHKSQDET
AGRLSSLLTSHEBEVTKNGYLQKNVSLSDITSTYSLLRTCGSSVATRAVMKH
LAAVYOGCLGSLIARKPLROESLYNTEEOELIKAININSFVECGIHHYOEST
SKSALISOEFELFGKSLYINSGNIPYLDFFHEPLNCASALDFIKLDFYGAAMSM
EKAAEDGGIIMEAPETVIPSRAVSLEFNMKQEFRTLEVTLRDFSKLNODIRYLCK
IFSSATSLRIQKRCAGVAGSLSLVSTCKNYSIMWEASPLTIEDRHTTSYNNKT
LSIHDLONORLPGSLTDSLGKRLKRLTINDNIKMNEEDAIKLAEGIKNNKCLPRL
THSDIGEGNDYIVKSLSSSEPCDLEELQVSCCLSAANVITLQNLNLVKLSLIDS
ENYLEKNGENALHELIDRMNVLEQLTALMLCPMGCDVGSLSLKLHLEVPOLVKGL
KNWRILDTETRIILGAFEGKNDLKNFQDLNLAGNVSSDGLAFGVEENLKOYFDF
STKEFLDPPALVRLSOVLSTKFLPQEARLVGMQFDDDDSVITGARKLVTA"

BASE COUNT 1011 a 718 c 768 g 863 t

ORIGIN

Alignment Scores:
Pred. No.: 7,17e-95 Length: 3360
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Gaps: 0
Indels: 0
Gaps: 0

US-09-697-089-2_COPY_762_965 (1-204) x BC031555 (1-3360)

QY 1 LeuysasleuThrlsleuilemetaspasniileysmetasngluaspalaile 20
|||||
Db 2515 TTGAAGAACCTTACAAAGCTCTATATGATATACATTAAGATGAAGAAGATGCTATA 2574

QY 21 LysleualagluGlyLeuylsasnleuylslysmetCysleuphehisleuthrisleu 40
|||||
Db 2575 AAACAGCTGAAGGCCCTGAAAAAAGCTGAAGAAGATGTGTATTTTCATTGACCCACTTG 2634

QY 41 SeraspillegluGlymetaspryrllevalysSerleuserSerGluProcysasp 60
|||||
Db 2635 TCTGACATTGGAGAGGAGGATGATTACATGCTCTCTCAAGTCAAGAACCCCTGTGAC 2694

QY 61 LeuglugluileglnleuValserCysCysleuserAlaasnAlValylsileleuala 80
|||||

Db	2695	CTGAGAAATTCATTAGTCTAGCTCCGCGCTGTGTCTGCAAAATGCAGCTGAAATTCCTAGCT	2754
QY	81	GIuAsnLeuHISAsnLeuValLysLeuSerILEuAspLeuSerGIuAsnTYrLeuGIu	100
Db	2755	CAGAACTTTCACAAATTTGGTGCAAACTGAGCATTCTTGATTTATCAGAAATTAACCTGGAA	2814
QY	101	LysAspGIuAsnGIuAlaLeuHISGIuLeuILEAspArgMetAsnValLeuGIuLeu	120
Db	2815	AAAGATGCAAAATGAAGCTCTTCATCAACTGATGCAGAGATGAAGCTGCTAGAACAGCTC	2874
QY	121	ThrAlaLeuMetLeuProTyrPGLysAspValGInGlySerLeuSerSerLeuLeuLys	140
Db	2875	ACCGCACTGAGCTGCCCTGGGGCGTGTACCGTGCAGGACGCCCTGAGCAGCCTGTGGAAA	2934
QY	141	HISLeuGIuGIuValProGInLeuValLysLeuGlyLeuLysAsnTTPArgLeuThrAsp	160
Db	2935	CATTGGAGGAGGAGTCCCACTCCTCAAGCTTGGGTTGAAAAAAGCTGGAGACTCACAGAT	2994
QY	161	ThrGIuILEArgILEuGlyAlaIlePheHecGlyLysAsnProLeuLysAsnHecGInGIn	180
Db	2995	ACAGAGATTAGAAATTTTGTGGTGCATTTTGTGAAAGAACCCCTCTAATAAACTTCAGCAG	3054
QY	181	LeuAsnLeuAlaGlyLysAsnArgValSerSerAspGlyTTPLeuAlaIleHecGlyValPhe	200
Db	3055	TTGAAATTTGGCGGGGAAATCGTGTGACAGTGTGATGGATGGCTTGCCTCATGGGTGTATTT	3114
QY	201	GIuAsnLeuLys	204
Db	3115	GAGAAATCTTAAAG	3126

LOCUS	AX318091	3396 bp	DNA	linear	PAT 14-DEC-2001			
DEFINITION	Sequence 96 from Patent WO0190156.							
ACCESSION	AX318091							
VERSION	AX318091.1	GI:17900820						
KEYWORDS	.							
SOURCE	human.							
ORGANISM	Homo sapiens							
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.							
AUTHORS	1 Reed, J.C., Plo, F.F., Godzik, A., Stenhlik, C., Damiano, J.S., Lee, S.H., Oliveira, V.A., Hayashi, H., and Pawlowski, K.							
TITLE	Card domain containing polypeptides, encoding nucleic acids, and methods of use							
JOURNAL	Patent: WO 0190156-A 96 29-NOV-2001; The Burnham Institute (US)							
FEATURES	Location/Qualifiers							
source	1..3396							
CDS	/organism="Homo sapiens"							
	/db_xref="taxon:9606"							
	277..3351							
	/note="unnamed protein product"							
	/codon_start=1							
	/protein_id="CAD19340.1"							
	/db_xref="GI:17900821"							
	/translation="MNFITKDSRALIORMGTYVTKQTTDDLFWNNVLRREYNIICCC							
	KVEDDAARGIIHMLTKRGSESCNLFSLSLKWMNPPLFODLNGOQLPQTSGDDLDDL							
	LOKLDIAHTPSFLFYPLDGEDIDIFNLKSFTEPIILMKROGHHRRBOALLNGLQQL							
	QDSCLIIIEGSGKSTLQRIAMLWSGKCALTFKFFPLRSRAOGLFETICL							
	QLDDIPCTRIKQFPMAMLLKROVFLPLDQNEKFPONCEIALLKENRFRKMV							
	VTPTTECLHRIROGALTAEGDWTESAALLIREVLLKELAEGLLQIQKSRCLRN							
	MKPPLPVYINCALDMGSESPHSHTQTTLLFFHYDILLQKHKHKGVASDFPISLSD							
	RGDLALGVFSHKRFDELQDVSVNEDVLLTGLLCKTAQRFPKYTFKFSQETVY							
	AGRLSLILTSHEPEVTKNGVYLQKWSISDITPTYSLLRYTGGSEVFETKRVMTK							
	LAAYVQHGCLGLGISIAKRLPMRQESLSYKNTQTEILKAININSFVCGIHLVQEST							
	SKSLAQGEFAFGQKSLYINGSNIPYLPDFEHLPRGCAALDFIKLDFEGMAAS							
	EKAEDAGGIHMEEAPEYTIIPSRVSLFPMNKQERTEVLRLEPSTKNDQDITYG							
	IFSSATSLRIQIKACVAGSLSTVLSCKKYSILNMPASPTLDEBHTSYNTRK							
	LSTHDLDNQRLLPGLDLSGLKLUKTLINDINIMANEDAIKLDEGLNLRKMLCFH							
	THSIDEGMDYIVKLSLSEPCDLEETIVSCSLAANVKTLLAQNLANLVSLTIDLS							
	ENYLEKQENALHLELDIRMNVLDELTLNMLPWGCDVGSLSLSLKHLIEEYQVLKGI							

BASE COUNT	992 a	737 c	793 g	874 t
ORIGIN	KNNMLTDTETIEIRILGAFEGCKNPLKNEQOQLNLAGNRYSSGMLAENGVEFNKLQOLYFEDDE STKEELDPALVRLISQVLSKTFEJOEARLIGWQFDDDDSVITGAEFLVTA"			

Alignment Scores:		
Pred. No.:	7, 26e-95	Length: 3396
Score:	1046.00	Matches: 204
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
Db:	6	Gaps: 0

US-09-697-089-2_copy_762_965 (1-204) x AX318091 (1-3396)

OY	1	LeuLysAsnLeuThrLysLeuIleMetHisPasnIleLysMetAsnGluAspAlaIle	20
Db	2560	TTGAAGAACCTTACAAAGCTCATATGATGATTAACATTAAGATGAATGAAGAACATGCTATA	2619
OY	21	LysLeuAlaGluGlyLeuLysAsnLeuLysMetCysLeuPheIstLeuThrIstLeu	40
Db	2620	AAACTAGCTGAGAGCCCTGAAAAAAGCTGAGAAAGATGTGTTTATTTTCATTGACCCACTTG	2679
OY	41	SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp	60
Db	2680	TCTGACATTTGAGAGAGGAATGATTAACATAGTCAAGTCTCTGTCAAGTAACCTGTGAC	2739
OY	61	LeuGluGluIleGluLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla	80
Db	2740	CTTTGAAGAAATTCATTTAGTCTCTGCTGCTGTCTGTGCAAAATGACAGTCAAAATCTTACCT	2799
OY	81	GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu	100
Db	2800	CAGAACTTTCACAAATTTGGTCAAACTGACCATTTCTTGATTATACAAAAATTACCTGGAA	2859
OY	101	LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGluLeu	120
Db	2860	AAAGATGGAATAGAAAGCTCTTCATGACTGATGACAGAGATGACGCTAGAACAGCTC	2919
OY	121	ThrAlaLeuMetLeuProTyrPclYcyAspValGlnGlySerLeuSerSerLeuLys	140
Db	2920	ACCGGACGATGCTCCCTCGGGGCTGTGACGTCGCAAGGACGCTGAGCCGTGTGAA	2979
OY	141	HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp	160
Db	2980	CATTTGGAGAGAGTCCCACTCGTCAAGCTTGGGTTTAAAAAATCGGAGACTCACAGAT	3039
OY	161	ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln	180
Db	3040	ACAGAGATTAGAAATTTTAGTGTCATTTTGTGAAAGAACCCCTGAAAAAATCTTCAGCAG	3099
OY	181	LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPLeuAlaPheMetGlyValPhe	200
Db	3100	TTGAATTTGGCGCGGAAATCGTGTGAGCAGATGATGATGGCTTGCCCTTCATGGGTGTATTT	3159
OY	201	GluAsnLeuLys 204	
Db	3160	GAGAACTTTAAG 3171	
RESULT 9	AY027787	3396 bp mRNA linear	PRI 20-JUL-2001
LOCUS	AY027787		
DEFINITION	Homo sapiens CLAN1 (CLAN1) mRNA, complete cds.		
ACCESSION	AY027787		
VERSION	AY027787.1	GI:14324112	
KEYWORDS			
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 3396)		
	Danilauo,U.S., Stehlik,C., Pio,F., Godzik,A. and Reed,J.C.		
	Clan, a novel human ced-4-like gene		

JOURNAL Genomics 75 (1-3), 77-83 (2001)
MEDLINE 21365712
PUBMED 11472070
REFERENCE 2 (bases 1 to 3396)
AUTHORS Stehlik,C., Damiano,J.S., Pio,F., Godzik,A. and Reed,J.C.
TITLE Direct Submission
JOURNAL Submitted (21-FEB-2001) Program on Apoptosis and Cell Death
Research, The Burnham Institute, 10901 North Torrey Pines Road, La
Jolla, CA 92037, USA

FEATURES
source location/Qualifiers
1..3396
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/map="2p22-p21"
/tissue_type="lung"
1..3396
/gene="CLAN1"
277..3351
/gene="CLAN1"
/note="alternatively spliced; similar to Ced-4"
/codon_start=1
/product="CLAN1"
/protein_id="AAK14776.1"
/db_xref="GI:14324113"
/translation="MNFIKDNRALLIORMGMTVIKQITDDLEFVNVNLRREVNITICE
KVEDDAARGIITHMLKGSSECNFLSKLKMNPPLFDLNGOSLFHOTSGDIDDLA
ODKLDYHTPSGFLPEDIDIIIFNLKSTPEPILKRFVDFHLSRAOGSLPEFLCD
LQSPCLIEGESGKSTYLORIAMWSGSKALKTKKPEFVDFHLSRAOGSLPEFLCD
OLDIPGIRKQTFMAMLIKLRQVLEFLDYNFKPQNCPEITALLKENRFRNMYI
VTTEICRHRIRGAGALTAEGDMTEDSAQLIREVLIKELAEGLLOIQSRCLRL
MKTPLFVYITCAIOMGSEFHSHTQTLFHFYDLLLOKNHKKHGVAAASPLSLDH
RGDLALRGVFSHKEDEFLQDVSVNEDALTTGLCKTAQRFKPKYEFKFSQEYT
AGRLSSILTSHEPEEYTKGNGYLOKNVSIIDITSTYSLLRYTCGSSVEATRAVMKH
LAAYHOGCLIGLSIARPLIMROESIOSVKTTQTECIIKAININSPVSGHLYQEST
SKALSQEFENFPGKSGIYINSNIPDLEPFEHPLPCASALDPFIKIDPFGAMASH
EKAEDTGGIIMEAPETIYPSRAVSLEFNKOEPRILEVLRDPSKLNKODIRLKG
IESATSRLQIKRCAGVAGSLSVLSTCKNIYSILMEASPLTEDEHRIYSNLKT
LSIHDQNRPLPGJLTDLSLKNITKIMNIMKNEEDAKIKLAEGLNKKMCLFHL
THSIDIGEMDIYKLSSEPCDELEIOLVCCSANAIVKILIAONLHNLVSLTSDLS
ENYLEKQNEALHELDIMNVLBDLTALMLPWCDDVGSLSLKHLEEVPOLYKGLI
KNMRLTPEIRIILAFEGKPNLKNFOOLNAGNRYSSGMLAFMGPVENLKOYVFFDF
STKEFLPEPALVKLSOYLSKLTFLDQEARLVKQFDDDDLSVITGAFLVYA"

BASE COUNT 992 a 737 c 793 g 874 t

ORIGIN

Alignment Scores:
Pred. No.: 7.26e-95 Length: 3396
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-697-089-2_COPY_762_965 (1-204) x AY027787 (1-3396)

QY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIle 20
DB 2560 TTGAAGAAGACCTTAACAAGCTCATTAATGATTAACAATGAAGATGAAGAAGATGCTATA 2619

QY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40
DB 2620 AAACAGCTGAAGGCCCTGAAGAAACCTGAAGAGATGCTTTATTCATTGACCCACCTTG 2679

QY 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60
DB 2680 TCTGCATTGGAGAGGAGATGATTACATAGCAAGTCTCTGTCAGTGAACCCCTGTGAC 2739

QY 61 LeuGluGluIleGluLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80
DB 2740 CTTGAAGAAGATTCATTAAGTCTCCCTGCTGCTGTGCAAAATGCAAGTGAATAATCTAGCT 2799

QY 81 GluAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100

DB 2800 CAGAACTTCACAAATTTGGTCAAACTGAGACATTTTGAATTTATCAGAAAATTAACCTGGAA 2859
QY 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluIleu 120
DB 2860 AAAGATGGAAGAAAGAGCTTCTCATCACTGACGACAGATGAAGTCTGTAGAACAGCTC 2919

QY 121 ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140
DB 2920 ACCGCATCATCTCTCCCTCGGCGCTGTGACGTGCAAGCAGCAGCTTACAGACCTGTGAAA 2979

QY 141 HisLeuGluGluValProGluLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160
DB 2980 CATTTGGAGAGAGCTCCCAACACTGCTCAAGCTTGGTGTGAATAACTGACAGACTCACAGAT 3039

QY 161 ThrGluIleArgIleLeuGlyAlaPheGlyLysAsnProLeuLysAsnPheGlnIle 180
DB 3040 ACAGAGATTGAATTTAGTGCATTTTGGAAAACCCCTGTGAATAAACTTCCAGCAG 3099

QY 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPLeuAlaPheMetGlyValPhe 200
DB 3100 TTGAATTTGGCGGGAATTCGTGTGACAGTGAATGATGCTGCTGCTCATGGGTGATTT 3159

QY 201 GluAsnLeuLys 204
DB 3160 GAGAACTTTAAG 3171

RESULT 10
LOCUS AF376061
DEFINITION Homo sapiens caspase recruitment domain protein 12 mRNA, complete cds.
ACCESSION AF376061
VERSION AF376061.1 GI:14040074
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3581)
AUTHORS Gingras,M.-C., Olin,J. and Margolin,J.F.
TITLE Differential expression of the caspase recruitment domain protein 12 (CARD12) during monocytic differentiation
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3581)
AUTHORS Gingras,M.-C., Olin,J. and Margolin,J.F.
TITLE Submitted (03-MAY-2001) Pediatric/Texas Children's Cancer Center, Baylor College of Medicine, 6621 Fannin St. MC3-3320, Houston, TX 77030, USA

FEATURES
source location/Qualifiers
1..3581
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/map="2p21-22"
/cell_line="U937"
/note="CARD12"
/codon_start=1
/product="caspase recruitment domain protein 12"
/protein_id="AAK3443.1"
/db_xref="GI:14040075"
/translation="MNFIKDNRALLIORMGMTVIKQITDDLEFVNVNLRREVNITICE
KVEDDAARGIITHMLKGSSECNFLSKLKMNPPLFDLNGOSLFHOTSGDIDDLA
ODKLDYHTPSGFLPEDIDIIIFNLKSTPEPILKRFVDFHLSRAOGSLPEFLCD
LQSPCLIEGESGKSTYLORIAMWSGSKALKTKKPEFVDFHLSRAOGSLPEFLCD
OLDIPGIRKQTFMAMLIKLRQVLEFLDYNFKPQNCPEITALLKENRFRNMYI
VTTEICRHRIRGAGALTAEGDMTEDSAQLIREVLIKELAEGLLOIQSRCLRL
MKTPLFVYITCAIOMGSEFHSHTQTLFHFYDLLLOKNHKKHGVAAASPLSLDH
CGDLALRGVFSHKEDEFLQDVSVNEDALTTGLCKTAQRFKPKYEFKFSQEYT
AGRLSSILTSHEPEEYTKGNGYLOKNVSIIDITSTYSLLRYTCGSSVEATRAVMKH

LAAYVQHGCLLGISIARRPLMRQESLQSVKNTTEOELIKAININSFVECGIHLVOEST
SKASLQEFEPFQKSLIYNSGNIPLYLPEFFPHLPLNCASLALFKIDFQGMASW
EKRAEDGTGHHMEAPETIYPSRAVSLIPFNKQPELLEVLRFPSKLNKODIVYLGK
IFSSATSLRIQKRCACVAGSLSTVSTCKNITYSLMTEASLTTEDEDRHTSYVNKT
LSTHDLONRPLPGCLTDSLGNKRLTKLMDNITWNEBDAIKLEGNKMKCLFHL
THSIDGEMDYIVKSLSSSEPCDLEELQVSCCISANAANKLIAONLNLVLSLIDLS
ENYLEKDNALHELDIDRMVLEQTLALMPWGDVGSLSLTKHLEEVQALVGL
KNMLTDEIRLGAFFGNPKLNFQOLNLAGNVSDDGMLAFMGVFNELQVLEFFDF
STKEFLDPALVRKLSQVLSKLFLEQARLVQMFDDDDLSVITGARKLVYA"

misc_feature

502..741

/note="Region: caspase recruitment domain"

BASE COUNT 1033 a 781 c 843 g 924 t

ORIGIN

Alignment Scores:

Pred. No.: 7.72e-95 Length: 3581
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-697-089-2_COPY_762_965 (1-204) x AF376061 (1-3581)

Oy 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIle 20
Db 2773 TTGAAGAAACCTTACAACCTCATTAATGATTAACATAAAGATGAAGAAACATCTATA 2832
Oy 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40
Db 2833 AAACAGCTGAAGGCTGAAAAACCTGAAGAAGATGTTTATTCATTGACCCACTTG 2892
Oy 41 SerAspIleGlyGlyGlyMetAspTyrIleValLysSerLeuSerSerGluProCysasp 60
Db 2893 TCTGCATTTGAGAGAGGATGATGATTAACATGCAAGTCTCTGCAAGCAAGCCCTGAGC 2952
Oy 61 LeuGluGluIleGlnLeuValSerCysLeuSerSerAlaAsnAlaValLysIleLeuAla 80
Db 2953 CTGGAAGAAATTCATTAATGCTCTCGCTGCTTGTCTGCAATGCAAGTGAATCTTACT 3012
Oy 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100
Db 3013 CAGAAATCTTCAACAATTTGGTCAAACTGAGACATTTTGAATTTATCAGAAATTAACCTG 3072
Oy 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120
Db 3073 AAAGATGGAATGAAGCTCTTCATGAACTGACAGAGATGAAGCTGCTGAACACGCTC 3132
Oy 121 ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140
Db 3133 ACCGACATGATGCTGCTGCTGCGGCTGTGACGTGCAAGGCAAGCTGAGACGCTGTTGAAA 3192
Oy 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrPargLeuThrAsp 160
Db 3193 CATTTGGAGAGGTCCACCACTGCTCAAGCTTGGGTGAAAAAATGAGACTCACAGAT 3252
Oy 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPhelGln 180
Db 3253 ACAGAGATTGAATTTAGGTCATTTTGTGAAAACCCCTGTAACAACTTCCAGCAG 3312
Oy 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPLeuAlaPheMetGlyValPhe 200
Db 3313 TTGATTTGGCGGGAATCGTGAGCAGTGATGATGATGCTTGCCTTCAATGGGTATATT 3372
Oy 201 GluAsnLeuLys 204
Db 3373 GAGATCTTAAG 3384
RESULT 11
LOCUS AK095467 3355 bp mRNA linear PRI 15-JUL-2002
DEFINITION Homo sapiens cDNA FLJ38148 f1s, clone D90ST2003791, highly similar
to Homo sapiens ICE-protease activating factor mRNA.

ACCESSION AK095467
VERSION AK095467.1 GI:21754727
KEYWORDS Oligo capping: f1s (full insert sequence).
SOURCE Homo sapiens CD34+ Cells cDNA to mRNA, clone_1ib:D90ST2
clone:D90ST2003791.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ninomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T.,
Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K.,
Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
Kikuchi,H., Murakawa,K., Kanenori,K., Takahashi-Fujii,A.,
Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
Nagahara,K., Masuo,Y., Nagai,K. and Isogai,T.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 3355)
REFERENCE 2
AUTHORS Isogai,T. and Yamamoto,J.
TITLE Direct Submission
JOURNAL Submitted (04-JUL-2002) Takao Isogai, FRJ Project(HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'-6 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
FEATURES
source
1..3355
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="D90ST2003791"
/cell_type="CD34+ Cells"
/clone_1ib="D90ST2"
/note="cloning vector: PME18SFx3-mRNA from CD34+ cells
after 9-days ODF induction. -primary culture, CD34+ Cells"
BASE COUNT 986 a 726 c 774 g 869 t
ORIGIN
Alignment Scores:
Pred. No.: 1.8e-94 Length: 3355
Score: 1042.00 Matches: 203
Percent Similarity: 100.00% Conservative: 1
Best local Similarity: 99.51% Mismatches: 0
Query Match: 99.62% Indels: 0
Gaps: 0
US-09-697-089-2_COPY_762_965 (1-204) x AK095467 (1-3355)
Oy 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIle 20
Db 2545 TTGAAGAAACCTTACAACCTCATTAATGATTAACATAAAGATGAAGAAACATCTATA 2604
Oy 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40
Db 2605 AAACAGCTGAAGGCTGAAAAACCTGAGAGAAGATGTTTATTTTCATTGACCCACTTG 2664
Oy 41 SerAspIleGlyGlyGlyMetAspTyrIleValLysSerLeuSerSerGluProCysasp 60
Db 2665 TCTGCATTTGAGAGAGGATGATTAACATGCAAGTCTCTGCAAGCAAGCCCTGTCAGC 2724
Oy 61 LeuGluGluIleGlnLeuValSerCysLeuSerSerAlaAsnAlaValLysIleLeuAla 80
Db 2725 CTGGAAGAAATTCATTAATGCTCTCGCTGCTTGTCTGCAAGCAAGTGAATTAATCTTACT 2784
Oy 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100

|||||
Db 2785 CACAATCTTCAACATTTGGTCAAACTGACATCTTGTATTATCAGAAATTTACTCTGAA 2844
QY 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValIleGluGlnLeu 120
|||||
Db 2845 AAAGATGGAATGATGAGCTCTTTCATGAACTGATGCACAGATGAACGCTGCTAAGAACACTC 2904
QY 121 ThrAlaLeuMetLeuProTyrPglyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140
|||||
Db 2905 ACCGACTGATGCTGCCCTGGGCTGTGAGCTGCAGAGCCGCTGACAGCCTGTGTAA 2964
QY 141 HisLeuGlnGluValProGlnLeuValIleGluGlyLeuLysAsnTPArgLeuThrAsp 160
|||||
Db 2965 CATTTGGAGGAGGCTCCACACACTGCTCAAGCTTGAGTGAAGAACTGAGACTCACAGAT 3024
QY 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPhelGlnGln 180
|||||
Db 3025 ACAGAGATTGAATTTAGTGCGCATTTTGGAAAGAACCTCTGAAATTTCCAGAG 3084
QY 181 LeuAsnLeuAlaGlyAsnAlaGlyValSerSerAspGlyTyrPheAlaPheMetGlyValPhe 200
|||||
Db 3085 TTGAATTTGGCGGGAATCGTGTGAGCAGATGATGATGCTTGCCTTCATGCTGTATTT 3144
QY 201 GluAsnLeuLys 204
|||||
Db 3145 GAGATCTTAAAG 3156
RESULT 12
CNS01DS3 138909 bp DNA linear PRI 18-APR-2002
LOCUS
DEFINITION BAC sequence from the SPG4 candidate region at 2p21-2p22 BAC 164M19
of library CITB_978_SKB from chromosome 2 of Homo sapiens (Human).
ACCESSION AL121653
VERSION AL121653.2 GI:7159616
KEYWORDS SPG4 genomic DNA interval.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 138909)
AUTHORS Hazan,J., Fonknechten,N., Mavel,D., Paternotte,C., Samson,D.,
Artiguenave,F., Davoine,C.S., Cruaud,C., Durr,A., Wincker,P.,
Brotier,P., Gattolico,L., Barde,V., Burgunder,J.M.,
Prud'Homme,J.F., Brice,A., Fontaine,B., Heilig,R. and
Weissenbach,J.
TITLE Spastin, a novel AAA protein, is altered in the most frequent form
of autosomal dominant spastic paraplegia
JOURNAL Nat. Genet. (1999) In press
REFERENCE 2 (bases 1 to 138909)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (18-APR-2002) Genoscope - Centre National de Sequencage :
BP 101 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT On Mar 6, 2000 this sequence version replaced gi:6002386.
FEATURES
source
Location/Qualifiers
1..138909
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/clone="164M19"
/clone_1id="CITB_978_SKB"
BASE COUNT 39243 a 28424 c 29121 g 42121 t
ORIGIN

Alignment Scores:

Pred. No.: 1.53e-21 Length: 138909
Score: 331.00 Matches: 91
Percent Similarity: 28.10% Conservative: 2
Best Local Similarity: 27.49% Mismatches: 6
Query Match: 31.64% Indels: 232
DB: 9 Gaps: 2

US-09-697-089-2_COPY_762_965 (1-204) x CNS01DS3 (1-138909)
QY 80 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 99
|||||
Db 60048 GCTCAGATCTTTCACATTTGGTCAAACTGAGCATCTTGTATTATCAGAAATTTACTCTG 59989
QY 100 GluLysAspGlyAsnGluAlaLeuHisGluLeu----- 110
|||||
Db 59988 GAAAAGATGGAATGAAAGCTCTTCATGAACTGTAAGAAATGACAATTCAGCCAAATT 59929
QY 110 ----- 110
Db 59928 AGATACCTGAATATGATCTAGTGGGTAGTCGAAATACATAGCCTGGTGCAGGCTCTTT 59869
QY 110 ----- 110
Db 59868 ATACCATGTGTGCTTACTACTAGATGACACCTCTTGAAGAAATCATTTAGGCTTCTTA 59809
QY 110 ----- 110
Db 59808 AACTGCCCTTAAGAACACAGGCCCATGTCTTTTAAGTCAACAGTTACATATGCTCACT 59749
QY 110 ----- 110
Db 59748 GCACTTGAGCGGTATCCACCTGCTTCTCTCTTGAAGAGGCACTGCAAGAGTAG 59689
QY 110 ----- 110
Db 59688 CCGATGTGCAAGACAAATTTGCTTAAGGAATGTGATATGATTTTGTAGTGTGATAGT 59629
QY 110 ----- 110
Db 59628 GATATGTGATTATGTTAAAAAGAAAAAGAAAGAACTGATTCAATTTGTCATGATTT 59569
QY 110 ----- 110
Db 59568 TGCTTTGAATTAATACAGAGGAATTAGTTCAGATTAAAGCAAGTTGCCATATTAA 59509
QY 110 ----- 110
Db 59508 TGTTTTGAAGGTGCTTATTATGATATATATATATATCTTCGATATATGTTT 59449
QY 110 ----- 110
Db 59448 GTATATGCTTGAAATACCTTCCAAAAAACCAAAATTAAGTAGATTTCATTACAGAT 59389
QY 110 ----- 110
Db 59388 TGAGTAGGCTCAGAGCCACCAACATTAAGATCATTCCTCCCTAACACCCCTTTGTC 59329
QY 111 -----1LeAspArg 113
Db 59328 TTCCCTGATTTTGAACACATCCAGTCCCTGAATGCTCTTGTTCCTCCAGTCGACAGG 59269
QY 114 MetAsnValIleGluGlnLeuThrAlaLeuMetLeuProTyrPglyCysAspValGlnGly 133
|||||
Db 59268 ATGAACGTGCTAGAACACGCTCACCGCATGTGCTGCCCTGGGCTGTGAGCTGCAAGGC 59209
QY 134 SerLeuSerSerLeuLeuHisLeuGlnGluValProGlnLeuValLysLeuGlyLeu 153
|||||
Db 59208 AGCCTGAGCAGCCTGTGAAACATTTGGAGGAGGTCCACACAGCTGTCACACTGGGCTTG 59149
QY 154 LysAsnTyrPArgLeuTyrAspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsn 173
|||||
Db 59148 AAAAAGTGGAGACTCACAGATACAGAGATTGATTTAGTAGTAGTACACATACAGAG 59089
QY 174 Pro-----LeuLysAsnPhe 178
|||||
Db 59088 CCAAGATTAACATGATTTGGCCCTTAAAAAATTC 59056
RESULT 13
AC011232/c 185281 bp DNA linear HTG 10-MAR-2001
LOCUS

```

DEFINITION Homo sapiens chromosome 2 clone RP11-78E13, WORKING DRAFT SEQUENCE,
7 unordered pieces.
ACCESSION AC011232
VERSION AC011232.7
KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE 1 (bases 1 to 185281)
JOURNAL Waterston,R.H.
REFERENCE The sequence of Homo sapiens clone
AUTHORS Unpublished
TITLE 2 (bases 1 to 185281)
JOURNAL Waterston,R.H.
REFERENCE Direct Submission
AUTHORS Submitted (04-OCT-1999) Genome Sequencing Center, Washington
TITLE University School of Medicine, 4444 Forest Park Parkway, St. Louis,
JOURNAL MO 63108, USA
COMMENT On Mar 10, 2001 this sequence version replaced gi:9799811.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH0078E13
----- Summary Statistics -----
Sequencing vector: M13; 57%
Sequencing vector: plasmid; 40%
Chemistry: dye-primer ET; 48% of reads
Chemistry: dye-terminator Big Dye; 50% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 182798 bases at least Q40
Consensus quality: 183538 bases at least Q30
Consensus quality: 184045 bases at least Q20
Insert size: 168000; agarose-fp
Insert size: 184681; sum-of-contigs
Quality coverage: 7.07 in Q20 bases; agarose-fp
Quality coverage: 7.33 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1985: contig of 1985 bp in length
* 1986 2085: gap of unknown length
* 2086 8183: contig of 6098 bp in length
* 8184 8283: gap of unknown length
* 8284 22741: contig of 14458 bp in length
* 22742 22841: gap of unknown length
* 22842 41446: contig of 18605 bp in length
* 41447 41546: gap of unknown length
* 41547 69182: contig of 27636 bp in length
* 69183 69282: gap of unknown length
* 69283 112131: contig of 42849 bp in length
* 112132 112231: gap of unknown length
* 112232 185281: contig of 73050 bp in length.
*
Location/Qualifiers
1. 185281
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/clone="RP11-78E13"
1. 1985
/note="assembly_name:Contig11"
2086. 8183
/note="assembly_name:Contig12"
8284. 22741

```

	misc_feature	/note="assembly_name:Contig13" 22842..41446 /note="assembly_name:Contig14"	
	misc_feature	41547..69182 /note="assembly_name:Contig15"	
	misc_feature	69283..112131 /note="assembly_name:Contig16"	
	misc_feature	112232..185281 /note="assembly_name:Contig17"	
BASE COUNT	52719 a	36957 c	37187 g 57816 t 602 others
ORIGIN			
Alignment Scores:			
Pred. No.:	2.13e-21	Length:	185281
Score:	331.00	Matches:	91
Percent Similarity:	28.10%	Conservative:	2
Best Local Similarity:	27.49%	Mismatches:	6
Query Match:	31.64%	Indels:	232
DB:	2	Gaps:	2
US-09-697-089-2_COPY_762_965 (1-204) x AC011232 (1-185281)			
OY	80	AAGGnAsnLeuHIsAsnLeuValLyIsLeuSerIleLeuSpLeuSerGArgLysnTyrrLeu	99
Db	171729	GCTCGAATCTTCACAAATTGTGGTAAACTGACGACTTTTGATTATTCAGAAAATTACCTG	171670
OY	100	GlulYsAspGlyAsnGluAlaLeuHISgluLeu-----	110
Db	171669	GAAAAAGATGGAAATGAAGAGCTTCATGAACTAGTAAGAATGCATTCAGCCAAAATT	171610
OY	110	-----	110
Db	171609	AGATACTGAATATGTATCTGGGTAGTCGAAATACATACCTGGGCTCGAGGCTCTTTT	171550
OY	110	-----	110
Db	171549	ATACCAGTGTGCTTACTGATGCACCCCTCCTTAGGAAAATCATTTAGGCCCTTCTTA	171490
OY	110	-----	110
Db	171489	AACGTCCTTAAAGAACAGAGCCCATGTCTTTTAAGTCACAGTTTACATATGTCACGT	171430
OY	110	-----	110
Db	171429	GCACCTTGGAGCGGTATCCACCTGCTTCTCCTTTGAAGAGCAACTGCAAGAGTAG	171370
OY	110	-----	110
Db	171369	CCGATGTGCACAACAAATTGCTTAAAGAAATTGCTGATGATGTTTTTTAGTGCTGATPACT	171310
OY	110	-----	110
Db	171309	GATATGCTATTATGTGTTAAAGAAAAAAGAAAGAAAGAACTGATTCAATTGTCCACAGATT	171250
OY	110	-----	110
Db	171249	TGCTTTAGATAATATACAGAGAGGAAATTAGTGCAGGATTAAGCAACATTGCCATGATTTAA	171190
OY	110	-----	110
Db	171189	TGTTTTGAGAGGTCTTATTATGATATATAGTTTCATTAATTCCTGCAATAATGTTT	171130
OY	110	-----	110
Db	171129	GTAATGCTTGAATACTTCCAAAAAACCAAAATTAAGTAGATTCATTAACAGAT	171070
OY	110	-----	110
Db	171069	TGAGTAGGCTGCAGAGCCCAACATAAAGATCATCTCCCTTACACCCCTTTGTTTC	171010
OY	111	-----IIeaapag 113	
Db	171009	TTTCCTAGCTTTTGAGACCATCCAGTCCCTGAACGTCTTTGTTCTCTCCAGTCGACAGG	170950

QY 114 MetasynValleugluInleuThAlaLeuMetleuProtrpglyCysaspValGlnly 133
 |||||||
 Db 170949 ATGAACGTGTAGAAGACAGCTACCGCACTGATGCTGCCCTGGGGCTGTGAGCTGAAGC 170890
 QY 134 SerleuserSerleuLeuLysHisleuGluValProGlnleuValLysleuGlyLeu 153
 |||||||
 Db 170889 AGCCTGAGACACCTGTGAAACATTTGGAGGAGGTCGCCAACATCTGTCACAGCTTGGGTTG 170830
 QY 154 LysasnPrpAgtleuThAspThrGluIleuArgIleuLeuGlyAlaPhePhgGlyLysasn 173
 |||||||
 Db 170829 AAAAAGTGAAGACTCAGATACAGAGATTGAAATTTAGTAGTACACACATACAGAG 170770
 QY 174 Pro-----leuLysasnPhe 178
 |||||
 Db 170769 CCAAGATPACTGATTTGGCCCTTAAAAAATTC 170737
 RESULT 14
 AC010968 160583 bp DNA linear HTG 18-AUG-2000
 LOCUS
 DEFINITION
 Homo sapiens chromosome 2 clone RP11-9302, WORKING DRAFT SEQUENCE,
 11 unordered pieces.
 AC010968
 VERSION
 AC010968.5 GI:9845170
 KEYWORDS
 HTG; HTGS_PHASE1; HTGS_DRAFT.
 SOURCE
 Homo sapiens.
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE
 TITLE
 Waterston,R.H.
 JOURNAL
 The sequence of Homo sapiens clone
 2 (bases 1 to 160583)
 REFERENCE
 TITLE
 Waterston,R.H.
 JOURNAL
 Direct Submission
 AUTHORS
 Submitted (28-SEP-1999) Genome Sequencing Center, Washington
 UNIVERSITY
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 COMMENT
 On Aug 18, 2000 this sequence version replaced g1:8439959.

----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc/index.shtml
 ----- Project Information -----
 Center project name: H.NH0093002
 ----- Summary Statistics -----
 Sequencing vector: M13; 598
 Sequencing vector: plasmid; 418
 Chemistry: Dye-primer ET; 47% of reads
 Chemistry: Dye-terminator Big Dye; 53% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: bases at least Q40
 Consensus quality: bases at least Q30
 Consensus quality: bases at least Q20
 Insert size: 14700; agarose-fp
 Insert size: 159583; sum-of-contigs
 Quality coverage: 6.64 in Q20 bases; agarose-fp
 Quality coverage: 6.38 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 11 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 1 1080: contig of 1080 bp in length
 * 1081 1180: gap of unknown length
 * 1181 2476: contig of 1296 bp in length
 * 2477 2576: gap of unknown length

FEATURES
 source
 1. 160583
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="2"
 /clone="RP11-9302"
 1. 1080
 /note="assembly_name:Contig9"
 1181. 2476
 /note="assembly_name:Contig12"
 2577. 5035
 /note="assembly_name:Contig13"
 5136. 9606
 /note="assembly_name:Contig14"
 9707. 17078
 /note="assembly_name:Contig15"
 17179. 27158
 /note="assembly_name:Contig16"
 27259. 45137
 /note="assembly_name:Contig17"
 45238. 65522
 /note="assembly_name:Contig18"
 clone_end:r7
 vector_side:right
 65623. 91498
 /note="assembly_name:Contig19"
 91599. 116835
 /note="assembly_name:Contig20"
 clone_end:sp6
 vector_side:right
 116936. 160583
 /note="assembly_name:Contig21"
 BASE COUNT 44349 a 33843 c 33703 g 47641 t 1047 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 5.7e-21 length: 160583
 Score: 326.00 Matches: 91
 Percent Similarity: 28.10% Conservative: 2
 Best local Similarity: 27.49% Mismatches: 6
 Query Match: 31.17% Indels: 232
 DB: 2 Gaps: 2
 US-09-697-089-2_COPY_762_965 (1-204) x AC010968 (1-160583)
 QY 80 AlaglnAsnleuNhisAsnleuValLysleuSerlleuAspLeuSerGluAsnTyrleu 99
 |||||||
 Db 64448 GTGAGATCTTTCACAAATTTGGTCAAACTGAGCATTTCTGTATTCAGAAATTTACTCG 64507
 QY 100 GtubysaprglyAsnGluAlaLeuHisGluLeu----- 110
 |||||||
 Db 64508 GAAAAGATGGAATGGAAGGCTTCATGAGTACAGTAGAATGACAAATTCAGCAAAAT 64567
 QY 110 ----- 110
 Db 64568 AGATACTTGAAATGATGATGAGTACTGGAATGCAATACATAGCCTGGGTCTGAGGTCTTTT 64627

```

Qy 110 ----- 110
Db 64688 ATACCAGTGTGCCTTACTAGATGACCCCTCCTTAGGAAATCATTTAGGCTTTCTTA 64687
Qy 110 ----- 110
Db 64688 AACTGCCCTTAGGAAACAGAGGCCCATGTCTTTTAAGTACACAGTTTACATATGCTCACT 64747
Qy 110 ----- 110
Db 64748 GCACCTTGAGCGGTATCCACACTGCTTCTCCTTGAGAGGCACTGTCAAGATAG 64807
Qy 110 ----- 110
Db 64808 CCGATGTGCAAGACAAATTTGCTTAGGAATTTGGATATGATTTTGTAGTGTGATAGT 64867
Qy 110 ----- 110
Db 64868 GATATGATATGCTTAAAGAAAAAAGAAAGAACTATTCATATTTGTCACAGAT 64927
Qy 110 ----- 110
Db 64928 TGCTTTAGAAATATACAGAGGAATTAGTCAAGATTAAGCAACATGCCATGATTTAA 64987
Qy 110 ----- 110
Db 64988 TGTTTTGAAGGTCTTATTAATATATATAGTTTCATATATTTCTTCCATTAATGTTT 65047
Qy 110 ----- 110
Db 65048 GATATGCTTGAATACCTTTCCAAAAAACCACAAATTAAGTAGATTTCTCATTCAGAT 65107
Qy 110 ----- 110
Db 65108 TGAGTAGCTGCAGAGCCACCAAAATTAAGATCATTCCTCCATACACCCCTTTGTTTC 65167
Qy 111 ----- 113
Db 65168 TTCCATGCTTTTGAGACCATTCAGCTCCGTAACGTCTTTGTTTCTTCCAGTCCACAGG 65227
Qy 114 MetasValLeuGlInLeuThrAlaLeuMetLeuProTprGlCysAspValGlnGly 113
Db 65228 ATGAACGTGTAGAACACACTCACCGCATGATGCTGCGCTGGGCTGTGAGCTGCAAGG 65287
Qy 134 SerLeuSerSerLeuLeuLysHisLeuGluValProGlnLeuValLysLeuGlyLeu 153
Db 65288 AGCCTGACGACCTGCTGTGAACATTTGGAGGAGGTCCCAACTGCTCAAGCTTGTTG 65347
Qy 154 LysAsnTPArgLeuThrAspThrGluLeuArgTlleLeuGlyAlaPhePheGlyLysAsn 173
Db 65348 AAAAAGCTGGAAGCTCACAGATACAGAGATTGAATTTAGGTAGGTACACACATACAGAG 65407
Qy 174 Pro-----LeuLysAsnPhe 178
Db 65408 CCAAGATTAACGTGATTTGGCCCTTAATAAAATTTC 65440
RESULT 15
G55568/c 553 bp DNA linear STS 30-MAR-2000
DEFINITION SHGC-100923 Human Homo sapiens STS genomic, sequence tagged site.
ACCESSION G55568
VERSION G55568.1 GI:6120887
KEYWORDS STS.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 553)
AUTHORS Olivier,M. and Cox,D.R.
TITLE Unpublished, Olivier, M., Cox, D.R. (2000)
JOURNAL Unpublished (2000)
COMMENT

```

Contact: Michael Olivier, David R. Cox
Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave., 2nd Fl., Palo Alto, CA 94025, USA
Tel: (650) 320-5800
Fax: (650) 320-5801
Email: olivier@shgc.stanford.edu
Primer A: AATGAGGGGCAAAATAGCAAA
Primer B: TACACCCCTTGTCTCTCTCA
STS size: 322
PCR Profile:

Initial incubation: 95 degrees C for 10 minutes
Denaturation: 94 degrees C for 30 seconds
Annealing: 60 degrees C for 30 seconds
Polymerization: 72 degrees C for 23 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9700
Protocol:

Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
AmpliTaq Gold Polymerase: 0.07 units/ul
Total Vol: 5 ul

Buffer: MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 8.3

BAC ends sequenced at TIGR from the RPC11 BAC library. Designed and developed at the Stanford Human Genome Center.

FEATURES
Location/Qualifiers
1..553
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="2"
/clone_lib="Human"

STS
primer_bind 5..27
primer_bind 107 c 114 g 162 t
BASE COUNT 170 a complement(304..326)
ORIGIN

Alignment Scores:
Pred. NO.: 5.24e-21 Length: 553
Score: 298.00 Matches: 60
Percent Similarity: 83.78% Conservative: 2
Best Local Similarity: 81.08% Mismatches: 6
Query Match: 28.49% Indels: 6
DB: 11 Gaps: 1

US-09-697-089-2_COPY-762_965 (1-204) x G55568 (1-553)

```

Qy 111 IleaSPArGMeTAsValLeuGluInLeuThrAlaLeuMetLeuProTprGlCysAsp 130
Db 259 GTCGACAGATGACGTCTAGAACAGCTCACCGCATGATGCTGCGGCTGTGAC 200
Qy 131 ValGlnGlySerLeuSerSerLeuLeuLysHisLeuGluValProGlnLeuValLys 150
Db 199 GTGCAGAGCAGCCTGAGCAGCTGTTGAACATTTGGAGGAGGTCCCAACTGCTCAAG 140
Qy 151 LeuGlyLeuLysAsnTPArgLeuThrAspThrGluLeuArgTlleLeuGlyAlaPhePhe 170
Db 139 CTGGGTGAAAAAAGCTGAGACTCACAGATACAGAGATTGAATTTAGGTAGGTACACA 80
Qy 171 GlyLysAsnPro-----LeuLysAsnPhe 178
Db 79 CATACAGAGCCAGATTAACGTGATTTGGCCCTTAATAAAATTTC 38

```

Search completed: January 31, 2003, 15:16:30
Job time : 3019.36 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 31, 2003, 10:49:01 ; Search time 241.662 Seconds
(without alignments)
1901.038 Million cell updates/sec

Title: US-09-697-089-2_COPY_762_965
Perfect score: 1046
Sequence: 1 LKMLTKLIMDNKNEBDAL.....GNRYSDDGLAFMGVFENLK 204

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 segs, 1125999159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame_plus_p2n.model -DEV=xlh
-O=/cga2_1/OSPTO.spool/US09697089/runtat_29012003_092753_19709/app_query.fasta_1.981
-DB=N_Geneseq.101002 -QFWT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum2 -TRANS=human40.cdi
-LIST=45 -LOCALALIGN=200 -THR SCORE=Pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09697089_ECGN1.1_276_etunat_29012003_092753_19709 -ICPU=6 -ICPU=3
-NO_XLPHY -NO_MMAR -LARGESUBSTRY -NEG_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N_Geneseq.101002: *
1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT: *
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT: *
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT: *
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT: *
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT: *
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT: *
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT: *
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT: *
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT: *
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT: *
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT: *
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT: *
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT: *
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT: *
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT: *
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT: *
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT: *
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT: *
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT: *
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT: *
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT: *
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001a.DAT: *
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001b.DAT: *
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1046	100.0	618	24	ABK22767	Human cDNA encodin
2	1046	100.0	1395	24	ABK22732	Human cDNA encodin
3	1046	100.0	2950	22	AAH309581	Human protein enco
4	1046	100.0	3133	22	AAH303945	Human caspase recr
5	1046	100.0	3213	22	AAH78219	Nucleotide sequenc
6	1046	100.0	3396	24	ABK22731	Human cDNA encodin
7	1046	100.0	3545	22	AAH98254	Murine EST-derived
8	1046	100.0	3615	22	AAH30946	Human caspase recr
9	626	59.8	2735	22	AAH34171	Human colon cancer
10	202	19.3	421	22	ABA45612	Human breast cell
11	202	19.3	421	22	ABA56119	Human foetal liver
12	202	19.3	421	22	ABA25770	Probe #4236 for ge
13	202	19.3	421	22	AAK04305	Human brain expres
14	202	19.3	421	22	AAK29801	Human bone marrow
15	202	19.3	421	22	AAI14389	Probe #4322 for ge
16	202	19.3	421	22	AAI35764	Probe #4450 used t
17	202	19.3	421	22	AAI04213	Probe #4204 used t
18	202	19.3	421	24	ABSO4362	Human genome-deriv
19	147.5	14.1	3447	23	ABK48611	Mouse MATR cDNA.
20	124.5	11.9	2748	23	ABLI0007	Drosophila melanog
21	122.5	11.7	4926	23	ABLI0006	Drosophila melanog
22	121.5	11.6	3069	24	ALA47134	Pyrim domain conta
23	121	11.6	7324	23	ABLO9367	Drosophila melanog
24	121	11.6	7324	23	ABLO9366	Drosophila melanog
25	120	11.5	2846	24	ABNS9870	Novel human coding
26	120	11.5	2846	24	AAH24250	Human Ras-binding
27	120	11.5	2847	22	AAH17735	Human cDNA sequenc
28	119.5	11.4	3525	20	AAH31788	Porphorymonas ging
29	119.5	11.4	3696	20	AAH31787	Porphorymonas ging
30	119.5	11.4	3798	20	AAH31786	Porphorymonas ging
31	119.5	11.4	3807	20	AAH31785	Porphorymonas ging
32	118	11.3	1386	19	AAV18082	Human liver ribonm
33	118	11.3	1426	17	AAH33115	Human placental r1
34	118	11.3	1614	11	AAH77394	Human placental r1
35	118	11.3	1698	9	AAH81083	Encodes human plac
36	116.5	11.1	2479	20	AAH52219	Protein PRO265 CDN
37	116.5	11.1	2479	22	AAH21418	Human cDNA sequenc
38	116.5	11.1	2479	22	AAH87044	Nucleotide sequenc
39	116.5	11.1	2479	22	AAH72377	Human PRO265 cDNA.
40	116.5	11.1	2479	24	ABL95383	Human angiogenesis
41	116.5	11.1	2479	24	ABL88094	Human PRO265 cDNA
42	116.5	11.1	2545	22	AAH36059	Human cardiovascular
43	116.5	11.1	2545	22	AAH33458	DNA encoding human
44	115	11.0	220	22	ABA50734	Human breast cell
45	115	11.0	220	22	ABA68704	Human foetal liver

ALIGNMENTS

RESULT 1
ABK22767
ID ABK22767 standard; cDNA: 618 BP.
XX
AC ABK22767;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human cDNA encoding CLAN LRR.
KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
KW autoimmune disease; inflammation; keratinocyte hyperplasia;
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
KW balloon angioplasty; stenosis; glioma; carcinoma; sarcoma; melanoma;
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;
KW Crohn's disease; graft-versus-host disease; stroke;
KW myocardial infarction; heart failure; neurodegenerative disease;

KW Parkinson's disease; Alzheimer's disease; HIV;
 KW human immunodeficiency virus infection.
 OS Homo sapiens.
 XX MO200190156-A2.
 XX 29-NOV-2001.
 XX 24-MAY-2001; 2001WO-US17158.
 XX 24-MAY-2000; 2000US-0579240.
 PR 10-OCT-2000; 2000US-0686347.
 PR 14-MAR-2001; 2001US-275980P.
 PR 23-MAY-2001; 2001US-0864921.
 XX (BURN-) BURHAM INST.
 XX Reed JC, Plo FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
 PI Oliveira VAM, Hayashi H, Pawlowski K;
 XX WPI: 2002-083086/11.
 DR P-PSDB; AAU80873.
 XX New caspase recruitment domain (CARD)-containing polypeptides and
 PT encoding nucleic acids, useful for treating abnormal cell proliferation
 PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
 PT arthritis or stroke -
 XX Claim 1; Page 202-203; 216pp; English.
 PS The invention relates to an isolated caspase recruitment domain (CARD)
 CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
 CC from it, and the polynucleotides encoding them. Also included are a
 CC recombinant vector comprising the polynucleotide, recombinant cells
 CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
 CC and insect cells) and an anti-CARD antibody. The CARD-containing
 CC polypeptide and CARD-encoding nucleic acid are useful for treating a
 CC pathology characterised by abnormal cell proliferation (e.g. cancer),
 CC abnormal cell death (apoptosis), autoimmune diseases or inflammation.
 CC Particular, the polypeptide and nucleic acid are useful for treating
 CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
 CC muscle cell proliferation in arteries following balloon angioplasty
 CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,
 CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
 CC graft-versus-host disease, stroke, myocardial infarction, heart failure,
 CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
 CC disease) or immunodeficiency associated disease (e.g. human
 CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
 CC in a variety of diagnostic applications. The present sequence is a
 CC cDNA encoding a CARD domain containing protein.
 XX Sequence 618 BP; 194 A; 113 C; 148 G; 163 T; 0 other:
 Alignment Scores:
 Pred. No.: 1,09e-106 Length: 618
 Score: 1046.00 Matches: 204
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0
 US-09-697-089-2_COPY_762_965 (1-204) x ABR22767 (1-618)
 QY 1 LeuysAsnLeuThrLysLeuIleMerAspAsnIleLysMeLanGluAspAlaIle 20
 DB 7 TTGAAGAAGCTTACAAAGCTCATATGATACATAAAGATGAAGAAGATGCTATA 66
 QY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40
 DB 67 AACTAGAGCTGAAGGCTGAAAAACCTGAGAAAGATGCTTTATTTCATTGACCACTTG 126
 QY 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60

DB 127 TCTACACATTGGAGAGGGAATGATACATAGTCAAGCTCTGTCAAGTGAACCTGTGAC 186
 QY 61 LeuGluGluIleGlyLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80
 DB 187 CTGGAAGAAATTCATTAGTCTCTGCTGCTGTCTCCAAATGCAAGAAATCTTAGCT 246
 QY 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100
 DB 247 CAGAAATCTTCACATTTTGGTCAAACTGACATCTTGTATTATACGAAATTTACTGGAA 306
 QY 101 LysAspGlyAsnGluAlaLeuHisGlyLeuIleAspArgMetAsnValLeuGluGlnLeu 120
 DB 307 AAAGATGGAATGAAAGCTCTTCATGAACCTGATCCACAGATGAACCGCTAGAAACAGCTC 366
 QY 121 ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLys 140
 DB 367 ACCGCACTGATGCTGCGCTGGGCTGTGACGTGCACAGCCAGCTGACCACTGTTTAAA 426
 QY 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160
 DB 427 CATTGGAGGAGGTCCCAACACCTGCAAGCTTGCTGAAAACTGGAGACTCAGAGAT 486
 QY 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln 180
 DB 487 ACAGAGATTGAATTTAGTGCAATTTTGGAAAAAGAACCTTGAAAACTTCACAGAG 546
 QY 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspLysTyrIleuAlaPheMetGlyValPhe 200
 DB 547 TTGAATTTGGCGGGAATTCGTGTGACGATGATGATGATGGCTTGCCTTCATGGGTATTT 606
 QY 201 GluAsnLeuLys 204
 DB 607 GAGAAATCTTAAAG 618
 RESULT 2
 ABR22732
 ID ABR22732 standard; cDNA; 1395 BP.
 AC ABR22732;
 XX 26-MAR-2002 (first entry)
 DT Human cDNA encoding CIAN B.
 DE Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
 KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
 KW autoimmune disease; inflammation; keratinocyte hyperplasia;
 KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
 KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
 KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;
 KW Crohn's disease; graft-versus-host disease; stroke;
 KW myocardial infarction; heart failure; neurodegenerative disease;
 KW Parkinson's disease; Alzheimer's disease; HIV;
 KW human immunodeficiency virus infection.
 KW Homo sapiens.
 OS MO200190156-A2.
 XX 29-NOV-2001.
 XX 24-MAY-2001; 2001WO-US17158.
 XX 24-MAY-2000; 2000US-0579240.
 PR 10-OCT-2000; 2000US-0686347.
 PR 14-MAR-2001; 2001US-275980P.
 PR 23-MAY-2001; 2001US-0864921.
 XX (BURN-) BURHAM INST.
 XX Reed JC, Plo FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
 PI Oliveira VAM, Hayashi H, Pawlowski K;


```
XX WPI: 2002-083086/11.
DR P-PSDB: AAU80862.
XX
PT New caspase recruitment domain (CARD)-containing polypeptides and
PT encoding nucleic acids, useful for treating abnormal cell proliferation
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
PT arthritis or stroke
XX
PS Claim 1; Page 174-176; 216pp; English.
XX
CC The invention relates to an isolated caspase recruitment domain (CARD)
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, IRR or SAM domain
CC from it, and the polynucleotides encoding them. Also included are a
CC recombinant vector comprising the polynucleotide, recombinant cells
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
CC and insect cells) and an anti-CARD antibody. The CARD-containing
CC polypeptide and CARD-encoding nucleic acid are useful for treating a
CC pathology characterised by abnormal cell proliferation (e.g. cancer),
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In
CC particular, the polypeptide and nucleic acid are useful for treating
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
CC muscle cell proliferation in arteries following balloon angioplasty
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
CC disease) or immunodeficiency associated disease (e.g. human
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
CC in a variety of diagnostic applications. The present sequence is a
CC cDNA encoding a CARD domain containing protein.
XX
SQ Sequence 1395 BP; 436 A; 248 C; 327 G; 384 T; 0 other:
Alignment Scores:
Pred. No.: 3.28e-106 Length: 1395
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-697-089-2_COPY_762_965 (1-204) x ABR22732 (1-1395)
QY 1 LeuysaenleuThryleuilemetaspnnlelysmetAsnGlunAspAlaIle 20
DB 565 TTGAAGAACTTACAAACCTCATATAGATGAATGAAGAAAGAAATGCTATTA 624
QY 21 LysleuAlaGlugLyLeuLyAsnleuLySlysmetCysLeuPheHisleuThriSleu 40
DB 625 AAACAGCTGAAGGCGCTGAAAAACCTGAAGAAGATGTTTATTCATTGACCCACTTG 684
QY 41 SeraspIleGlyGluGlyMetaspTyrIleVallySerleuSerSerGluProCysasp 60
DB 685 TCTGACATGAGAGGGAATGATACATAGCAAGCTCTGCTCAAGTGAACCCCTGTGAC 744
QY 61 LeuGlugluIleGlnleuValSerCysCysleuSerAlaAsnAlaVallySleuAla 80
DB 745 CTGGAAGAAATTCATATAGTCTCCGCTGCTGTCTGCAAAATGACGTGAATAATCCTACT 804
QY 81 GlnAsnleuHisAsnleuVallySleuSerIleLeuAspLeuSerGlnAsnTyrleuGlu 100
DB 805 CAGAAATCTTCAACATTTGGTCAAACTGAGCATTTCTTGATTTATATCGAAATAATGCTGGA 864
QY 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValleuGluGlnleu 120
DB 865 AAAGATGGAATAAGAGCTTCATGCAACTGATCGACAGAGAAAGAGCTGTGAACAGCTC 924
QY 121 ThrAlaIleMetLeuProTyrGlyCysAspValGlnGlySerleuSerSerleuLeuLys 140
DB 925 ACCGACATGATGCTGCTCCCTGGGGCTGTGACGTGCAAGGCAAGCCTGTGTGAAA 984
QY 141 HisleuGluGluValProGlnleuVallySleuGlyLeuLysAsnTyrArgleuThrAsp 160
```

```
DB 985 CATTGGAGAGAGCTCCCAACACTGCTCAAGCTTGGGTGAAAACGAGACTCACAGAT 1044
QY 161 ThrGluIleArgIleleuGlyAlaPhePheGlyLysAsnProleuLysAsnPheGlnGln 180
DB 1045 ACAGAGATTGAAATTTTGGGTGCATTTTGGAAAAGAACCTTGAAAAAATCTCCAGCAG 1104
QY 181 LeuAsnleuAlaGlyAsnArgValSerSerAspGlyTyrPleuAlaPheMetGlyValPhe 200
DB 1105 TTGAATTTGGCGGGAATTCGTGTGAGCACTGATGATGCTGCTTCATGGGTGATATT 1164
QY 201 GlnAsnleuLys 204
DB 1165 GAGAAATCTTAAG 1176
RESULT 3
AAH99581
ID AAH99581 standard; cDNA; 2950 BP.
XX
AC AAH99581;
XX
DE 16-OCT-2001 (first entry)
XX
XX Human protein encoding cDNA sequence SEQ ID NO:416.
KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
KW antibacterial; endocrine; cardiant; central nervous system; vitruode;
KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
KW antiagregant; haemostatic; vulnerary; antulcer; osteopathic; eczema;
KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
KW antiaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
KW cardiac dysfunction; neuropathology; cardiac anapylaxis; autoimmunity;
KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
KW thrombocytopenia; osteoporosis; severe combined immunodeficiency;
KW allergic rhinitis; diabetes; multiple sclerosis; depression;
KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
KW neurological disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200153455-A2.
XX
PD 26-JUL-2001.
XX
XX 22-DEC-2000; 2000WO-US35017.
XX
PR 23-DEC-1999; 99US-0471275.
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
XX
XX (HXSE-) HXSEQ INC.
PA
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI: 2001-457603/49.
DR P-PSDB: AAM25640.
XX
XX Isolated human polynucleotides encoding polypeptides, useful for the
XX treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
PS Claim 1; Page 511-512; 1217pp; English.
XX
XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
XX AA25963. The proteins can have activities based on the tissues and
XX cells they are expressed in, such as: antiinflammatory; antirheumatic;
XX antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
XX central nervous system; vitruode; anti-HIV; fungicide; antimutagen;
XX cardiovascular; antianaemic; antiagregant; haemostatic; vulnerary;
XX antulcer; osteopathic; dermatological; antiallergic; antiasthmatic;
XX antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
```

CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
CC encoding them can be used in gene therapy, antisense therapy and vaccine
CC production. The proteins and polynucleotides are useful for screening for
CC agonists or antagonists of a protein and for the treatment and diagnosis of
CC disorders associated with the activity of a protein e.g. inflammation,
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
CC osteoporosis, severe combined immunodeficiency, eczema, allergic
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
CC neurological disorders.

XX Sequence 2950 BP; 915 A; 592 C; 628 G; 815 T; 0 other;

Alignment Scores:
Pred. No.: 9.04e-106 Length: 2950
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-697-089-2_COPY_762_965 (1-204) x AAH99581 (1-2950)

QY 1 LeuysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIle 20
Db 1139 TTGAAGAAGCCTTACAAACCTCATATGATGATACATAAAGATGAAAGATGATCTTATA 1198
QY 21 LysIleuAlaGluGluLysLeuLysAsnLysLysMetCysLeuPheHisLeuThrHisLeu 40
Db 1199 AAACGTAGCTGAAGGCTGAAACCTGAAAGATGATGATGATGATGATGATGATGATG 1258
QY 41 SerAspIleGluGluGluMetAspPyrIleValLysSerLysSerSerGluAsnProCysAsp 60
Db 1259 TCTGCATTTGAGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1318
QY 61 LeuGluGluIleGluLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80
Db 1319 CTTGAGAGAAATTCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1378
QY 81 GluAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100
Db 1379 CAGAAATCTTCACAAATTTGCTCAAACTGAGACATTTCTGATTTATCAGAAAATTACCTG 1438
QY 101 LysAspGlyAsnGluAlaIleLeuHisGluLeuIleAspArgMetAsnValLeuGluGlu 120
Db 1439 AAAGATGGAAATGAAAGCTCTTCATGATGATGATGATGATGATGATGATGATGATG 1498
QY 121 ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140
Db 1499 ACCGACACTGATGCTCCCTCGGGGCTGTACGTGCAAGGACAGCTTACAGACCTGTTGAAA 1558
QY 141 HisLeuGluGluValProGlnLeuValLysLeuGluLysLeuLysAsnTyrPargLeuThrAsp 160
Db 1559 CATTGGAGGAGGCTCCACCACTGCTCAAGCTGGGTTGAAAACCTGAGACTCAGACT 1618
QY 161 ThrGluIleArgIleLeuGluGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln 180
Db 1619 ACAGAGATTAAGAAATTTTGGGTCATTTTGGAAAAGAACCTCTGAAAACCTTCAGACAG 1678
QY 181 LeuAsnLeuAlaGlyLysAsnArgValSerSerAspGlyTyrPheAlaPheMetGlyValPhe 200
Db 1679 TTGAATTTGGGGGGAATCGTGTGAGCAGTGTGATGCTTGCCTTCATGGGTATATTT 1738
QY 201 GluAsnLeuLys 204
Db 1739 GAGAAATCTTAAG 1750

RESULT 4
AAS03945
ID AAS03945 standard; cDNA; 3133 BP.

XX AAS03945;
XX 12-SEP-2001 (first entry)
XX Human caspase recruitment domain 12 (CARD-12) cDNA.

Caspase recruitment domain: CARD-12; apoptosis; stress-related pathway;
cancer; viral infection; poxvirus; adenovirus; autoimmune disorder;
systemic lupus erythematosus; arthritis; neurological disorder; stroke;
Alzheimer's disease; amyotrophic lateral sclerosis; haematologic disease;
aplastic anaemia; myocardial infarction; inflammatory disorder;
Crohn's disease; insulin-dependent diabetes; contact dermatitis;
psoriasis; graft rejection; bacterial infection; lepromatous leprosy;
tuberculosis; ischemic brain injury; hypoxic brain injury; ss;
kidney ischaemia; reperfusion injury; acute bacterial meningitis;
excitotoxic brain damage; liver disease.

XX Homo sapiens.

Key Location/Qualifiers
CDS 36..3110
/tag= a
/product= "Human CARD-12"

XX MO200130971-A2.

XX 03-MAY-2001.

XX 26-OCT-2000; 2000WO-US29643.

XX 27-OCT-1999; 99US-0161822.

XX (MILL-) MILLENNIUM PHARM INC.

XX Bertin J, Robison KE;

XX WPI; 2001-308628/32.

XX P-PSDB; AAU02880.

XX Isolated caspase recruitment domain-12 polypeptide and nucleic acids
XX encoding them, useful for treating and diagnosing disorders associated
XX with abnormal apoptosis such as cancer, arthritis and Alzheimer's
XX disease -

XX Claim 2; Fig 1; 93pp; English.

XX The sequence represents a cDNA which encodes the human caspase
XX recruitment domain 12 (CARD-12) polypeptide. CARD domains are found in a
XX number of proteins that transmit signals that activate apoptosis and
XX inflammatory pathways in response to stress and other stimuli. Therefore,
XX CARD-12 and its corresponding nucleic acid may be used in treatment and
XX diagnosis of patients suffering from disorders associated with an
XX abnormal level (an increase or a decrease) of apoptotic cell death or
XX abnormal activity of stress-related pathways. The disorders include
XX cancer, viral infections (e.g. caused by poxviruses, adenoviruses),
XX autoimmune disorders (e.g. systemic lupus erythematosus, arthritis),
XX neurological disorders (e.g. Alzheimer's disease, amyotrophic lateral
XX sclerosis), haematologic diseases (e.g. aplastic anaemia, myocardial
XX infarction, stroke), inflammatory and immune system disorders (e.g.
XX Crohn's disease, insulin-dependent diabetes, contact dermatitis,
XX psoriasis, graft rejection), bacterial infections (e.g. tuberculosis,
XX lepromatous leprosy), ischemic and hypoxic brain injury, kidney
XX ischaemia/reperfusion injury, excitotoxic brain damage, acute bacterial
XX meningitis and liver disease.

XX Sequence 3133 BP; 903 A; 691 C; 729 G; 810 T; 0 other;

Alignment Scores:
Pred. No.: 9.81e-106 Length: 3133
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0
US-09-697-089-2_COPY_762_965 (1-204) x AAS03945 (1-3133)

QY 1 LeuLysAsnLeuThrIleuLysLeuIleMetAspAsnIleLysMetAsnGluLysAlaIle 20
DB 2319 TTGAAGAACCCTTACAAACCTCATATGATTAACATAAAGATGAAGATGATCTCTATA 2378
QY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40
DB 2379 AAACCTAGCTGAAGGCCCTGAAAAACCTGAAGAAGATGCTTTATTTCAATTGACCCACTTG 2438
QY 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLysSerSerGluProCysAsp 60
DB 2439 TCTGACATTTGAGAGGAGGAAATGATTAATCAAGTCTCTGTCAGTGAACCTGTGAC 2498
QY 61 LeuGluGluIleGluIleuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80
DB 2499 CTTGAAGAATTTCAATTTAGTCTCCGTGCTGCTGCAAAATGCAAGTGAATCTTACT 2558
QY 81 GluAsnLeuHisAsnLeuValLysLeuSerIleLeuAsnLeuSerGluAsnTyrLeuGlu 100
DB 2559 CAGATCTTCAACAATTTGGTCAAACTGAGCATCTTGATTTATCAGAAATTAACCTGGAA 2618
QY 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGluIleu 120
DB 2619 AAAGTGAAGAAATGAGCTCTTCAATGAACTGATCGACAGAGATGAGCTGTGAACAGCTC 2678
QY 121 ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140
DB 2679 ACCGACATGATGCTCCCTCGGGGCTGTGACGTCGCAAGCAGCCTGAGACGCTGTGAA 2738
QY 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160
DB 2739 CATTTGGGAGGCTCCCAACCTGCTCAAGCTTGGGTGAAAAAACTGGAGACTCCAAAT 2798
QY 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGlu 180
DB 2799 ACAGGATTTAATAATTTTGGTGCATTTTGGAAAGAACCTCTGAAAAAACTCCAGCAG 2858
QY 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPheAlaPheMetGlyAlaPhe 200
DB 2859 TTGATTTGGGCGGAAATCGTGTGAGCAGTATGATGCTTGGCTTCATGGGTATTT 2918
QY 201 GluAsnLeuLys 204
DB 2919 GAGAACTTTAAG 2930

RESULT 5
AAH78219
ID AAH78219 standard; DNA: 3213 BP.

XX AC AAH78219;

XX XX 26-NOV-2001 (first entry)

DE Nucleotide sequence of a human secreted polypeptide.

XX Human; secreted polypeptide; nervous disease; muscular disease; tumour;
KW gastrointestinal ulceration; spinal cord disease; trachea disease;
KW thyroid gland disease; ovary disease; prostate disease; heart disease;
KW renal gland disease; small intestine disease; thymus disease;
KW lymph node disease; muscular system disease; colon disease;
KW lipase deficiency; cystic fibrosis; pancreatitis; clot formation;
KW myocardial infarction; angiodysplasia; liver disease; coagulation disorder;
KW microbial disease; immune disorder; inflammation; transplant rejection;
KW bone thickness; bone density; ferroxidase loss; apoptosis;
KW vascular smooth cell proliferation; vaccine; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..3213
FT /tag= a
FT /product= "secreted polypeptide"

PN WO200166690-A2.

PD 13-SEP-2001.

PP 05-MAR-2001; 2001WO-US07143.

PR 06-MAR-2000; 2000US-0187107.

PR 13-MAR-2000; 2000US-0188916.

PR 03-OCT-2000; 2000US-0236874.

PR 03-OCT-2000; 2000US-0237846.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;

DR WPI: 2001-570768/64.

DR P-PSDB; AAG67527.

PT Novel isolated secreted polypeptide useful for treating nervous and

PT muscular diseases, gastrointestinal ulceration, coagulation and immune

PT disorders, microbial diseases, inflammation and transplant rejection -

PS Claim 2; Page 53-54; 102pp; English.

XX The present sequence encodes a human secreted polypeptide. The
CC secreted polypeptides and polynucleotides are useful for treating
CC nervous and muscular diseases, for inhibiting tumour formation and
CC metastasis, for treating gastrointestinal ulceration, for preventing
CC and treating diseases in spinal cord, thyroid gland, ovary, prostate,
CC renal gland, small intestine, heart, trachea, thymus, lymph node,
CC muscular system and colon, for treating lipase deficiency in cystic
CC fibrosis and pancreatitis, for treating undesirable clot formation
CC such as myocardial infarction, during angioplasty and all surgical
CC procedures that require decreased blood clot formation, for treating
CC liver diseases, coagulation disorders and microbial diseases, for
CC treating immune disorders, for treating inflammation and transplant
CC rejection, for enhancing bone thickness and increasing bone density,
CC for reducing the loss of essential ferroxidases, for suppressing
CC apoptosis, and for regulating vascular smooth cell proliferation. They
CC may also be used as vaccines.

XX Sequence 3213 BP, 916 A; 704 C; 756 G; 837 T; 0 other:

Alignment Scores:

Pred. NO.: 1.01e-105 Length: 3213
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 22 Gaps: 0

US-09-697-089-2_COPY_762_965 (1-204) x AAH78219 (1-3213)

QY 1 LeuLysAsnLeuThrIleuLysLeuIleMetAspAsnIleLysMetAsnGluLysAlaIle 20

DB 2422 TTGAAGAACCCTTACAAACCTCATATGATTAACATAAAGATGAAGAAGATCTCTATA 2481

QY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40

DB 2482 AAACCTAGCTGAAGGCCCTGAAAAACCTGAAGAAGATGCTTTATTTCAATTGACCCACTTG 2541

QY 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLysSerSerGluProCysAsp 60

DB 2542 TCTGACATTTGAGAGGAGGAAATGATTAATCAAGTCTCTGTCAGTGAAGAACCTGTGAC 2601

QY 61 LeuGluGluIleGluIleuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80

DB 2602 CTTGAAGAATTTCAATTTAGTCTCCGTGCTGCTTGTGCAAAATGCAAGTGAATCTTACT 2661

QY 81 GlnAsnLeuH1sAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100
Db 2662 CAGATCTTCACAAATTTGGTCAAACTGAGCATTTCTGATTATCATGAAATTAACCTGGAA 2721
QY 101 LysAspGlyAsnGluAlaLeuH1sGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120
Db 2722 AAAAGATGGAATGGAAGCTCTTCATGAACTGATCGACAGATGAACGCTCTGAAACAGCTC 2781
QY 121 ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerIleSerSerLeuLeuLys 140
Db 2782 ACCGCACTGATGCTGCTCCCTGGGCTGTGACGTGCAAGGACGCTGAGCAGCTGTGAAA 2841
QY 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160
Db 2842 CATTTGGAGGAGGTCCCAACACTGCTCAAGCTTGGCTTGAAACCTGGAGACTCACAT 2901
QY 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln 180
Db 2902 ACAGAGATTAGAAATTTTGTGTCATTTTGTGAAAGAACCTCTGAAACCTCCACAG 2961
QY 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPheAlaPheMetGlyValPhe 200
Db 2962 TTGAATTTGGCGGGAATCGTGTAGCAGTATGATGATGCTTGCCTTCATGGGTATTT 3021
QY 201 GluAsnLeuLys 204
Db 3022 GAGAACTTTAAG 3033
RESULT 6
ABK22731
ID ABK22731 standard; CDNA; 3396 BP.
XX AC ABK22731:
XX 26-MAR-2002 (first entry)
DT Human CDNA encoding CLAN A.
DE
XX Caspase recruitment domain; CARD; ss: NB-ARC; ANGIO-R; LRR; SAM;
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
KW autoimmune disease; inflammation; keratinocyte hyperplasia;
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
KW leukemia; allergy; arthritis; lupus; Schrodgen's syndrome;
KW Crohn's disease; graft-versus-host disease; stroke;
KW myocardial infarction; heart failure; neurodegenerative disease;
KW Parkinson's disease; Alzheimer's disease; HIV;
KW human immunodeficiency virus infection.
XX Homo sapiens.
OS
XX W0200190156-A2.
PN
XX 29-NOV-2001.
PD
XX 24-MAY-2001: 2001WO-US17158.
PF
XX 24-MAY-2000: 2000US-0579240.
PR 10-OCT-2000: 2000US-0666347.
PR 14-MAR-2001: 2001US-275980P.
PR 23-MAY-2001: 2001US-0864921.
XX
XX (BURN-) BURNHAM INST.
PA
XX Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
PI Oliveira VAM, Hayashi H, Pawlowski K;
XX WPI: 2002-083086/11.
DR P-PSDB; AAU80861.
XX New caspase recruitment domain (CARD)-containing polypeptides and
PT encoding nucleic acids, useful for treating abnormal cell proliferation

PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
XX arthritis or stroke
PS Claim 1; Page 166-171; 216pp; English.
XX
CC The invention relates to an isolated caspase recruitment domain (CARD)
CC containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
CC from it, and the polynucleotides encoding them. Also included are a
CC recombinant vector comprising the polynucleotide, recombinant cells
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
CC and insect cells) and an anti-CARD antibody. The CARD-containing
CC polypeptide and CARD-encoding nucleic acid are useful for treating a
CC pathology characterised by abnormal cell proliferation (e.g. cancer),
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation.
CC In particular, the polypeptide and nucleic acid are useful for treating
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
CC muscle cell proliferation in arteries following balloon angioplasty
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukemias,
CC allergies, arthritis, lupus, Schrodgen's syndrome, Crohn's disease,
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
CC disease) or immunodeficiency associated disease (e.g. human
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
CC in a variety of diagnostic applications. The present sequence is a
CC CDNA encoding a CARD domain containing protein.
XX
SS Sequence 3396 BP; 992 A; 737 C; 793 G; 874 T; 0 other;
SS
Alignment Scores:
Pred. No.: 1,09e-105 Length: 3396
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
B: 24 Gaps: 0
US-09-697-089-2_COPY_762_965 (1-204) x ABK22731 (1-3396)
QY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluAspAlaIle 20
Db 2560 TTGAAGAAGCTTCAACAACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2619
QY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheH1sLeuThrH1sLeu 40
Db 2620 AAACAGCTGGAAGGCTCAAAACCTGGAAGAAGATGTTTATTTCAATTTGACCACCTG 2679
QY 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60
Db 2680 TCTGACATTTGAGAGGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2739
QY 61 LeuGluGluIleGlnLeuValSerCysCysLeuSerIleAsnAlaValLysIleLeuAla 80
Db 2740 CTTGAGAGAAATTCATTTAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2799
QY 81 GlnAsnLeuH1sAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100
Db 2800 CAGATCTTCACAAATTTGGTCAAACTGAGCATTTCTGATTATCATGAAATTAACCTGGAA 2859
QY 101 LysAspGlyAsnGluAlaLeuH1sGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120
Db 2860 AAAAGATGGAATGGAAGCTCTTCATGAACTGATCGACAGATGAACGCTCTGAAACAGCTC 2919
QY 121 ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerIleSerSerLeuLeuLys 140
Db 2920 ACCGCACTGATGCTGCTCCCTGGGCTGTGACGTGCAAGGACGCTGAGCAGCTGTGAAA 2979
QY 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160
Db 2980 CATTTGGAGGAGGTCCCAACACTGCTCAAGCTTGGCTTGAAACCTGGAGACTCACAGAT 3039
QY 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln 180
Db 3040 ACAGAGATTAGAAATTTTGTGTCATTTTGTGAAAGAACCTCTGAAACCTCCACAG 3099

OY 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetClyValAlphe 200
Db 3100 TTGAATTGGGGGAAATCGTGTGACAGTGTGATGGCTTGCCTTCATGGGTATATT 3159
OY 201 GluAsnLeuLys 204
Db 3160 GAGAACTTTAAG 3171
RESULT 7
AAH98254
ID AAH98254 standard; cDNA: 3545 BP.
AC AAH98254;
XX
DT 12-OCT-2001 (first entry)
XX
DE Murine EST-derived coding sequence SEQ ID NO: 111.
XX
XX Human: sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition; ss.
XX
OS Mus musculus.
XX
PN WO200154477-A2.
XX
PD 02-AUG-2001.
XX
PE 25-JAN-2001; 2001WO-US02687.
XX
PR 25-JAN-2000; 2000US-0491404.
PR 17-JUL-2000; 2000US-0617746.
PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663870.
XX
XX
PA (HYSEQ-) HYSEQ INC.
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Dzmanac RA, Zhang J, Werthman T;
XX
DR WPI: 2001-476164/51.
DR P-PSDB: AAM23595.
XX
XX Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
PS
PS Claim 1; Page 250-251; 1275pp; English.
XX
XX The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a cDNA
CC of the invention.
XX
SQ Sequence 3545 BP; 1038 A; 755 C; 816 G; 936 T; 0 other;
Alignment Scores:
Pred. No.: 1.16e-105 Length: 3545
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0
US-09-697-089-2_COPY_762_965 (1-204) x AAH98254 (1-3545)
OY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIle 20
|||||

Db 2515 TTGAAGAACTTACCAAGCTCATATGATTAACATTAAGATGATGAAAGATGCTATA 2574
OY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysMetCysLeuPheHisLeuThrHisLeu 40
Db 2575 AAACATGATGGAAGGCGCTGAAAAAACCCTGAAGAAGATGTGTTTATTCATTGACCCACATGG 2634
OY 41 SerAspIleGlyGlyIleMetAspTyrIleValLysSerLeuSerSerClyProCysAsp 60
Db 2635 TCTGACATTGGAGAGGAATGATTAACATAGTCMAAGTCTCTGTCAAGTCAACCCCTGTGAC 2694
OY 61 LeuGluGluIleGlnLeuValSerCysLeuSerAlaAsnAlaValLysIleLeuAla 80
Db 2695 CTTGAAGAAATTCATTAATAGTCTCTGCTGCTGTCTGCAAAATGACAGTAAATCCTAGCT 2754
OY 81 GluAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerClyAsnTyrIleGlu 100
Db 2755 CAGAACTTTCACAAATTTGGTCAAACTGAGCAATTCCTGATTATTCAGAAAATTAATCCTGGAA 2814
OY 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120
Db 2815 AAAAGATGGAATGAAGACCTTTCATGACTGATCGACAGATGAACGTCTAGAACAGCTC 2874
OY 121 ThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLys 140
Db 2875 ACCGCACTGATGCTGCTGCGGGCTGTGACGTGCAAGGAGCGCTGAGCAGCTGTGAAA 2934
OY 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAsp 160
Db 2935 CATTTGGAGGAGGCTCCCAACACTGCAAGCTTGGGTGAAGAACTGGAGACTCAAGAT 2994
OY 161 ThrGluIleArgIleLeuGlyValAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln 180
Db 2995 ACAGAGATTAGATTTAGATTCATTTTGGAAAAAACCCCTGAAAAAACCCTCCAGCAG 3054
OY 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetClyValAlphe 200
Db 3055 TTGAATTGGCGGAAATCGTGTGAGCAGTGTGATGATGCTGCTTCATGGGTATATT 3114
OY 201 GluAsnLeuLys 204
Db 3115 GAGAACTTTAAG 3126
RESULT 8
AAS03946
ID AAS03946 standard; DNA: 3615 BP.
AC AAS03946;
XX
XX 12-SEP-2001 (first entry)
DT
DT
XX
XX Human caspase recruitment domain 12 (CARD-12) genomic DNA.
DE
XX
XX Caspase recruitment domain; CARD-12; apoptosis; stress-related pathway;
KW cancer; viral infection; poxvirus; adenovirus; autoimmune disorder;
KW systemic lupus erythematosus; arthritis; neurological disorder; stroke;
KW Alzheimer's disease; amyotrophic lateral sclerosis; haematologic disease;
KW aplastic anaemia; myocardial infarction; inflammatory disorder;
KW Crohn's disease; insulin-dependent diabetes; contact dermatitis;
KW psoriasis; graft rejection; bacterial infection; lepromatous leprosy;
KW tuberculosis; ischaemic brain injury; hypoxic brain injury; ds;
KW kidney ischaemia; reperfusion injury; acute bacterial meningitis;
KW excitotoxic brain damage; liver disease.
XX
XX Homo sapiens.
XX
OS
XX
XX Key Location/Qualifiers
FH 1.3615
FH CDS /tag= a
FT /product= "Human CARD-12"
FT
PN WO200130971-A2.
XX
XX 03-MAY-2001.
PD

XX 26-OCR-2000; 2000WO-US29643.
XX
XX 27-OCT-1999; 99US-0161822.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Berlin J, Robison KE;
XX
XX WPI: 2001-308628/32.
XX P-PSDB: AAU02881.
XX
XX Isolated caspase recruitment domain-12 polypeptide and nucleic acids
XX encoding them, useful for treating and diagnosing disorders associated
XX with abnormal apoptosis such as cancer, arthritis and Alzheimer's
XX disease -
XX
XX PS Disclosure; Fig 2; 93pp; English.
XX
XX The sequence represents a genomic DNA which encodes the human caspase
XX recruitment domain 12 (CARD-12) polypeptide. CARD domains are found in a
XX number of proteins that transmit signals that activate apoptosis and
XX inflammatory pathways in response to stress and other stimuli. Therefore,
XX CARD-12 and its corresponding nucleic acid may be used in treatment and
XX diagnosis of patients suffering from disorders associated with an
XX abnormal level (an increase or a decrease) of apoptotic cell death or
XX cancer, viral infections (e.g. caused by poxviruses, adenoviruses),
XX autoimmune disorders (e.g. systemic lupus erythematosus, arthritis),
XX neurological disorders (e.g. Alzheimer's disease, amyotrophic lateral
XX sclerosis), hematologic diseases (e.g. aplastic anaemia, myocardial
XX infarction, stroke), inflammatory and immune system disorders (e.g.
XX Crohn's disease, insulin-dependent diabetes, contact dermatitis,
XX psoriasis, graft rejection), bacterial infections (e.g. tuberculosis,
XX lepromatous leprosy), ischemic and hypoxic brain injury, kidney
XX ischemia/reperfusion injury, excitotoxic brain damage, acute bacterial
XX meningitis and liver disease.
XX
XX SQ Sequence 3615 BP; 1041 A; 811 C; 845 G; 918 T; 0 other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 1 19e-105 Length: 3615
XX Score: 1046.00 Matches: 204
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 22 Gaps: 0
XX
XX US-09-697-089-2_COPY_762_965 (1-204) x AAS03946 (1-3615)
XX
XX QY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluAspAlaIle 20
XX |||||||
XX Db 2755 TTGAAGAAGACCTTACAAACCTCATATGATTAACATAAGAGATGAGAAAGATCTCTATA 2814
XX |||||||
XX QY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40
XX |||||||
XX Db 2815 AAAGTAAAGTGAAGGCGCTGAAAAACCTGAAGAGATGTTTATTCATTGACCCACTG 2874
XX |||||||
XX QY 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60
XX |||||||
XX Db 2875 TCTGACATGTGAGAGCGAATGATTACATCAAGTCTCTGTCAGGAACCCCTGTAC 2934
XX |||||||
XX QY 61 LeuGluGluIleGlnLeuValSerCysLysLeuSerAlaAsnAlaValLysIleLeuAla 80
XX |||||||
XX Db 2935 CTTGAAGAATAATTCATTAGTCTCTGCTGCTTGTCTGCAATGAGTGAAATCTTACT 2994
XX |||||||
XX QY 81 GluAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrIleGlu 100
XX |||||||
XX Db 2995 CAGAAATCTTCACAAATTTGGTCAAACTGAGCATTTCTTGATTATATCGAAAAATTAACCTG 3054
XX |||||||
XX QY 101 LysAspGlyAsnGluAlaLeuHisGluLeuLeuLysAspGlyMetAsnValLeuGluGlnLeu 120
XX |||||||
XX Db 3055 AAAAGTGAATGAAGAGCTTCTCATGAACTGATCGACAGAGATGAACGTCCTGAAACAGCTC 3114
XX |||||||

QY 121 ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLys 140
XX |||||||
XX Db 3115 ACCGACATGATGCTGCCCTGGGGCTGTGACGTGCAAGGACACCTGAGAGAGCTTTGAAA 3174
XX |||||||
XX QY 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrPArgLeuThrAsp 160
XX |||||||
XX Db 3175 CATTTGGAGGAGGCTCCCAACATCGTCAAGCTTGCTGGTGAATAAAGCTGAGCTCAGAT 3234
XX |||||||
XX QY 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln 180
XX |||||||
XX Db 3235 ACAGAGATTAGAAATTTTGGTGCATTTTGGAAAGAACCTCTGAAATACTCCAGCAG 3294
XX |||||||
XX QY 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrLeuAlaPheMetGlyValPhe 200
XX |||||||
XX Db 3295 TTGAATTTGGCGGGAATACGTCGTGACGACGATGATGATGCTTGCTTCATGCGTATTT 3354
XX |||||||
XX QY 201 GluAsnLeuLys 204
XX |||||||
XX Db 3355 GAGAAATCTTAAG 3366
XX |||||||
XX
XX RESULT 9
XX ID AAH34171/c
XX AAH34171 standard; cDNA; 2735 BP.
XX
XX AAH34171:
XX AC
XX 03-SEP-2001 (first entry)
XX
XX DE Human colon cancer antigen encoding cDNA SEQ ID NO:1253.
XX
XX KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
XX KW colorectal carcinoma; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200122920-A2.
XX
XX PD 05-APR-2001.
XX
XX PF 28-SEP-2000; 2000WO-US26524.
XX
XX PR 29-SEP-1999; 99US-0157137.
XX PR 03-NOV-1999; 99US-0163280.
XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
XX DR WPI: 2001-235357/24.
XX DR P-PSDB: AAG74766.
XX
XX PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX useful for preventing, diagnosing and/or treating colorectal cancers -
XX
XX PS Claim 1; Page 3017; 9803pp; English.
XX
XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
XX cancer-associated nucleic acid molecules (N) and proteins (P), where
XX the proteins are collectively known as colon cancer antigens. The colon
XX cancer antigens have cytostatic activity and can be used in gene
XX therapy and vaccine production. N and P may be used in the prevention,
XX diagnosis and treatment of diseases associated with inappropriate P
XX expression. For example, N and P may be used to treat disorders
XX associated with decreased expression by rectifying mutations or deletions
XX in a patient's genome that affect the activity of P by expressing
XX inactive proteins or to supplement the patients own production of P.
XX Additionally, N may be used to produce the colon cancer-associated Ps,
XX by inserting the nucleic acids into a host cell and culturing the cell
XX to express the proteins. N and P can be used in the prevention, diagnosis
XX and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
XX and AAB77789 represent sequences used in the exemplification of the
XX present invention.

CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
missing at time of publication, meaning no sequences are present for
CC SEQ ID NO:1027 to 1052, 7921 and 7922.

XX SQ Sequence 2735 BP; 791 A; 555 C; 512 G; 876 T; 1 other;

Alignment Scores:

Pred. No.:	3,03e-59	Length:	2735
Score:	626.00	Matches:	121
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	59.85%	Indels:	0
DB:	22	Gaps:	0

US-09-697-089-2_COPY_762_965 (1-204) x AAB34171 (1-2735)

OY 84 HisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGluLysAspGly 103

DB 2727 CACAATTGTCGCAACGTGAGCATCTTGATTTATCAGAAATTTACTGTGAAAAAGATGGA 2668

OY 104 AsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThrAlaLeu 123

DB 2667 AATGAAGCTCTTCATGACATGATCGACAGATGAACGTGCTGAAACAGCTCCGACATG 2608

OY 124 MetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLeuLysHisLeuGlu 143

DB 2607 ATGCTGCTCGGCGCTGTACGTGCAAGCAGCAGCTGTAGAGCTTGTTGAAACATTTGGAG 2548

OY 144 GluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAspThrGluLe 163

DB 2547 GAGGTCCCAACAGCTGCTCAAGCTGGGTGAAAACTGAGACTCAGATACAGAGATT 2488

OY 164 ArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLeu 183

DB 2487 ACAAATTTTGGTCATTTTGGAAAGAACCTCTGAAAACTTCCAGCAGTTGAATTGG 2428

OY 184 AlaGlyAsnArgValSerSerAspGlyTyrPheAlaPheMetGlyValPheGluAsnLeu 203

DB 2427 GCGGGAATCGTGTGAGCAGTGTGATGATGCTTGCCTTATGGGTATTGGAATCTT 2368

OY 204 Lys 204

DB 2367 AAG 2365

RESULT 10

ABA45612 ID ABA45612 standard; DNA; 421 BP.

XX ABA45612;

XX 01-FEB-2002 (first entry)

DE Human breast cell single exon nucleic acid probe #4307.

XX Human: microarray; single exon probe; gene expression; breast;

KW disease; cancer; ss.

XX Homo sapiens.

XX WO200157271-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00662.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0236359.

PA (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-496933/54.

PT New spatially-addressable set of single exon nucleic acid probes,
useful for measuring gene expression in sample derived from human
breast, comprises number of single exon nucleic acid probes -

PS Claim 1; SEQ ID NO 4307; 327pp + sequence listing; English.

CC The invention relates to a spatially-addressable set of single exon
nucleic acid probes for measuring gene expression in a sample derived
from human breast and BR 474 cells. The method involves contacting
CC the probes with a collection of detectably labelled nucleic acids
CC derived from mRNA of human breast, and then measuring the label
CC bound to each probe of the microarray. The probes are useful for
CC verifying the expression of regions of genomic DNA predicted to
CC encode proteins. They are useful for gene discovery, and for
CC determining predisposition and/or prognosing breast disease. Gene
CC expression analysis is useful for assessing the toxicity of chemical
CC agents on cells. The microarray of this invention presents a far greater
CC diversity of probes for measuring gene expression, with far less bias
CC than expressed sequence tag microarrays. The method is suitable for
CC rapid production of functional information from genomic sequence. The
CC present sequence is a single exon nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 421 BP; 126 A; 69 C; 77 G; 149 T; 0 other;

Alignment Scores:

Pred. No.:	2.49e-13	Length:	421
Score:	202.00	Matches:	38
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	19.31%	Indels:	0
DB:	22	Gaps:	0

US-09-697-089-2_COPY_762_965 (1-204) x ABA45612 (1-421)

OY 167 GlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnAlaGlyAsn 186

DB 181 GGTGCAATTTTGGAAAGAACCTCTGAAAACTTCCAGCAGTTGAATTGGCGGGAAT 240

OY 187 ArgValSerSerAspGlyTyrPheAlaPheMetGlyValPheGluAsnLeuLys 204

DB 241 CGTGTGACAGATGATGATGCTTGCCTTCAATGGGTATTGGAATCTTAAAG 294

RESULT 11

ABA56119 ID ABA56119 standard; DNA; 421 BP.

XX ABA56119;

XX 01-FEB-2002 (first entry)

DE Human foetal liver single exon nucleic acid probe #4424.

XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

XX Homo sapiens.

XX WO200157277-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00669.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-063366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0234687.
PR 04-OCT-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483447/52.
XX
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human fetal liver -
XX
XX Claim 1: SEQ ID NO 4424; 639pp + sequence listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for
XX measuring human gene expression in a sample derived from human foetal
XX liver. The single exon nucleic acid probes may be used for predicting,
XX measuring and displaying gene expression in samples derived from human
XX fetal liver. The present sequence is a single exon nucleic acid
XX probe of the invention.
XX Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
XX
XX Sequence 421 BP; 126 A; 69 C; 77 G; 149 T; 0 other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 2,49e-13 Length: 421
XX Score: 202.00 Matches: 38
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 19.31% Indels: 0
XX DB: 22 Gaps: 0
XX
XX US-09-697-089-2_COPY_762_965 (1-204) x ABA56119 (1-421)
XX
QY 167 GtAlaPhePheGlyLysAsnProLeuLysAsnPhenGlnGlnLeuAsnLeuAlaGlyAsn 186
DB 181 GGTGATTTTTTGGAAAGAACCTCTGAAACCTTCACAGCTTGAATTTGGCGGAAT 240
QY 187 ArgValSerSerAspGlyTyrPheAlaPheMetGlyValPheGluAsnLeuLys 204
DB 241 CGTGGAGCAGATGATGATGCTTCCTTCATGGGTATTTGAGAACTTTAAG 294
XX
XX RESULT 12
XX ABA25770
XX ID ABA25770 standard; DNA; 421 BP.
XX
XX ABA25770;
XX
XX 23-JAN-2002 (first entry)
XX
XX Probe #4236 for gene expression analysis in human heart cell sample.
XX
XX Human; gene expression; heart; microarray; vascular system; probe;
XX cardiovascular disease; hypertension; cardiac arrhythmia;
XX congenital heart disease; ss.
XX
XX Homo sapiens.
XX
XX WO200157274-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00666.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-063366.

PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488899/53.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX hearts -
XX
XX Claim 1: SEQ ID NO 4236; 530pp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart. The
XX present sequence is one such probe. The probes may be used for
XX predicting, measuring and displaying gene expression in samples derived
XX from the human heart via microarrays. By measuring gene expression, the
XX probes are useful for predicting, diagnosing, grading, staging,
XX monitoring and prognosing diseases of the human heart and vascular system
XX e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX congenital heart disease.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pcl_sequences.
XX
XX Sequence 421 BP; 126 A; 69 C; 77 G; 149 T; 0 other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 2,49e-13 Length: 421
XX Score: 202.00 Matches: 38
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 19.31% Indels: 0
XX DB: 22 Gaps: 0
XX
XX US-09-697-089-2_COPY_762_965 (1-204) x ABA25770 (1-421)
XX
QY 167 GtAlaPhePheGlyLysAsnProLeuLysAsnPhenGlnGlnLeuAsnLeuAlaGlyAsn 186
DB 181 GGTGATTTTTTGGAAAGAACCTCTGAAACCTTCACAGCTTGAATTTGGCGGAAT 240
QY 187 ArgValSerSerAspGlyTyrPheAlaPheMetGlyValPheGluAsnLeuLys 204
DB 241 CGTGGAGCAGATGATGATGCTTCCTTCATGGGTATTTGAGAACTTTAAG 294
XX
XX RESULT 13
XX AAK04305
XX ID AAK04305 standard; DNA; 421 BP.
XX
XX AAK04305;
XX
XX 05-NOV-2001 (first entry)
XX
XX Human brain expressed single exon probe SEQ ID NO: 4296.
XX
XX Human; brain expressed exon; gene expression analysis; probe;
XX microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
XX epilepsy; cancer; ss.
XX
XX Homo sapiens.
XX
XX WO200157275-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00667.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
DR
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
XX
PS Example 4; SEQ ID NO: 4296; 650pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system,
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention.
XX
SQ Sequence 421 BP; 126 A; 69 C; 77 G; 149 T; 0 other;
XX
Alignment Scores:
Pred. No.: 2,49e-13 Length: 421
Score: 202.00 Matches: 38
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 19.31% Indels: 0
DB: 22 Gaps: 0
US-09-697-089-2_COPY_762_965 (1-204) x AAK04305 (1-421)
QY 167 GYAlaphepGhGlyLysAsnProLeuYsAsnPhgInGlnLeuAsnLeuAagLysn 186
DB 161 GGTGCAATTTTGGAAAGAACCCCTGTGAAAACTTCACAGCACTTGAATTTGGCGGGAAT 240
QY 187 ArgValSerSerAspGlyTTrpLeuAlaPheMetGlyValPheGluAsnLeuYs 204
DB 241 CGTGTGAGCAGATGATGATGGCTTCCTTCATGTGATTTGAGAACTCTTAAG 294
RESULT 14
AAK29801
ID AAK29801 standard; DNA; 421 BP.
XX
AC AAK29801;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed single exon probe SEQ ID NO: 4358.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
OS Homo sapiens.
XX
PN WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PE 30-JAN-2001; 2001WO-US00668.
XX
PF 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX

PA (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488900/53.
DR
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human bone marrow -
XX
PS Example 4; SEQ ID NO: 4358; 658pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention.
XX
SQ Sequence 421 BP; 126 A; 69 C; 77 G; 149 T; 0 other;
XX
Alignment Scores:
Pred. No.: 2,49e-13 Length: 421
Score: 202.00 Matches: 38
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 19.31% Indels: 0
DB: 22 Gaps: 0
US-09-697-089-2_COPY_762_965 (1-204) x AAK29801 (1-421)
QY 167 GYAlaphepGhGlyLysAsnProLeuYsAsnPhgInGlnLeuAsnLeuAagLysn 186
DB 161 GGTGCAATTTTGGAAAGAACCCCTGTGAAAACTTCACAGCACTTGAATTTGGCGGGAAT 240
QY 187 ArgValSerSerAspGlyTTrpLeuAlaPheMetGlyValPheGluAsnLeuYs 204
DB 241 CGTGTGAGCAGATGATGATGGCTTCCTTCATGTGATTTGAGAACTCTTAAG 294
RESULT 15
AAI14389
ID AAI14389 standard; DNA; 421 BP.
XX
AC AAI14389;
XX
DT 12-OCT-2001 (first entry)
XX
DE Probe #4322 for gene expression analysis in human cervical cell sample.
XX
KW Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PE 30-JAN-2001; 2001WO-US00670.
XX
PF 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488901/53.
XX

PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells -

PS Claim 25; SEQ ID No 4322; 487bp; English.

XX
CC The present invention relates to human single exon nucleic acid probes
CC (SNP). The present sequence is one such probe. The SNPs are derived
CC from human HeLa cells. The SNPs can be used to produce a single exon
CC microarray, which can be used for measuring human gene expression in a
CC sample derived from human cervical epithelial cells. By measuring gene
CC expression, the probes are therefore useful in grading and/or staging
CC of diseases of the cervix, notably cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 421 BP; 126 A; 69 C; 77 G; 149 T; 0 other;

Alignment Scores:

Pred. No.:	2.49e-13	Length:	421
Score:	202.00	Matches:	38
Percent Similarity:	100.00%	Conservative:	0
Best local Similarity:	100.00%	Mismatches:	0
Query Match:	19.31%	Indels:	0
DB:	22	Gaps:	0

US-09-697-089-2_COPY_762_965 (1-204) x AA114389 (1-421)

QY	167	GIYAlAPhePheGlyLySAsnProLeuLYSAsnPheGlnGlnLeuAsnLeuAlaGlyAsn	186
DB	181	GGTGCATTTTTGGAAAGAACCCCTCTGAAAAACTTCACAGCACTTGAATTTGGCGGGAAT	240
QY	187	ArgValSerSerAspGlyTTrPLeuAlaPheMetGlyValPheGluAsnLeuLYS	204
DB	241	CGTGAGACAGATGATGATGCTTCATGCGGTATTTGAGAAATCTTAAG	294

Search completed: January 31, 2003, 13:24:27
Job time : 245.662 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 31, 2003, 11:50:07 : Search time 1666.97 Seconds

(without alignments)
1981.965 Million cell updates/sec

Title: US-09-697-089-2_COPY_762_965

Perfect score: 1046

Sequence: 1 LKNTKLIMONIKMNEDEL.....GNRYSDDGLAFMGVFENLK 204

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+g2n_model -DEV=xlh
-O=/cgn2.1/USPTO_spool/US09697089/runat_29012003_092754_19729/app_query.fasta_1.981
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blsum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptco -NORM=ext -HEAPSIZE=500 -MTLEN=0 -MAXLEN=200000000
-USER=US09697089_@cgn_1.1_1985_@runat_29012003_092754_19729 -MCPU=6 -ICPU=3
-NO_XLIPX -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	506	48.4	480	10 AV719179	AV719179 AV719179
2	347	33.2	775	13 B1854236	B1854236 603381263
3	313	29.9	637	9 AL782121	AL782121 AL782121
c 4	298	28.5	553	17 A0320928	A0320928 RPI11-93
c 5	290	27.7	364	9 A1263294	A1263294 qx57b01.x
c 6	279	26.7	719	14 B0204082	B0204082 UT-R-DN1-
7	255	24.4	630	17 A0112439	A0112439 CIT-HSP-2
c 8	184.5	17.6	476	12 Bg210375	Bg210375 RST29913
c 9	176.5	16.9	728	17 A2720059	A2720059 RPCI-24-8
10	173	16.5	637	9 AL639997	AL639997 AL639997
11	142.5	13.6	577	13 B7037401	B7037401 B7037401
12	140.5	13.4	714	9 AL657756	AL657756 AL657756
13	137.5	13.1	1913	11 AK016782	AK016782 Mus muscu
14	127	12.1	805	12 Bg684008	Bg684008 602635613
15	126	12.0	619	13 B7361756	B7361756 B3161756
16	124.5	11.9	630	12 Bg081770	Bg081770 H3068H04-
17	121.5	11.6	806	9 A7455014	A7455014 A7455014
18	121	11.6	1019	13 B4470084	B4470084 AGENCOURT
19	120	11.5	961	13 B4458722	B4458722 AGENCOURT
20	119.5	11.4	745	14 B779763	B779763 EST590339
21	119.5	11.4	862	14 B779781	B779781 EST590357
22	119.5	11.4	1490	11 AY103901	AY103901 zea. mays
23	119	11.4	893	12 Bg831716	Bg831716 602766010
24	118.5	11.3	985	14 B0645517	B0645517 AGENCOURT
25	118	11.3	625	12 Bf309088	Bf309088 601890996
26	118	11.3	737	13 BMO20728	BMO20728 603644242
27	118	11.3	849	9 AL555302	AL555302
28	118	11.3	883	13 B761214	B761214 603043447
29	118	11.3	892	9 AL540576	AL540576 AL540576
30	118	11.3	906	14 B0961941	B0961941 AGENCOURT
31	118	11.3	924	9 AL541714	AL541714 AL541714
32	118	11.3	926	9 AL557388	AL557388
33	118	11.3	1020	13 BMS52397	BMS52397 AGENCOURT
34	118	11.3	1067	13 BMS45249	BMS45249 AGENCOURT
35	118	11.3	1085	14 B9319092	B9319092 AGENCOURT
36	117.5	11.2	733	14 B0042443	B0042443 UT-M-EMO-
37	117.5	11.2	805	12 Bf384755	Bf384755 602046246
38	117.5	11.2	1034	14 B0059434	B0059434 AGENCOURT
39	117	11.2	586	12 Bf718051	Bf718051 fd55905.y
40	116.5	11.1	543	9 AA426831	AA426831 vf20e04.s
41	116.5	11.1	848	9 A0118229	A0118229 A0118229
42	116	11.1	599	9 AL651084	AL651084 AL651084
43	116	11.1	667	12 Bf718068	Bf718068 fd55h11.y
44	116	11.1	758	12 Bg750840	Bg750840 602707366
45	116	11.1	865	13 B1668326	B1668326 603295689

ALIGNMENTS

RESULT 1
AV719179/c
LOCUS AV719179 480 bp mRNA linear EST 16-OCT-2000
DEFINITION AV719179 GLC Homo sapiens CDNA clone G1CEQA10 5', mRNA sequence.
ACCESSION AV719179
VERSION AV719179.1 GI:10816331
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 480)
Qian,B., Wu,T., Huang,Q., Kang,B., Gao,X., Xu,Z., Xiao,H.,
Qian,X., Li,N., Peng,Y., Liu,F., Ou,J., Song,H., Cheng,Z., Zeng,L.,
Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang

TITLE
JOURNAL
COMMENT

,Y., Gu,Y., Chen,Z. and Han,Z.
Homo sapiens cDNA GLC clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES

SOURCE

Location/Qualifiers

1..480

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="GLCE0A10"

/clone_1lb="GLC"

/tissue_type="corresponding non cancerous liver tissue"

/dev_stage="Adult"

/lab_host="SOLR"

/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 138 a 120 c 85 g 137 t

ORIGIN

Alignment Scores:

Pred. No.: 2,47e-52 Length: 480
Score: 506.00 Matches: 97
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 48.37% Indels: 0
DB: 10 Gaps: 0

US-09-697-089-2_COPY_762_965 (1-204) x AV19179 (1-480)

QY 108 HisGlueuileaspargmetsValleuclnleuthralaleumetleuprottr 127
DB 480 CATCACTGATGACAGATGACGCTGTAACACGCTGATGCTGCTGCTGCTGCTG 421
QY 128 GGCCTGATGACGACGACGACGCTGATGACGCTGATGACGCTGATGACGCTG 147
DB 420 GGCCTGATGACGACGACGACGCTGATGACGCTGATGACGCTGATGACGCTG 361
QY 148 LeuVallyleuGlyleuLysAsnTrpArgleuthrAsprrhguilleargilleuGly 167
DB 360 CTCGTCACAGCTTGGTGAACAACTGAGACTACAGATACAGATTAAGTTAGCT 301
QY 168 AlaPhepneGlyLysAsnProleuLysAsnPhedngineLysAsnleuAlaGlyAsnArg 187
DB 300 GCATTTTGGAAAGAACCTCTGAAAACCTCCAGCAGTTGGAATTTGGCGGAATCGT 241
QY 188 ValserSerAspGlyTrpLeuAlaPheMetGlyValPheGluAsnLeuLys 204
DB 240 GTGACGACTGATGATGAGCTTGCCTTCATGGGTGATTTGAGAACTTTAAG 190

RESULT 2
BI854236 775 bp mRNA linear EST 10-OCT-2001
LOCUS 603381263F1 NCI_GCAP_Mam4 Mus musculus cDNA clone IMAGE:5389239 5',

DEFINITION MRNA sequence.
ACCESSION BI854236
VERSION BI854236.1 GI:15994983

KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 775)
NIH-MGC <http://mgs.nci.nih.gov/>.

TITLE
JOURNAL
COMMENT
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
plate: LHAM1991 row: m column: 16
High quality sequence stop: 764.

FEATURES

SOURCE

Location/Qualifiers

1..775

/organism="Mus musculus"

/strain="NMRI"

/db_xref="taxon:10090"

/clone="IMAGE:5389239"

/clone_1lb="NCI_GCAP_Mam4"

/tissue_type="tumor, gross tissue"

/dev_stage="5 months"

/lab_host="DH10B"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Priscilla Furth,
NIH Reference for transgenic model: Li et al., Cell Growth
and Differentiation 7, 3-11 (1996)."

BASE COUNT 226 a 162 c 196 g 191 t

ORIGIN

Alignment Scores:

Pred. No.: 2,64e-32 Length: 775
Score: 347.00 Matches: 71
Percent Similarity: 74.29% Conservative: 7
Best Local Similarity: 67.62% Mismatches: 27
Query Match: 33.17% Indels: 0
DB: 13 Gaps: 0

US-09-697-089-2_COPY_762_965 (1-204) x BI854236 (1-775)

QY 100 GluLysAspGlyAsnGluAlaLeuHisGluLeuLeuAspArgmetAsnValleucln 119
DB 2 GAAAAGATGGGAATGAAGACTCTACAGACTGATGCGAGCTTGGGCTCTGGAGAG 61
QY 120 LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerLeu 139
DB 62 CTCACCTACATTGATGCTGCTTGGGCTGGATGCGACACAGAGCTGCCAAGCTGTG 121
QY 140 LysHisLeuGluGluValProGlnLeuValLysLeuGlyLysAsnTrpArgleuthr 159
DB 122 AAGCAGTTGGAGGGGACCCAGGACTTCCCAAACTTGATGTAAGAACTGAGACTCAGA 181
QY 160 AsprrhguilleargilleuGlyAlaPhepneGlyLysAsnProleuLysAsnPhedn 179
DB 182 GACGAGAGATTAAGATTTAGTGAATTTCTGAGATGAATCTCTGAGAGACTGACAG 241
QY 180 GlnLeuAsnLeuAlaGlyAsnArgValserSerAspGlyTrpLeuAlaPheMetGlyVal 199
DB 242 CAGTTGATTTAGCGGGGCACTGTGACAGTACGAGATGCTTACTTCATGATGATGTG 301
QY 200 PheGluAsnLeuLys 204
DB 302 TTTGAGATCTGAAG 316

RESULT 3

AL782121

LOCUS AL782121 637 bp mRNA linear EST 25-JUN-2002

DEFINITION AL782121 XGC-neurula silurana tropicalis cDNA clone TNeu076a12 5',
MRNA sequence.

ACCESSION AL782121

VERSION AL782121.1 GI:21567825

KEYWORDS EST.

SOURCE western clawed frog.

ORGANISM Silurana tropicalis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Silurana.
1 (bases 1 to 637)
Taylor, R., Ashurst, J.L., Croning, M.D.R., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2002
Unpublished (2001)
Contact: Taylor R
Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TNeu076a12.p1csp6
Sequencing primer: P1CSP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.

FEATURES
source
1..637
/organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="TNeu076a12"
/clone_lib="XGC-neurula"
/dev_stage="neurula"
/lab_host="Escherichia coli DH10B"
/note="vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."

BASE COUNT
211 a 103 c 138 g 185 t

ORIGIN

Alignment Scores:
Pred. No.: 3.14e-28 Length: 637
Score: 313.00 Matches: 66
Percent Similarity: 61.90% Conservative: 38
Best Local Similarity: 39.29% Mismatches: 64
Query Match: 29.92% Indels: 0
DB: 9 Gaps: 0

US-09-697-089-2_COPY_762_965 (1-204) x AL782121 (1-637)

QY 1 LeuLysAsnLeuThLysLeuIleMetAspAsnIleLysMetAsnGluLysAlaIle 20
DB 133 CTAGTAAGGGCTGAAATAATGTTCCATACATTAAATAGACAGAAATGCGAAA 192
QY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40
DB 193 ACTCTGGCTGAGGCGATTTTAACTGTAAGAGATTAAAGAGTTATCCATATCTCATATC 252
QY 41 SerAspIleGlyGlyMetAspTyrIleValLysSerLeuSerSerLeuProCysAsp 60
DB 253 TCCAACTATTGGAGTGGCGATGGAGATGATTCGAGAAATCAATTCCTATGTTCCATGAG 312
QY 61 LeuGluGluIleGlnLeuValSerCysLeuSerAlaAsnAlaValLysIleLeuAla 80
DB 313 CTTAAGAAGCAATTAATTAATGACTGTTGAGTGTGAAGCTCTCATGAGTCTGCA 372
QY 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100
DB 373 TTCCTCTTAAATAATGTTCTCTAGCATTTGAAATATGATGATTTCTGCGAATATTATTA 432
QY 101 LysAspArgLysAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120
DB 433 CAGAGAGGGAAGAAATCAATGATAGAAAGAGCTGCCAACTGATATCTTATGCGAATA 492
QY 121 ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLys 140
DB 493 AAGACACTTATGCTGCTGAGAGACATATGTAAAGTTTGGCTGAGGACATATTACT 552
QY 141 HisLeuGluGluValProGlnLeuValLysGlyLeuLysAsnTyrArgLeuThrAsp 160
DB 553 ACATTGAGGCGCATCTCTACTGTCAGAACTTGTCTTAAAGATGAACTTGACCAAT 612

QY 161 ThrGluIleArgIleLeuGluAla 168
DB 613 GATGACTGATGACATTACCTTGG 636

RESULT 4
AO320928/c
LOCUS
DEFINITION
AO320928 553 bp DNA linear GSS 06-MAY-1999
RPC111-93C9.TV RPC111 Homo sapiens genomic clone RPC11-93C9, DNA
sequence.
ACCESSION
AO320928
VERSION
AO320928.1 GI:4053662
KEYWORDS
GSS.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 553)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
Use of human BAC End Sequences for Sequence-Ready Map Building
Unpublished (1998)
Other GSSs: RPC111-93C9.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org

REFERENCE
AUTHORS
JOURNAL
COMMENT
The Institute for Genomic Research
Department of Eukaryotic Genomics
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org

Clones are derived from the human BAC library RPC11-11. For BAC library availability, please contact Pieter de Jong (pieter@ed.jong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/hunguen/bac_end_search/bac_end_search.html
Seq primer: 17
Class: BAC ends.

FEATURES
source
1..553
/organism="Homo sapiens"
/db_xref="GDB:7535384"
/db_xref="taxon:9606"
/clone="RPC11-93C9"
/clone_lib="RPC11-93C9"
/sex="Male"
/cell_type="Lymphocytes"
/note="vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPC11 Human Male BAC library"

BASE COUNT
170 a 107 c 114 g 162 t

ORIGIN

Alignment Scores:
Pred. No.: 1.8e-26 Length: 553
Score: 298.00 Matches: 60
Percent Similarity: 83.78% Conservative: 2
Best Local Similarity: 81.08% Mismatches: 6
Query Match: 28.49% Indels: 6
DB: 17 Gaps: 1

US-09-697-089-2_COPY_762_965 (1-204) x AO320928 (1-553)

QY 111 TLeAspArgMetAsnValLeuGluGlnIleuThrAlaLeuMetLeuProTyrGlyCysAsp 130
DB 259 GTGCGACAGATGATGAGCTGTAGAACGCTCACCGCATGATGCTGCCGCGGCTGTGAC 200
QY 131 ValGlnGlySerLeuSerSerLeuLysHisLeuGluGluValProGlnLeuValLys 150
DB 199 GTGCAAGGCGAGCTGAGCGCTGTGGAACATTTTGAGAGAGCTCCACAACTGCTCAAG 140
QY 151 LeuGlyLeuLysAsnTyrArgLeuThrAspThrGluIleArgIleLeuGluAlaPhePhe 170
DB 139 CTTGGGTTGAAAAGCTGAGACTACAGATACAGAGATTGATTTTACGTAGTACACA 80

QY 171 GlytysAsnPro-----LeutysAsnPie 178
Db 79 CATACAGAGCCAGATACTGATTGGCCCTTAAATAATTC 38

RESULT 5
AI263294/c 364 bp mRNA linear EST 03-FEB-1999
LOCUS q957b01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2005417 3',
DEFINITION mRNA sequence.
ACCESSION AI263294
VERSION AI263294
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
1 (bases 1 to 364)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Life Technologies catalog #: 11548-013
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/BLM at:
www-bio.llnl.gov/bdrrp/image/image.html
Insert length: 2146 Std Error: 0.00
Seq primer: -40UP from Glibco
High quality sequence stop: 364.
Location/Qualifiers
1. 364
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2005417"
/clone_lib="NCI_CGAP_Pan1"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site:1: Salt:
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"

BASE COUNT 117 a 84 c 55 g 108 t
ORIGIN

Alignment Scores:
Pred. NO.: 9.05e-26 Length: 364
Score: 290.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 27.72% Indels: 0
DB: 9 Gaps: 0

US-09-697-089-2_COPY_762_965 (1-204) x AI263294 (1-364)

QY 150 LysleuGlyLeuLysAsnTrpArgLeuThrAspThrGluIleArgIleLeuGlyAlaPhe 169
Db 364 AAGCTGGCTTGAATAAAGTGGAGACTCAGATACAGATTAGATTTTACGTGCATT 305

QY 170 PheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsnArgValSer 189
Db 304 TTTTGAAAGAACCTCTGTAATAAAGCTTCACAGAGTTGAGTGGCGGAATCGTGTGAGC 245

QY 190 SerAspGlyTrpLeuAlaPheMetGlyValPheGluAsnLeuLys 204
Db 244 AGTATGATGGATGGCTTGCCTTCATGGGTGATATTGAGAACTTTAAG 200

RESULT 6
BQ204082/c 719 bp mRNA linear EST 02-MAY-2002
LOCUS BQ204082
DEFINITION UT-R-DNI-cmv-e-08-0-UT.s1 UT-R-DNI Rattus norvegicus cDNA clone
UT-R-DNI-cmv-e-08-0-UT 3', mRNA sequence.

ACCESSION BQ204082
VERSION BQ204082.1 GI:20420547
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
1 (bases 1 to 719)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704447
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: masoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
normalized distal colon library cDNA library preparation: M.B.
Soares lab clone distribution: clones will be available through
Research Genetics (www.resgen.com) The following repetitive
elements were found in this cDNA sequence: 12-210, >L1P3#LINE/L1
Seq primer: M13 Forward
POLY-A=yes.
Location/Qualifiers
1. 719
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UT-R-DNI-cmv-e-08-0-UT"
/clone_lib="UT-R-DNI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site:1: Not I; Site:2: Eco RI; The UT-R-DNI
library is a normalized Rat Distal Colon library (NRCC)
constructed in pT37 PAC vector according to the procedure
described by Bonaldo, Lennon & Soares (Normalization and
Subtraction: Two Approaches to Facilitate Gene Discovery.
Genome Research 6: 791-806, 1996). The oligonucleotide
used to prime first strand synthesis contained the
sequence tag GAAGTGTCTC between the Not I cloning site and
DT8 stretch. The Rat Distal Colon tissue was provided by
Tom Freeman of the Sanger Center.
TAG_LIB=UT-R-DNI
TAG_TISSUE=distal colon
TAG_SEQ=GAAGTGTCTC"

BASE COUNT 184 a 185 c 146 g 203 t 1 others
ORIGIN

Alignment Scores:
Pred. NO.: 6.2e-24 Length: 719
Score: 279.00 Matches: 57
Percent Similarity: 75.29% Conservative: 7
Best local Similarity: 67.06% Mismatches: 21
Query Match: 26.67% Indels: 0
DB: 14 Gaps: 0

US-09-697-089-2_COPY_762_965 (1-204) x BQ204082 (1-719)

QY 120 LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerLeuLeu 139
Db 718 CTAAGCGGCTGATGCTGCTTGGTGGCGGAGATCGTACATGATCTGCCAACATCTGCTG 659

QY 140 LysHisLeuGlnGluValProGlnLeuValLysleuGlyLeuLysAsnTrpArgLeuThr 159

```
Db 658 AACCACTGAGGAGGAGCCAGGCGTTGTCAAACTTGATGATAAAAGCTGAGCTGAGA 599
QY 160 ASPTThGlul1eargilleuGlyAlaAphPheGlyLysanProleuLysasnPheGln 179
Db 598 GACGAGAGATTTAGAAATTCGGTGAATTTTGAGATGAATCCTCGAGAGACTTGACAG 539
QY 180 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpPheLeuAlaPheMetGlyVal 199
Db 538 CAGTTGGATTTCAGCAGACAGCGGTGTGACAGATGATGATGCTTCTTCATGATGATGTG 479
QY 200 PheGluAsnLeuLys 204
Db 478 TTGAGATCTTAAAG 464

RESULT 7
LOCUS A0112439 630 bp DNA linear GSS 29-AUG-1998
DEFINITION CIT-HSP-2372C1.TR CIT-HSP Homo sapiens genomic clone 2372C1, DNA
sequence.
ACCESSION A0112439
VERSION A0112439.1 GI:3484599
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 630)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
Venter,J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building (1998)
Unpublished (1998)
Other_GSSs: CIT-HSP-2372C1.TR
COMMENT Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
FEATURES
Location/Qualifiers
source 1..630
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBelobAC11. site_1: HindIII. site_2:
HindIII"
BASE COUNT 188 a 126 c 124 g 192 t
ORIGIN

Alignment Scores:
Pred. No.: 4,71e-21 length: 630
Score: 255.00 Matches: 48
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 24.38% Indels: 0
DB: 17 Gaps: 0

US-09-697-089-2_COPY_762_965 (1-204) x A0112439 (1-630)
QY 23 AlagluGlyLeuLysanLeuLysLysMetCysLeuPheHisLeuThrHisLeuSerAsp 42
Db 486 GCTGAAGGCGCTGAATAACGTAAGAGATGTGTTTATTTCATTGACCCACTTGCTGAC 545
```

```
QY 43 TleGlyGluGlyMetAspTrlIleValLysSerLeuSerSerLeuProCysAspLeuGlu 62
Db 546 ATTGGAGAGGGAATGTGATTACATAGTCACAGTCTCTGCAAGTGAACCTGTGACCTTGA 605
QY 63 GluIleGlnLeuValSerCysCys 70
Db 606 GAAATTCATTTAGTCTCTCTGCTGC 629

RESULT 8
LOCUS BG210375 476 bp mRNA linear EST 21-APR-2001
DEFINITION RST29913 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG210375
VERSION BG210375.1 GI:13732062
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 476)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith
,E., Veloso,N., Kika,A., Hess,J., Cochren,K., Lo,K., Offenbacher
,J., Danzig,J. and Ducat,M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
21227151
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 360.
FEATURES
Location/Qualifiers
source 1..476
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
BASE COUNT 120 a 99 c 107 g 149 t 1 others
ORIGIN

Alignment Scores:
Pred. No.: 1.63e-12 length: 476
Score: 184.50 Matches: 47
Percent Similarity: 55.91% Conservative: 5
Best Local Similarity: 50.34% Mismatches: 24
Query Match: 17.64% Indels: 17
DB: 12 Gaps: 3

US-09-697-089-2_COPY_762_965 (1-204) x BG210375 (1-476)
QY 121 ThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLys 140
Db 10 ACTGCAGGTGGTGGTCTTGCTGCTACACCGACCTCCGCTTCGCGGATTCCTGTTCTCT 69
QY 141 -----HisLeuGluGluValProGlnLeuValLysLeu 151
Db 70 ATTTGCTTCTCTGAGATCTGAGATGATTCCTCTCCCTCAGCTCCAG-----TAGCTG 123
QY 152 GlyLeuLysanTrpArgLeuThrAspThrGluIleArgIleLeuGlyAlaPheGly 171
Db 124 GGATTACCGGTGCATGCGCGCACT-----ATAAGTGATTTCTTGGGA 165
```

QY	192	glyttrpleuA1aphemeclyValphnegluA5nleuLys 204
Db	226	GGATGGCTTGCCCTTGTTGGTGTATTGAGATCTTAAG 264
RESULT 9		
LOCUS	A2720059	728 bp DNA linear GSS 24-JAN-2001
DEFINITION	RPci-24-88D12.TVC RPci-24 Mus musculus genomic clone RPci-24-88D12.	
ACCESSION	A2720059	
VERSION	A2720059.1	GI:12461375
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 728)	
AUTHORS	Zhao,S., Niemman,W., Malek,J., Shatsman,S., Akintet,B., Levins,M., Tesgaie,G., Geel,K.K., Krol,M., Shavitsbeyn,A., Gebregeorgis,E., Russell,D., de Jong,P. and Friser,C.M.	
TITLE	Mouse BAC End Sequences from Library RPci-24	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: szhao@tigr.org Clones are derived from the mouse BAC library RPci-24. For BAC library availability, please contact Pieter de Jong (pdejong@tigr.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end page: http://www.tigr.org/tigr/tdb/bac/ends/mouse/bac_end_intro.html Plate: 88 row: D column: 12 Seq primer: 77 Class: BAC ends.	
FEATURES	Location/Qualifiers	
SOURCE	1. 728	
	/organism="Mus musculus"	
	/strain="C57BL/6J"	
	/db_xref="taxon:10090"	
	/clone="RPci-24-88D12"	
	/clone_1lb="RPci-24"	
	/sex="Male"	
	/cell_type="Spleen/Brain"	
	/note="Vector: pPRABAC1. Site.1: BamHI. Site.2: BamHI. RPci-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pPRABAC1 cloning vector at the BamHI sites using MboI partially digested male C57BL/6J DNA."	
BASE COUNT	193 a 194 c 145 g 196 t	
ORIGIN		
Alignment Scores:		
Pred. No.:	3,15e-11	Length: 728
Score:	176.50	Matches: 41
Percent Similarity:	55.32%	Conservative: 11
Best local Similarity:	43.62%	Mismatches: 35
Query Match:	16.87%	Indels: 7
DB:	17	Gaps: 2
US-09-697-089-2_COPY_762_965 (1-204) x A2720059 (1-728)		
QY	111	lileasparMetAsnValleuclnleuPrralaleuMetleuProtrpelyCysasp 130
Db	561	GTGCGACAGGCTTGCGCTTCTGTGGAGAGCTCACTACATTGATGCTGCTGGGAGAT 522

Qy	131	ValgInglySerIeuSerSerIeuIeuYsHtIeuGluGluValProGInIeuValYs	150
Db	521	GTGCACACCAAGCCTCCCAAGCTGTTGAAAGCAGTTGGAGAGGACCCCAAGACTTGCCAAA	462
Qy	151	IeuGlyIeuYsAsnTTParGleuthrAspThrGluIeuIeuGlyIeuGlyAlaIeuPhe	170
Db	461	CTTGATTTGAATAAAGCTGGAGACTGAGACGCAAGAGATTAAAGTTTAGGTAGTACAC	402
Qy	171	GlyIeuAsnPro-----IeuYsAsnPheGln---GlnIeuAsnIeu	183
Db	401	CAAAAGGAGCCGAGGAGGACAGGAGCTGACTTTAAACAAGGCTTAGTTGGCCTTTATGTC	342
Qy	184	AlaGlyAsnArgValSerSerAspGlyThrIeuAlaIeuMet	197
Db	341	AGTCCTCAGAGAGCTGAGGACGCGGTCCTGCTTCCTTTC	300
RESULT 10			
AL639997			
LOCUS	AL639997	637 bp	mRNA linear EST 12-DEC-2001
DEFINITION	AL639997 XGC-neurula Silurana tropicalis cDNA clone TNeu003d13 5',		
ACCESSION	AL639997		
VERSION	AL639997		
KEYWORDS	AL639997.1 GI:16792128		
SOURCE	EST.		
ORGANISM	western clawed frog.		
	Silurana tropicalis		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;		
	Xenopodinae; Silurana.		
REFERENCE	1 (bases 1 to 637)		
AUTHORS	Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.		
TITLE	Sanger Xenopus tropicalis EST project 2001 (10_2001)		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Huckle E		
	Sanger Centre		
	Hinxton, Cambridgeshire, CB10 1SA, UK		
	Email: tropesanger.ac.uk		
	Sanger Xenopus tropicalis EST project 2001		
	TROPICALIS_SEQUENCE_ID: TNeu003d13.sp6		
	Sequencing primer: SP6		
	This sequence is from a Xenopus Gene Collection (XGC) library		
	constructed by Aaron M. Zorn.		
FEATURES			
source	Location/Qualifiers		
	1..637		
	/organism="Silurana tropicalis"		
	/db_xref="taxon:8364"		
	/clone="TNeu003d13"		
	/clone_lib="XGC-neurula"		
	/dev_stage="neurula"		
	/lab_host="Escherichia coli DH10B"		
	/note="Vector: pCS107; Site.1: EcoRI; Site.2: NotI; cDNA		
	was oligo dT primed from 5ug of poly A+ RNA from neurula.		
	EcoRI-NotI cut cDNA was then ligated into pCS107 with		
	EcoRI at the 5' end and NotI at the 3' end."		
BASE COUNT	226 a 93 c 132 g 185 t	1 others	
ORIGIN			
Alignment Scores:			
Pred. NO.:	6,89e-11	Length:	637
Score:	173.00	Matches:	36
Percent Similarity:	68.67%	Conservative:	21
Best Local Similarity:	43.37%	Mismatches:	26
Query Match:	16.54%	Indels:	0
DB:	9	Gaps:	0
US-09-697-089-2_COPY_762_965 (1-204) x AL639997 (1-637)			
Qy	1	IeuYsAsnIeuThrIeuYsIeuIeuMetAspAsnIleYsMetAsnGluGluAspAlaIle	20
Db	387	CTAGTAGGGCTTGAATAAATTGGTTTCCATTAACATTAAATAGACAAAGATGATCAAAA	446
Qy	21	LysIeuAlaGluGlyIeuYsAsnIeuYsIeuYsMetCysIeuPheHisIeuThrHisIeu	40


```

Db 447 ACTGCGCTGAAGCATTTAAGTCTGAAGAAGTTAAAGCTTATCATCTCATC 506
Qy 41 SeraspilleglygluGlymetaspyrrilValylsSerleuSerleuProCysasp 60
Db 507 TCCACATGATGGAGATGGAGATGATTCGACAAATCTTCTTATGTCATGG 566
Qy 61 LeugluGluGluGluLeuValserCysleuSerAlaAsnAlaValylleuAla 80
Db 567 CTTAAGAACTCAATTAATTAATGACTGTGTGTCAGTGTGAAGCTCTCAAGACTTGGCA 626
Qy 81 GlnAsnLeu 83
Db 627 TTCGCCTTA 635

RESULT 11
LOCUS B037401 577 bp mRNA linear EST 07-DEC-2001
DEFINITION B037401 NIBB Mochii normalized Xenopus neurula library Xenopus
laevis cDNA clone XL040g14 5', mRNA sequence.
ACCESSION B037401
VERSION B037401.1 GI:17420442
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 577)
Kikayama,A., Teresaka,C., Mochii,M., Ueno,N., Shin-I,T. and Kohara
Y.
REFERENCE 1
AUTHORS Y.
TITLE Expressed genes in X. laevis embryo
JOURNAL Unpublished (2001)
COMMENT Contact: Tadasu Shin-I
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
FEATURES
location/Qualifiers
source
1..577
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone_lib="XL040g14"
/clone_lib="NIBB Mochii normalized Xenopus neurula
library"
/tissue_type="whole embryo"
/dev_stage="stage 15"
/Note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
were oligo-dT primed and directionally cloned. Staging
according to Nieuwkoop and Faber. Library is substracted
and was constructed by N. Garrett. and A.M. Zorn,
(Wellcome/CRC Institute)."
BASE COUNT 176 a 107 c 114 g 179 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 3.53e-07 Length: 577
Score: 142.50 Matches: 39
Percent Similarity: 47.86% Conservative: 17
Best Local Similarity: 33.33% Mismatches: 47
Query Match: 13.62% Indels: 14
Gaps: 3
DB: 13
US-09-697-089-2_COPY_762_965 (1-204) x B037401 (1-577)
Qy 90 SerIleuAspLeuSerGluAsnTyrlleuGluLysAspGlyAsnGluAlaLeuHis-Gl 109
Db 81 TCTTCTTGAGATGATGCTGAAAT-----GTGCATGGG 113
Qy 109 uLeuIleAspArgMetAsnVal-----LeuGluGluLeuThrAlaLeuMetLeuProTr 127
Db 114 TTGTATTCACAGCTACCAACGCTCAGCTGATGCAATTAAGACACTTTCTGCTGCG 173

```

```

Qy 127 pGlyCysAspValGlnGlySerleuSerleuLeuYshISleuGluGluValProCl 147
Db 174 AGGACAGATGATGATTTTCCCTGGAGGGGTTATTACTTACTATTAAGCGCATTCCTAA 233
Qy 147 nLeuValylsLeuGlyLeuLysAsnTrpArgleuThrPrpArgThrGluIleArgIleLeuGl 167
Db 234 CTTGTCAAAACTTGGCTTTTAAACATGAAGACTGACAGCTGATGACATGAAATACGTTAGC 293
Qy 167 yAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGluLeuAsnLeuAlaGlyAsnAr 187
Db 294 TTCTCATCTT-----AGCAGCTTTTAAAAACCTTCATATTGAGATCTTGTGATTAATCG 347
Qy 187 yAlaSerSerAspGlyTrpLeuAlaPheMetGlyValPheGluAsnLeu 203
Db 348 TCGTCAAAGTGCAGCGCTTCTTCTGATCGCATTAATGATATCTG 396

RESULT 12
LOCUS AL657756 714 bp mRNA linear EST 13-DEC-2001
DEFINITION AL657756 XGC-neurula Silurana tropicalis cDNA clone TNeu037j15 5',
mRNA sequence.
ACCESSION AL657756
VERSION AL657756.1 GI:17670663
KEYWORDS EST.
SOURCE Western clawed frog.
ORGANISM Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopodinae; Silurana.
1 (bases 1 to 714)
Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
REFERENCE 1
AUTHORS Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
TITLE Sanger Xenopus tropicalis EST project 2001 (10-2001)
JOURNAL Unpublished (2001)
COMMENT Contact: Huckle E
Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TNeu037j15.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
FEATURES
location/Qualifiers
source
1..714
/organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone_lib="TNeu037j15"
/clone_lib="XGC-neurula"
/dev_stage="neurula"
/lab_host="Escherichia coli DH10B"
/Note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from neurula.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end."
BASE COUNT 220 a 156 c 128 g 209 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 8.78e-07 Length: 714
Score: 140.50 Matches: 30
Percent Similarity: 52.04% Conservative: 21
Best Local Similarity: 30.61% Mismatches: 46
Query Match: 13.43% Indels: 1
Gaps: 1
DB: 9
US-09-697-089-2_COPY_762_965 (1-204) x AL657756 (1-714)
Qy 106 ALAlaLeuHISGluLeuIleAspArgMetAsnValLeuGluGluLeuThrAlaLeuMetLeu 125
Db 3 TCAGTAAGAGACTGGCTGCCAAGCTTGAATGATGCAATTAAGACACTTATGCTG 62
Qy 126 ProTrpGlyCysAspValGlnGlySerleuSerleuLeuYshISleuGluGluVal 145

```

D6	CCTGGAGACAGATGTAAGTTTGGCTTGAGGCAGCATATTACTTACCATTGAGCCGCAATT	122
OY	ProGlIneuVallyLysLeuGlyLeuLysAsnTrpArgLeuThrAspHrgLilearGyle	165
D6	CCTACCTGTGACAACTTCCTTTAAACGATGAACCTGACCAATGATGATCATTGATGACA	182
OY	LeuGLyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLeuAlagly	185
D6	AACGTGCTCAAAGTGGCGGCTTCCCTTCCCTACCTGCCATCTACTACATAATCTCG	293
OY	AsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyValPheGluAsnLeu	203
D6	AK016782	1913 bp mRNA linear HTC 19-JAN-2002
LOCUS	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4933411P06:maternal effect gene, full insert sequence.	
DEFINITION	AK016782 GI:12855702	
ACCESSION	AK016782	
VERSION	AK016782.1	
SOURCE	HTC; CAP trapper. Mus musculus (strain:C57BL/6J) adult male testis cDNA to mRNA, clone:4933411P06.	
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	1 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)	
TITLE	2	
JOURNAL MEDLINE PUBMED	99279253 10349636	
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.	
TITLE	Normalizaation and subtraction of cap-trapper-selected cDNAs to Prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)	
JOURNAL MEDLINE PUBMED	20499374 11042159	
AUTHORS	3 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M., Sumi,I., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A., Yamamoto,R., Matsuno,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawaj,i., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y.	
TITLE	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer	
JOURNAL MEDLINE PUBMED	Genome Res. 10 (11), 1757-1771 (2000) 20530913 11076661	
REFERENCE	4	
AUTHORS	Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamataka,I., Salto,T., Katzaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Salto,R., Kadota,K., Matsuda,H., Ashburner,M., Batilov,S., Casavant,T., Kleihsman,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kiehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Mashio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Balderelli,R., Barsch,G., Blake,J., Botfelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bull,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombearts,P., Norione,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyooka,K., Wang,K.H., Weltz.C., Whiteker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kontsuki,S. and Hayashizaki,Y.	
TITLE	Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)	
JOURNAL MEDLINE	21085660 11217851	
PUBMED	5 (bases 1 to 1913)	
REFERENCE	Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bull,C., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hangaki,T., Hara,A., Hayatsu,N., Hill,D., Himomoto,K., Hiroaka,T., Horii,F., Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koja,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J., Salto,H., Salto,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Teijima,Y., Toya,T., Yamamura,T., Yamanka,I., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.	
COMMENT	Direct Submission Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsr.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216) Please visit our web site (http://genome.gsc.riken.go.jp/) for further details. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGGAGAGAGAAGATCCAGAGCTCTTTTTTTTTTTTTTTTAA 3'], cDNA was prepared by using trihalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGGAGAGATTCGATTAATTAATTAATCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. cDNA of size comprised between 0.5 and 3 kb was selected before cloning. Vector: a modified pluscript KS(+) after bulk excision from Lambda FIC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B. Location/Qualifiers	
FEATURES	source	
gene	1..1913	/organism="Mus musculus"
CDS	735..1544	/strain="C57BL/6J" /db_xref="FANTOM.DB:4933411P06" /db_xref="MGD:MGI:1903594" /gb_xref="taxon:10090" /clone="4933411P06" /sex="male" /tissue_type="testis" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev stage="adult"
putative	1..1913	/gene="WATER"
evidence:ISS	735..1544	/note="data source:MCD, source key:MGI:1345193," maternal effect gene evidence: /codon_start=1 /protein_id="BAB30427.1" /db_xref="GI:12855702" /db_xref="MGD:MGI:1345193"

TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409 (6821), 685-690 (2001)
PUBLISHED	21085660
REFERENCE	11217851
AUTHORS	Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bulic,C., Carninci,P., Fukuda,S., Fukushima,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hirooka,T., Horii,F., Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Katsukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Schriml,L., Shibata,K., Shibata,Y., Shingawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamada,K.I., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE	Direct Submission
JOURNAL	Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-1-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT	Please visit our web site (http://genome.gsc.riken.go.jp/) for further details. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGCAGAGAAGATCCAGACGCTTTTGTTCCTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGCAGAGACTTCGAGTTAAATTAAATCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. cDNA of size comprised between 0.5 and 3 kb was selected before cloning. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B. location/Qualifiers 1..1913 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="FANTOM_DB:4933411P06" /db_xref="MGD:MGI:1903594" /db_xref="taxon:10090" /cclone="4933411P06" /sex="male" /tissue_type="testis" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev stage="adult" 1..1913 /gene="Mater" /735..1544 /gene="Mater" /note="data source:MGD, source key:MGI:1345193, evidence:ISS maternal effect gene putative" /codon_start=-1 /protein_id="BAB30427.1" /db_xref="GI:12855703" /db_xref="MGD:MGI:1345193"

```

/translacion="MKDDMKIACEALEHPKCALEALRLDSCGLTPASCHLLVLSALFS
NONLTHLCLSNNSIGTEVQOLCOFLRPECALORLIHNINVIDADAFALRLANN
TKLFTLSTNPNVGDAMKILCEALKEPTCYLKEKLIVDCOLMNCDCDLACMTTTRK
HKLSIDLGNNALGDKVYTLTCEBGLKQSSSLRRIGLACETISMCBESLAIQSNPH
LNSLMLKNDPSTSGKLKLSAFQCPVSNLSTIGSNGLSPALFTLALRN"
polya_signal
/gene="Mater"
/locus="putative"
1886..1891
polya_site
/gene="Mater"
/locus="putative"
1913
BASE COUNT      556 a      439 c      494 g      424 t
ORIGIN
Alignment Scores:
Pred. No.:      1e-05      Length:      1913
Score:          137.50      Matches:      59
Percent Similarity: 36.68%      Conservative: 25
Best Local Similarity: 25.76%      Mismatches: 84
Query Match:    13.15%      Indels:      61
DB:             11      Gaps:        7
US-09-697-089-2_COPY_762_965 (1-204) x AK016782 (1-1913)
OY      2      LysAsnLeuThrIleuLleuMetAspAsnIleuMetAsnGluGluAspAlaIleuLys 21
DB      870      CAGAACTTGACACACCTGGCTGTCACAAACACACCTGGGACCTGAGAGAGTGCACACG 929
OY      22      LeuAlaGluGlyLeuLysAsn-----LeuLysLysMetCysLeuPheHis--- 36
DB      930      CTGTGTCAGAGTCTCTAGGAAATCCAGAAATGCTGCTCCACAGGCTGATGTAATCATCTGC 989
OY      37      -----Leu 37
DB      990      AACATGTAGATGATGCTTATGCTCTCTGCGCATTGACAGCTTGAACAACAACAAGCTG 1049
OY      38      ThrHisLeuSer-----AspIleGlyGluGly---MetAspTyrIleValLys 52
DB      1050      ACCCACTGAGGCTGACCATGACATGAACCCGTAAGGGGATGGTGCATGACATGAGCTACTGTGTGA 1109
OY      53      SerLeuSerSerGluProCysAspLeuGluGluIleGluLeuValSerCysCysLeuSer 72
DB      1110      GCTTTAAAGGAACCTACTGTGTAACCTTAAAGAACTGAAGAACTGAGTGCACCACTTATG 1169
OY      73      AlaAsnAlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeu 92
DB      1170      CAGAACTGCTGTGAGACCTGCGCTGTGATGATCACAACAACCAACCACTTAAAGATTG 1229
OY      93      AspLeuSerGluAsnTyrLeuGluLysAspGlyAsnGluAlaLeuHisGluLeuLeuAsp 112
DB      1230      GATCTTGGTACACACGCGCTGGGTGACAAAGGATGATTAACCTG----- 1274
OY      113      ArgMetAsnValLeuGluGlnLeuThrAlaLeuMetLeuProTyrGlyCysAspValGln 132
DB      1275      -----TGCAGAGGAGCTG 1286
OY      133      GlySerLeuSerSerLeuLeuLysHisLeuGluGluValProGlnLeuValLysLeuGly 152
DB      1287      AAGCAAAAGTACAGCTCCCTGAGG-----AGACTTGGG 1319
OY      153      LeuLysAsnTyrArgLeuThrAspThrGluIleArgIleLeuGlyAlaPhePheGlyLys 172
DB      1320      TTGGGGGCGATGTGAGTACTTCCAAATGCTGTGATGCTATTGTCATTGGCCATCTCTTGC 1379
OY      173      AsnProLeuLysAsnPheGlnIleLeuAsnLeuAlaGlyAsnArgValSerSerAspGly 192
DB      1380      AACCT-----CACCTGAACAGCCTTAACCTGATGAAGAATGACTTGAATGATCAGCGGG 1433
OY      193      TrpLeuAlaPheMetGlyValPheGlu 201
DB      1434      AAGTTGAAGCTGTGCTGTGCTTCCAA 1460
RESULT 14

```

```

BG684008
LOCUS      BG684008      805 bp      mRNA      linear      EST 01-MAY-2001
DEFINITION      602635613P1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4763594 5',
mRNA sequence.
ACCESSION      BG684008
VERSION      BG684008.1 GI:13915405
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 805)
NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS      National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE      Unpublished (1999)
JOURNAL
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: ILCM1619 row: 1 column: 03
High quality sequence stop: 802.
FEATURES
source
location/Qualifiers
1..805
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4763594"
/clone_lib="NIH_MGC_48"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pORF7; Site:1: XhoI;
Site:2: EcoRI; cDNA made by oligo-dT priming.
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAC(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."
BASE COUNT      147 a      273 c      249 g      136 t
ORIGIN
Alignment Scores:
Pred. No.:      5e-05      Length:      805
Score:          127.00      Matches:      41
Percent Similarity: 47.10%      Conservative: 32
Best Local Similarity: 26.45%      Mismatches: 76
Query Match:    12.14%      Indels:      6
DB:             12      Gaps:        4
US-09-697-089-2_COPY_762_965 (1-204) x BG684008 (1-805)
OY      41      SerAspIleGlyGlu---GlyMetAspTyrIleValLysSerLeuSerSerGluProCys 59
DB      353      AAGGAGCTGGGCGGATGCGCTGCATTCGCTCCAGAGGCTGCACACCCCTCTCTGC 412
OY      60      AspLeuGluGluIleGluLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 79
DB      413      AAGATCCAGAACTGAGCTCCAGAACTGCTCTGACGCGGGCGGCGGCGGCTG 472
OY      80      AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 99
DB      473      TCCACACACATAGACACCTGCGCCACCTGCGAGGAGCTGCACCTGACGACAACTCTTG 532
OY      100      GluLysAspGlyAsnGluAlaLeuHisGlu---LeuIleAspArgMetAsnValLeuGlu 118
DB      533      GGGATGCGGCGCTGACCTGTGCGCAAGGATCTGAGACCCCAATGCGCGCTGGA 592
OY      119      GlnLeuThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeu 138

```

```
Db 593 AAG-----CTGCACACTGCGAGTATGACACCTCTCGGCTGCACGCTCGGACGCCCTG 643
Qy 139 LeuysHsleuGlulValProGlnleuValLysleuGlyLeuLysAsnTirPargleu 158
Db 644 GCCGCCGCTGCGAGGCCAGCCGACTTCAAGAGCTCAGCGTTAGCAACAGCACTG 703
Qy 159 ThrAspTirGlnleuLysleuGlyLysleuLysAsnProleuLysAsnPh 178
Db 704 AATGAGCTGCGCTGCTGTCTATGCGAGGCGCTGAGAGACTCCCGCTGCAG---CTG 760
Qy 179 GlnGlnleuAsnleuAlaGlyAsnArgValSerSerAspGlyTir 193
Db 761 GAGGCGCTCAAGCTGAGAGCTGCGCTGATCAGACACTG 805

RESULT 15
LOCUS BJ361756 619 bp mRNA linear EST 07-MAR-2002
DEFINITION BJ361756 Dictyostelium discoideum cDNA library, CF Dictyostelium
discoideum cDNA clone ddc18j17 5', mRNA sequence.
ACCESSION BJ361756
VERSION BJ361756
KEYWORDS BJ361756.1 GI:19261351
SOURCE EST.
ORGANISM Dictyostelium discoideum.
REFERENCE Dictyostelium discoideum.
AUTHORS Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
TITLE Uruhashira, H., Tanaka, Y., Kohara, Y. and Shin-I, T.
Full length cDNA of Dictyostelium discoideum at the culmination
stage
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-I
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
Location/Qualifiers
FEATURES
source
1. 619
/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="ddc18j17"
/clone_id="Dictyostelium discoideum cDNA library, CF"
/sex="mat A"
/dev_stage="Culmination stage"
BASE COUNT 230 a 59 c 108 g 222 t
ORIGIN
```

```
Alignment Scores:
Pred. No.: 4.37e-05 Length: 619
Score: 126.00 Matches: 36
Percent Similarity: 52.03% Conservative: 28
Best Local Similarity: 29.27% Mismatches: 45
Query Match: 12.05% Indels: 14
DB: 13 Gaps: 4
```

US-09-697-089-2_COPY_762_965 (1-204) x BJ361756 (1-619)

```
Qy 5 ThrLysleuIleMetAspAsnIleLysMetAsnGlnGluAspAlaIleLysleuAlaGlu 24
|||||
Db 80 ACAAAATTAGTATTAAGTATGATTGATATGATACACACAGAGAAATTAATTAG 139
|||||
Qy 25 GlyLeuLysAsnleuLysLysMetCysLeuPheHisLeuSerAspIleGly 44
|||||
Db 140 GCATTATTAAGTAAATGATACATTCAGACAAATTA-----GATCTTGT 187
|||||
Qy 45 -----GlnGlyMetAspTyrIleValLysSerLeuSerSerGluPro 58
|||||
Db 188 AATAATTCAATTGAGATTAAGGATATGATGTTTGGGTGAATATTAAGATTACACCA 247
|||||
Qy 59 CysAspLeuGlnGluIleGlnleuValSerCysCysLeuSerAlaAsnAlaValLysIle 78
|||||
```

```
Db 248 TATGAAATTGAAGATTATTAATGAAATATTGTCACGCCGCTAAGAAATTCATGACAGTG 307
|||||
Qy 79 LeuAlaGln-----AsnleuHisAsnleuValLys---LeuSerIleLeuAspLeu 94
|||||
Db 308 ATTGGTGAAGCAGTTTCTAATTAATGAATAATATTTTAAAGAAATTTAAAGTATTTGAGATGC 367
|||||
Qy 95 SerGluAsnTyrLeuGlnLysAspGlyAsnGlnAlaLeuHisGlnLeuIleAspArgMet 114
|||||
Db 368 AGTGTATTAATTAAGATTAAGAGAAATGATGGTCATCATCATTTTCAAAAGCTATTTGAGAGATCA 427
|||||
Qy 115 AsnValleu 117
|||||
Db 428 AAAGTGTG 436
```

Search completed: January 31, 2003, 16:18:57
Job time : 1671.97 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 31, 2003, 11:43:51 ; Search time 46.1802 Seconds
(without alignments)
1354.737 Million cell updates/sec

Title: US-09-697-089-2_COPY_762_965

Perfect score: 1046
Sequence: 1 LKNLKLIMDKMNEEDAI.....GNRVSSDDGIAFMGVFENLK 204

Scoring table:
BLOSUM62
Xgapop 10.0 , Ygapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 segs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -DEV-X1H
-MODEL=frame.p2n.model -DEV-X1H
-Q=/cgn2_1/USPTO_pool/US09697089/runat_29012003_092754_19735/app_query.fasta.1.981
-DB=Issued_Patents_NA_QEFT-fastap-SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -SPART=1 -END=1 -MATRIX=blomsum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORR-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09697089_0CGN1.1.137_0runat_29012003_092754_19735 -NCPU=6 -ICPU=3
-NAR_X1PXY -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV.TIMECUT=120
-NAR.TIMECUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA.*

- 1: /cgn2_6/ptodata/2/ina/5A.COMB.seq.*
- 2: /cgn2_6/ptodata/2/ina/5B.COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A.COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B.COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PCTUS.COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	120.5	11.5	8722	4	US-09-221-017B-263
2	118	11.3	1386	2	US-08-910-731-5
3	112.5	10.8	1374	2	US-08-910-731-3
4	112.5	10.8	1374	2	US-08-910-731-3
5	111.5	10.7	1371	2	US-08-910-731-1
6	111.5	10.7	1371	2	US-08-910-731-1
7	111.5	10.7	1371	2	US-08-910-731-7
8	103	9.8	638	4	US-09-221-017B-1118
9	99.5	9.5	3879	4	US-09-180-438-1
10	99.5	9.5	3879	4	US-09-180-438-2
11	99.5	9.5	4123	4	US-09-180-439-7
12	99	9.5	2241	5	PCT-US95-10509-1

13	97	9.3	2859	4	US-09-099-041A-9	Sequence 9, Appl1
14	97	9.3	2859	4	US-09-245-281-9	Sequence 9, Appl1
15	97	9.3	2859	4	US-09-207-359B-9	Sequence 9, Appl1
16	97	9.3	3382	4	US-09-099-041A-7	Sequence 7, Appl1
17	97	9.3	3382	4	US-09-245-281-7	Sequence 7, Appl1
18	97	9.3	3382	4	US-09-207-359B-7	Sequence 7, Appl1
19	97	9.3	4302	4	US-09-245-281-38	Sequence 38, Appl
20	97	9.3	4302	4	US-09-207-359B-38	Sequence 38, Appl
21	91.5	8.7	633	4	US-09-385-982-206	Sequence 206, Appl
22	91	8.7	4758	3	US-09-191-647-1	Sequence 1, Appl1
23	91	8.7	4758	3	US-09-540-153-1	Sequence 1, Appl1
24	91	8.7	4758	4	US-09-540-153-1	Sequence 1, Appl1
25	90	8.6	3080	4	US-09-099-041A-25	Sequence 25, Appl
26	90	8.6	3080	4	US-09-245-281-25	Sequence 25, Appl
27	90	8.6	3080	4	US-09-207-359B-25	Sequence 25, Appl
28	89.5	8.6	2296	3	US-09-188-930-228	Sequence 228, Appl
29	88.5	8.5	4141	4	US-09-245-281-42	Sequence 42, Appl
30	88.5	8.5	4141	4	US-09-207-359B-42	Sequence 42, Appl
31	88	8.4	4843	3	US-08-986-485-1	Sequence 1, Appl1
32	87.5	8.4	3573	4	US-09-353-585-4	Sequence 4, Appl1
33	87.5	8.4	6471	4	US-09-353-585-1	Sequence 1, Appl1
34	86	8.2	3628	3	US-08-480-640A-113	Sequence 113, Appl
35	86	8.2	3628	3	US-08-295-802-113	Sequence 113, Appl
36	86	8.2	3628	4	US-08-488-237A-113	Sequence 113, Appl
37	86	8.2	3628	4	US-08-375-992A-113	Sequence 113, Appl
38	86	8.2	3842	3	US-08-480-640A-189	Sequence 189, Appl
39	86	8.2	3842	4	US-08-686-968C-189	Sequence 189, Appl
40	86	8.2	3942	4	US-08-488-237A-189	Sequence 189, Appl
41	86	8.2	3942	4	US-08-375-992A-189	Sequence 189, Appl
42	86	8.2	5785	3	US-08-480-640A-221	Sequence 221, Appl
43	86	8.2	5785	4	US-08-686-968C-221	Sequence 221, Appl
44	86	8.2	5785	4	US-08-488-237A-221	Sequence 221, Appl
45	85.5	8.2	2582	1	US-08-514-014-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-09-221-017B-263
; Sequence 263, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: Ross, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/221_017B
; FILING DATE: 23-DEC-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1182
; FILING DATE: 31-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1546
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP2911
; FILING DATE: 09-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU98/01023
; FILING DATE: 10-DEC-1998

ATTORNEY/AGENT INFORMATION:
NAME: Montoy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 263:
SEQUENCE CHARACTERISTICS:
LENGTH: 8722 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORPHYROMONAS GINGIVALIS
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1...8722
US-09-221-017B-263

Alignment Scores:
Pred. No.: 0.000101 Length: 8722
Score: 120.50 Matches: 55
Percent Similarity: 42.92% Conservative: 45
Best Local Similarity: 23.61% Mismatches: 72
Query Match: 11.52% Indels: 61
DB: 4 Gaps: 8

US-09-697-089-2_copy_762_965 (1-204) x US-09-221-017B-263 (1-8722)

Qy 1 LeuLysAsnLeuThrLeuLeuLeuMetAspAsnLeuLysMetAspGluGluAspAlaIle 20
Db 2293 CTGGACGCTCTCAGCTTCTGTAACAAGCTTCTGTAAGAGTAACAGATCAGTAACATA 2352

Qy 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPhe----- 35
Db 2353 GAGGGCTGTGATAGTCTCAGCTCAGTAACAAGCTTCTGTAAGTAACCAATCAGT 2412

Qy 36 -----HisLeuThrHisLeuSerAspIleGlyGlyMetAspTyr 49
Db 2413 AAGTAGAGGCTGTGGAACGCTCTCAGCTGTAAGCGAGCTT-----TAT 2457

Qy 50 IleValLysSerLeuSerSerGluProCysAspLeuGluIle---GlnLeuValSer 68
Db 2458 CTTTGGATTAACCAATCAGTAAGAGGCTGTGGAACGCTCAGCTCCTTAGCAACG 2517

Qy 69 CysCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuValLys 88
Db 2518 CTTGAATATCGGGTAACCAATCGTAAGCTG--GAGGGCTGTGGAACGCTCAGCTCC 2574

Qy 89 LeuSerIleLeuAspLeuSerGlnAsnTyrLeuGluLys----- 101
Db 2575 TTAGCAACGCTTGAATATCGGGTAACCAATCGTAAGCTGAGGCTGTGGAACGCTTC 2634

Qy 102 -----AspGlyAsnGlu 105
Db 2635 ACTTCGTTAAACAAGCTTCGCTAAGAAAGTAACCAATCAGTAACCTGAGGGCTGTGGA 2694

Qy 106 AlaLeuHisGluLeu-----IleAspArgMetAsnVal 116
Db 2695 CGTTCACAGCTCTTGAACAAGCTTGAATCGGGTAACCAATCGTAAGCTGAGGGT 2754

Qy 117 LeuGluGlnLeuThrAlaLeuMetLeuProTrrpGlyCysAspValGlnGlySerLeuSer 136
Db 2755 CTGGAACGCTTCACGCTCTGGAACAG-----CTTGAACCTCGGGTAACCAATC 2805

Qy 137 SerLeuLeuLysHisLeuGlnGluValProGlnLeuValLysLeuGlyLeuLysAsnTrrp 156
Db 2806 AGTAAGCTAGAGGGCTGTGGAACGCTCTCTTCGTTAACAAGCTTCGCTAAGAAAGTAAC 2865

Qy 157 ArgLeuThrAspThrGluIleArgIleLeuGlyAlaIlePheGlyLysAsnProLeuLys 176
Db 2866 CAGATCAGTAACCTAGAG-----GGCCTGGAACGCTCTCACC 2901

Qy 177 AsnPheGlnGlnLeuAsnLeuAlaGlyAsnArgValSer 189
Db 2902 TCGTAACAAACCTTCTCTCCGTAACCAATCAGT 2940

RESULT 2
US-08-910-731-5
Sequence 5, Application US/08910731
Patent No. 5932440
GENERAL INFORMATION:
APPLICANT: CHATTERJEE, DEB K.
APPLICANT: SHANDILYA, HARINI
TITLE OF INVENTION: Mammalian Ribonuclease Inhibitors and Use Thereof
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., N.W., SUITE 600
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910.731
FILING DATE: (Herewith)
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/795,395
FILING DATE: 04-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/794,546
FILING DATE: 03-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/024,057
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0942.3440003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1386 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
US-08-910-731-5

Alignment Scores:
Pred. No.: 1.13e-05 Length: 1386
Score: 118.00 Matches: 41
Percent Similarity: 45.96% Conservative: 33
Best Local Similarity: 25.47% Mismatches: 81
Query Match: 11.28% Indels: 6
DB: 2 Gaps: 4

US-09-697-089-2_copy_762_965 (1-204) x US-08-910-731-5 (1-1386)

Qy 41 SerAspIleGlyGlu---GlyMetAspTyrIleValLysSerLeuSerGluProCys 59
Db 196 AACGAGCTGGGCGATGTGCGGCTGATTCGCTCCAGGGCTGTGAGACCCCTCTCTCC 255

```

OY 60 AspleglnclutleleuValserCysCysleuserAlaasnaValylsleu 79
      ::::::::::: ||| :::::::::::
Db 256 AAGATCCAGAGCTGAGCCTCCAGAACTGCTGACGGGGCCGGCTCGCTG 315
OY 80 AlaGlnAsnleuHisasnleuValylsleuSerlleuAspleuserGluasnTyrleu 99
      ::::::::::: ||| :::::::::::
Db 316 TCCAGCAGCACTAGCAGCCTGCCACCCTGCAGAGAGCTGCACAGCAGCAACTCTTG 375
OY 100 GlnleuAspGlyasnGlnAlaMetHisGlu---leuIleAspArgMetAsnValleuGlu 118
      ::::::::::: ||| :::::::::::
Db 376 GGGGATGGGGCTGCAGCTCTCTCGAAGAGCTCTCGAAGCCTCCAGCTCCCTGGAA 435
OY 119 GlnleuThrAlaMetleuProTyrGlyCysAspValGlnleuSerleuSerleu 138
      ::::::::::: ||| :::::::::::
Db 436 AAG-----CTGCAGCTGGAGTATGAGCCTCTCGGCTCCAGCTCCGAGCCCTG 486
OY 139 leuIleuHisleuGlnleuValProGlnleuValylsleuGlyleuAsnTyrleu 158
      ::::::::::: ||| :::::::::::
Db 487 GCTCCGCTCAGGCGCAAGCCGCAAGCTTCAGAGAGCTCAGGCTGAGCAACAGCATC 546
OY 159 ThrAspThrGlnleuArglleuGlyAlaPheGlyleuAsnProleuIleuAsnPhe 178
      ::::::::::: ||| :::::::::::
Db 547 AATGAGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 603
OY 179 GlnGlnleuAsnleuAlaGlyAsnArgValserSerAspGlyTyrleuAlaPheMetGly 198
      ::::::::::: ||| :::::::::::
Db 604 GAGGCTCAGAGCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 663
OY 199 Val 199
      :::::::::::
Db 664 ATT 666

RESULT 3
US-08-910-731-3
; Sequence 3, Application US/08910731
; Patent No. 5932440
; GENERAL INFORMATION:
; APPLICANT: CHATTERJEE, DEB K.
; APPLICANT: SHANDILYA, HARINI
; TITLE OF INVENTION: Mammalian Ribonuclease Inhibitors and Use thereof
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., N.W., SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,731
; FILING DATE: (Herewith)
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/795,395
; FILING DATE: 04-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08-FEB-1997
; FILING DATE: 03-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/024,057
; FILING DATE: 16-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0942.3440003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540

```

```

; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1374 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1368
; US-08-910-731-3

Alignment Scores:
Pred. No.: 5, 88e-05 Length: 1374
Score: 112.50 Matches: 61
Percent Similarity: 38.708 Conservative: 28
Best Local Similarity: 26.528 Mismatches: 84
Query Match: 10.764 Indels: 57
DB: 2 Gaps: 9

US-09-697-089-2_COPY_762_965 (1-204) x US-08-910-731-3 (1-1374)
OY 4 leuThrIleuSerleuMetAsnIleuMetAsnGlnleuAspAlaIleuValleuAla 23
      ::::::::::: ||| :::::::::::
Db 244 ATCCAGAGAGCTGAGCCTTCAGAACTGACGAGCTGCTGCTGCTGCTGCTGCTG 303
OY 24 GlnGlyleuIleuAsnleuIleuValylsMetCysleuPheHisleuThrHis-----leuSer 41
      ::::::::::: ||| :::::::::::
Db 304 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 363
OY 42 AspIleGlyGlnleuMetAspTyrIleValylsSerleuSerleuProCysAspIleu 61
      ::::::::::: ||| :::::::::::
Db 364 GAT-----GAGGCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 417
OY 62 GlnGlnleuIleuValserCysleuSerAlaAsnAlaValylsIleuAlaGln 81
      ::::::::::: ||| :::::::::::
Db 418 GAGAGCTTCAGTGGAACTGTAACCTCAGCTGCAAGCTGCAAGCTGCAAGCTGCAAG 477
OY 82 AsnleuHisasnleuValylsleuSerlleuAspleuserGluasnTyrleuGluIle 101
      ::::::::::: ||| :::::::::::
Db 478 GTGCTCAGGCTGAACCTGACTTTAAAGAGCTGATGTGAGCAACATGCTTCATGAG 537
OY 102 AspGlyAsnGlnleuAlaMetHisGlu---leuIleAspArgMetAsnValleuGlnleu 120
      ::::::::::: ||| :::::::::::
Db 538 GCTGATATCCACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 597
OY 121 -----ThrAlaMetleuProTyrGlyCysAspValGlnGly 133
      ::::::::::: ||| :::::::::::
Db 598 AAGCTGAGAACTGCTGATCAGATCAGCAAGCTGCAAGAGATGCTGCTGCTGCTGCTG 657
OY 134 SerleuSerleuIleuValylsleuGlnleuValProGlnleuValylsleuGly--- 152
      ::::::::::: ||| :::::::::::
Db 658 TCCAAAGCTCAGCTG-----CAAGAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTG 693
OY 152 ----- 152
      :::::::::::
Db 694 AACAGCTGGGCAACAGAGCTTCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 753
OY 153 ---leuIleAsnTyrArgleuThrAspThrGlnleu----- 163
      ::::::::::: ||| :::::::::::
Db 754 AGCCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 813
OY 164 ---ArgIleleuGlnleuAlaPhePheGlyleuAsnProleuIleuAsnPheGlnleuAsn 182
      ::::::::::: ||| :::::::::::
Db 814 TGCCTGCTCTCAGAGCT-----AAGCAGAGCTGAGG-----GAACCTCAGC 855
OY 183 leuAlaGlyAsnArgValserSerAspGly 192
      ::::::::::: ||| :::::::::::
Db 856 CTAGCTGGCAATGAGCTGAGAGGATGAGGAT 865

RESULT 4
US-08-795-395-3
; Sequence 3, Application US/08795395

```

```

; Patent No. 5965399
; GENERAL INFORMATION:
; APPLICANT: CHATTERJEE, DEB K.
; APPLICANT: SHANDILYA, HARINI
; TITLE OF INVENTION: Cloning and Expression of Rat Liver and
; TITLE OF INVENTION: Porcine Liver Ribonuclease Inhibitor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVE., N.W., SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,395
; FILING DATE: 04-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/024,057
; FILING DATE: 16-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0942.3440002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1374 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1368
; US-08-795-395-3

```

```

Alignment Scores:
Pred. No.: 5.88e-05 Length: 1374
Score: 112.50 Matches: 61
Percent Similarity: 38.70% Conservative: 28
Best Local Similarity: 26.52% Mismatches: 84
Query Match: 10.76% Indels: 57
DB: 2 Gaps: 9

```

US-09-697-089-2_COPY_762_965 (1-204) x US-08-795-395-3 (1-1374)

```

QY 4 LeuThLysLeuLemetaSpasniLeLysMetasngluGluspaLaileLysLeuAla 23
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 244 ATCCAGAACAGCTGAGCTGACAGAACTGACCTGACGAGAGCTGGTGGGCTGCGCT 303
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 24 GluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThris-----LeuSer 41
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 304 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 363
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 42 AspIleGlyGlyMetAspTyrIleValLysSerLeuSerSerSerIleProCysAspLeu 61
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 364 GAT-----GAAGGCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 417
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 62 GluGluIleGluLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGln 81
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 418 GAGAGCTTCACTTGAATAGCTGTAACCTCACACAGCTACAGCTGAGCCCTGGGCTCA 477
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 82 AsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGluLys 101
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

```

DB 478 GTGCTCAGGCTGAACCTGACTTTAAAGACTAGATTTGAGCAACAGTTCATTCAGAG 537
QY 102 AspGlyAsnGluAlaLeuHisGlu---LeuIleAspArgMetAsnValLeuGluGlnLeu 120
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 538 GCTGATATCACACTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 597
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 121 -----ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGly 133
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 598 AAGCTGAGACACTGTGTATCATCATCAGCCAGCCAGCTGATGCTGTGTGTGTGTGTG 657
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 134 SerLeuSerSerLeuLeuLysHisLeuGluValProGlnLeuValLysLeuGly--- 152
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 658 TCCTAAGCCTCAGT-----CAAGAACTGACTGACTTGGGAGAGC 693
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 152 ----- 152
DB 694 AACAACTGGGCAACACAGGCACTTGCAGCAGCTGCTCAGGACTGCTGCTCCAGCTGC 753
QY 153 ---LeuLysAsnTyrArgLeuThrAspThrGluile----- 163
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 754 AGCTGAGAGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 813
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 164 ---ArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsn 182
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 814 TCCCGTGTCTTCAGAGCC-----AAGCAGAGCTGTAAG-----GAAGTCAAGC 855
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 183 LeuAlaGlyAsnArgValSerSerAspGly 192
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 856 CTAGCTGGCAATGAGCTGAGAGATGAGGT 885
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

```

RESULT 5
US-08-910-731-1
; Sequence 1, Application us/08910731
; Patent No. 5932440
; GENERAL INFORMATION:
; APPLICANT: CHATTERJEE, DEB K.
; APPLICANT: SHANDILYA, HARINI
; TITLE OF INVENTION: Mammalian Ribonuclease Inhibitors and Use Thereof
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., N.W., SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,731
; FILING DATE: (Herewith)
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/795,395
; FILING DATE: 04-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/794,546
; FILING DATE: 03-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/024,057
; FILING DATE: 16-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0942.3440003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

```



```

; LENGTH: 1371 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1368
US-08-910-731-1

Alignment Scores:
Pred. No.: 7.92e-05 Length: 1371
Score: 111.50 Matches: 48
Percent Similarity: 40.93% Conservative: 40
Best Local Similarity: 22.33% Mismatches: 90
Query Match: 10.66% Indels: 37
DB: Gaps: 7

US-09-697-089-2_COPY_762_965 (1-204) x US-08-910-731-1 (1-1371)
QY 9 MetAspAsnIleLeuMetAsnGluGuaSpAlaIleLeuAlaGluGluLeuLys---- 27
DB 88 CTCGAGAGCTGGCGGCTCTACGAGGAGCAGCTCGAAGAGCATCGCTTCCTCCGCGGCC 147
QY 28 -----AsnLeuLysLysMetCysLeuPheHisLeuThrHisLeuSerAspIleGlyIu 45
DB 148 AACCCCTCCCTGACGAGCTGTGCTC-----CGCACCAAGACAGCTGGCGCAT 195
QY 46 ---GlyMetAspTyrIleValLysSerLeuSerGluProCysAspLeuGluIle 64
DB 196 GCGGCGGTGACCTGCTGCTGACAGGCGCTGCAGAGCCCACTGCAAGATCCAGAGCTC 255
QY 65 GlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHis 84
DB 256 ACCCTGACAGACTGCTCCCTGACCGAGCGGCTCGCGGCTCGCCACGACGCTGCC 315
QY 85 AsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGluLysAspGlyAsn 104
DB 316 TCCCTGCCACAGCTGCGGAGCTGCATCTCAGCGACGACACCCACTGGGGAGACCGCGCTG 375
QY 105 GluAlaLeuHisGlu---LeuIleAspArgMetAsnValLeuGluGlnLeuThr----- 121
DB 376 CCGCTGCTCTGTGAGGGGCTCTGACCCCGAGCTGCACCTGAGAGAGCTGCAGTTGAG 435
QY 122 ---AlaLeuMetLeuProTyrPheLysAspValGlnGlySerLeuSerLeuLeuLys 140
DB 436 TACTGCGCGCTGACGCGCCGACGCTGCGAGCCCTGCGCTGCTGCTCAGGGCCACGCG 495
QY 141 HisLeuGlnGluValPro----- 146
DB 496 GCCTTGAAGAGCTCAGCGTGACGAACAGCATCGCGGAGCGCGCGCGGCTGCTG 555
QY 147 -----GlnLeuValLysLeuGlyLeuLysAsnTyrParg 157
DB 556 GGCAGGAGGTGTCGACAGCTGCTGCTGACGAGCTGAGAGAGCTGAGAGACTGAGAGCTG 615
QY 158 LeuThrAspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsn 177
DB 616 CTCAGCGCAGCCAACTGCAAAAGACTGTGCGGAAATGTGGCTCCACAG-----GCC 669
QY 178 PheGlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGly 192
DB 670 CTGAGGAGACTTGACCTGGGCGACGAACGGGCTGGCGGAGCGCGGCG 714

RESULT 6
US-08-910-731-7
; Sequence 7, Application us/08910731
; Patent No. 5932440
; GENERAL INFORMATION:
; APPLICANT: CHATTERJEE, DEB K.
; APPLICANT: SHANDILYA, HARINI
; TITLE OF INVENTION: Mammalian Ribonuclease Inhibitors and Use Thereof
; NUMBER OF SEQUENCES: 16

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., N.W., SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,731
; FILING DATE: (Herewith)
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/795,395
; FILING DATE: 04-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/794,546
; FILING DATE: 03-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/024,057
; FILING DATE: 16-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0942.3440003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1371 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
US-08-910-731-7

Alignment Scores:
Pred. No.: 7.92e-05 Length: 1371
Score: 111.50 Matches: 48
Percent Similarity: 40.93% Conservative: 40
Best Local Similarity: 22.33% Mismatches: 90
Query Match: 10.66% Indels: 37
DB: Gaps: 7

US-09-697-089-2_COPY_762_965 (1-204) x US-08-910-731-7 (1-1371)
QY 9 MetAspAsnIleLeuMetAsnGluGuaSpAlaIleLeuAlaGluGluLeuLys---- 27
DB 88 CTCGAGAGCTGGCGGCTCTACGAGGAGCAGCTCGAAGAGCATCGCTTCCTCCGCGGCC 147
QY 28 -----AsnLeuLysLysMetCysLeuPheHisLeuThrHisLeuSerAspIleGlyIu 45
DB 148 AACCCCTCCCTGACGAGCTGTGCTC-----CGCACCAAGACAGCTGGCGCAT 195
QY 46 ---GlyMetAspTyrIleValLysSerLeuSerGluProCysAspLeuGluIle 64
DB 196 GCGGCGGTGACCTGCTGCTGACAGGCGCTGCAGAGCCCACTGCAAGATCCAGAGCTC 255
QY 65 GlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHis 84
DB 256 ACCCTGACAGACTGCTCCCTGACCGAGCGGCTCGCGGCTCGCCACGACGCTGCC 315
QY 85 AsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGluLysAspGlyAsn 104
DB 316 TCCCTGCCACAGCTGCGGAGCTGCATCTCAGCGACGACACCCACTGGGGAGACCGCGCTG 375
QY 105 GluAlaLeuHisGlu---LeuIleAspArgMetAsnValLeuGluGlnLeuThr----- 121

```

Db 376 CGGCTGCTGTGAGGGGCTCCTGGAGCCCGCAGTCCACCTGAGAGAGCTGATGGAG 435
QY 122 ---AlaLeuMetLeuProTirpelysaspValGlnGlySerLeuSerSerLeuLeuys 140
Db 436 TACTGCCCGCTGACGGCCGCCAGCTGCGAGCCCTGGCTCGTCTCAGGGCCAGCGGG 495
QY 141 HisLeuGlnGluValPro----- 146
Db 496 GCCTTGAAAGAGCTCAGCGGTGAGCAACAGCATCGGCGAGCGCGCGCGCGGTGCTG 555
QY 147 -----GlnLeuValLysLeuGlyLeuLysAsnTirpArg 157
Db 556 GCCAGGGCTGCGCCGACTGCTCCCTGCGCAGCTGAGACCTCAGCTGAGAACTGCGGT 615
QY 158 LeuThrAspThrGlnIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsn 177
Db 616 CTCACGCCAGCACTGCAGAAAGACTGTGCGGAATTGGCTCCAC-----GCCCTG 669
QY 178 PheGlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGly 192
Db 670 CTGGCGGAGCTGGCCCTGGCGCAACAAGCTGGGTGATGTGGGC 714

RESULT 7

US-08-795-395-1
; Sequence 1, Application US/08795395
; Patent No. 5965399
; GENERAL INFORMATION:
; APPLICANT: CHATTERJEE, DEB K.
; APPLICANT: SHANDILYA, HARINI
; TITLE OF INVENTION: Cloning and Expression of Rat Liver and
; TITLE OF INVENTION: Porcine Liver Ribonuclease Inhibitor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVE., N.W., SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,395
; FILING DATE: 04-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/024,057
; FILING DATE: 16-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0942,3440002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1371 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1368
; US-08-795-395-1

Alignment Scores:

Pred. No.: 7,92e-05
Score: 111.50

Length: 1371
Matches: 48

Percent Similarity: 40.93% Conservative: 40
Best Local Similarity: 22.33% Mismatches: 90
Query Match: 10.66% Indels: 37
Db: 2 Gaps: 7

US-09-697-089-2_copy_762_965 (1-204) x US-08-795-395-1 (1-1371)

QY 9 MetAspAsnIleLysMetAsnGlnGluAspAlaIleLysIleAlaGlnGlyLeuLys--- 27
Db 88 CTCGACGAGCTGCGGCTCAGGAGAGACATGCAAGACATGGTTGCTCCGCGGCC 147
QY 28 -----AsnLeuLysLysMetCysLeuPheHisLeuThrHisLeuSerAspIleGly 45
Db 148 AACCCCTCCCTGACCGAGCTGTGCTC-----CGCACCAAGAGCTGGCGCAT 195
QY 46 ---GlyMetAspTyrIleValLysSerLeuSerSerGluProCysAspLeuGlnIle 64
Db 196 GCCGGCGTGCACCTGTGCTGCGAGGCGCTGCAGACCCACCTGCAGAAATCCAGAACTC 255
QY 65 GlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHis 84
Db 256 AGCTTCAGAACTGCTCCCTGACCGAGCGGCTGCGGGGTCTCTCCAGACGCTGCCG 315
QY 85 AsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlnLysAspGlyAsn 104
Db 316 TCCTGCGCCACGCTCGGAGCTGCATCTCAGCACCAACCCACTGGGGAGCGCGGCTG 375
QY 105 GlnAlaLeuHisGlu---LeuIleAspArgMetAsnValLeuGlnGlnLeuThr----- 121
Db 376 CGGCTGCTGTGAGGGCTCCTGAGACCCCGACCTGCACCTGCAAGAGCTGCAATTGGAG 435
QY 122 ---AlaLeuMetLeuProTirpelysaspValGlnGlySerLeuSerSerLeuLeuys 140
Db 436 TACTGCCCGCTGACGGCCGCCAGCTGCGAGCCCTGGCTGCTCAGGGCCAGCGGG 495
QY 141 HisLeuGlnGluValPro----- 146
Db 496 GCCTTGAAAGAGCTCAGCGGTGAGCAACAGCATCGGCGAGCGCGCGCGGTGCTG 555
QY 147 -----GlnLeuValLysLeuGlyLeuLysAsnTirpArg 157
Db 556 GCCAGGGCTGCGCCGACTGCTCCCTGCGCAGCTGAGACCTCAGCTGAGAACTGCGGT 615
QY 158 LeuThrAspThrGlnIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsn 177
Db 616 CTCACGCCAGCACTGCAGAAAGACTGTGCGGAATTGGCTCCAC-----GCCCTG 669
QY 178 PheGlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGly 192
Db 670 CTGAGGAGCTTGACCTGCGCAGCAACGCGGTGGCGGCGAGCGCGGCG 714

RESULT 8

US-09-221-017B-1118/C
; Sequence 1118, Application US/09221017B
; Patent No. 644799
; GENERAL INFORMATION:
; APPLICANT: ROSS, BRUCE C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/221,017B

FILING DATE: 23-DEC-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: MONROY, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 1118:
SEQUENCE CHARACTERISTICS:
LENGTH: 638 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORPHYROMONAS GINGIVALIS
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1...638
US-09-221-017B-1118

Alignment Scores:
Pred. No.: 0.000302 Length: 638
Score: 103.00 Matches: 43
Percent Similarity: 46.71% Conservative: 35
Best Local Similarity: 25.75% Mismatches: 55
Query Match: 9.85% Indels: 34
Gaps: 6

US-09-697-089-2_COPY_762_965 (1-204) x US-09-221-017B-1118 (1-638)

OY 45 GUGUyMetAspYrILeVallySerLeuSerGluProCysAspLeuGluGlu 64
DB 605 GAAAGCATGACTTGCTTATGATTCTCTCTAATAAAAGCTTGATCTATAC 546
OY 65 Gln-----LeuValSerCysCysLeuSer 72
DB 545 CAAATCAGTAGCTAGAGGCTGAGAACGCTCTACTTCTGTAACAAACTCGCTAGA 486
OY 73 AlaAsnAlaValysILeLeuAlaGlnAsnLeuHisAsnLeuVallyLeuSerILeLeu 92
DB 485 AGTAACCAAAATCCGTAACCTA--GAGGCTGATAGTCTACCTCGCTACCAAAACTT 429
OY 93 AspLeuSerGluAsnTYrLeuGluLys---AspGlyAsnGluAlaLeuHisGluLeu--- 110
DB 428 TCTCTCTCGATTAACCAATCAGTAGAGGCTCTGGAACGCTGCACTCGTTACG 369
OY 111 -----ILeAspArgMetAsnValLeuGluGlnLeuThra 122
DB 368 GAGCTTATCTTTGGATTAACCAATCAGTAACAGAGGCTGAGACGTCCTCAGTCC 309
OY 123 LeuMetLeuProTIPGlyCysAspValGlnGlySerLeuSerSerLeuLeuLysHisLeu 142
DB 308 TTAAACGAGCTTTAT-----CTGTCGGGTAAACCAATCAGTAAGAGGCTGTG 258
OY 143 GUGUyValProGlnLeuVallyLeuGluLysLeuLysAsnTYrArgLeuThrAspPheGlu 162

DB 257 GAACGTCTCATTGCTTAAACAAGCTCGCTTAAGAAGTAACCATAGTAACTAGAG 198
OY 163 IleArgILeLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnLeuAsn 182
DB 197 -----GGCCGTGATAGTCTCACCCTCGCTACCAAAACTTCT 162
OY 163 LeuAlaGlyAsnArgValSer 189
DB 161 CTCTCGATTAACCAATCAGT 141
RESULT 9
US-09-180-439-1
Sequence 1, Application US/09180439
Patent No. 6225532
GENERAL INFORMATION:
APPLICANT: Dixon, Mark S
APPLICANT: Hatzixanthis, Kostas
APPLICANT: Jones, David A
APPLICANT: Jones, Jonathan DG
TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof
FILE REFERENCE: 620 - 53
CURRENT APPLICATION NUMBER: US/09/180.439
EARLIER FILING DATE: 1998-12-06
EARLIER APPLICATION NUMBER: PCT/GB97/01249
EARLIER FILING DATE: 1997-05-08
EARLIER APPLICATION NUMBER: GB 9609681.3
EARLIER FILING DATE: 1996-05-09
EARLIER APPLICATION NUMBER: GB 9619924.5
EARLIER FILING DATE: 1996-09-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 3979
TYPE: DNA
ORGANISM: Lycopersicon esculentum
US-09-180-439-1

Alignment Scores:
Pred. No.: 0.0162 Length: 3979
Score: 99.50 Matches: 66
Percent Similarity: 39.57% Conservative: 44
Best Local Similarity: 23.74% Mismatches: 85
Query Match: 9.51% Indels: 83
Gaps: 16

US-09-697-089-2_COPY_762_965 (1-204) x US-09-180-439-1 (1-3979)

OY 1 LeuLysAsnLeuThrLysLeuLeuMetAspAsnILeLysMetAsnGluGluAspAlaIle 20
DB 2013 CTGAGTCTCTTACTGAACCTATTTTGGGTATTAACCTCTTAAAGGCTTATCTCTGCT 2072
OY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHis----- 36
DB 2073 TCATTTGGGG---AATCTTAACAACCTTGCTAGTGTGTAATTACAAATATCAGCTTCT 2129
OY 37 -----LeuThrHisLeuSerAsp 42
DB 2130 GGCCTTATCTCTGCTTCAATTGGCAATATGAGAAATGCAAACTGCTGTTCTCAGTGAT 2189
OY 43 -----ILeGlyGluGlyMetAspYrILeVallySerLeuSerSerGlu----- 57
DB 2190 AACGATCTCATTTGGGAAATTCCTTCATTTGTGTGCAATTTGACATCTGGAAGTGTG 2249
OY 58 -----ProCys-----AspLeuGluGlu 63
DB 2250 TATATGTCGAGAAACAATTTGAAGGGAAGATTCGCAATGTTGGTAATATCAGTGAC 2309
OY 64 ILeGlnLeuValSerCysCysLeuSerAlaAsnAlaValLys---ILeLeuAlaGlnsn 82
DB 2310 CTTCATATTTGTGCG-----ATGTCATCTAATTAATTTTCAGAGGAGAGCTCCCTTCATCT 2363
OY 83 LeuHisAsnLeuVallyLeuSerILeLeuAspLeuSerGluAsnTYrLeuGluLysAsp 102

```

Db 2364 ATTTCCAAATTTACATACATAAAATACTGATTTTGGCAGAAACAACTGAGGAGCA 2423
QY 103 -----GLYASngluAlaLeuHisgluLeuIleAspArgMetAsnValLeu 117
Db 2424 ATACCAAAATTTTGGCAATATTAGTAGCTCCAGGTTTGGATATGACAGAAAT----- 2477
QY 118 GluInleuThrAlaLeuMetLeuProTyrPglYcysAspValGlnGlySerLeuSerSer 137
Db 2478 AACAACTTCTCTGGG---ACTCTTCCAAACAATTTTAGCATTTGATGTCTACGTATAGT 2534
QY 138 LeuLeuLysHis-----LeuGluGluValPro----- 146
Db 2535 CTCACATTCGACGCAATGAACATGAGATGAATCCCTCGCTCTTGGCAATTTGCAAA 2594
QY 147 GluInleuValLysLeuGlyLeuLysAsnTyrParGlyLeuThrAspThr----- 161
Db 2595 AAGCTGCAAGTCTTGATTTAGAGACATCACTCAACGACACATTTCCCATGTGGTGG 2654
QY 162 -----GluIleArgIleLeuGlyAlaPhePheGlyLys-----AsnProLeu 175
Db 2655 GGAATCTTGCCAGAGCTGAGAGTTTAAAGTTGACATCGAATTAATTCATGACGACCTATA 2714
QY 176 Lys-----AsnPheGlnGlnLeuAsnLeuAlaGlyAsn 186
Db 2715 AGATCATCAGGGGCTGAATCATGTTCCTGATCTCCGAATCATAGATCTCTCGCAAT 2774
QY 187 ArgValSerSerAspGlyTyrPheAlaPheMetGlyValPheGluAsnLeuLys 204
Db 2775 GCATTCCTCGCAAGAC-----TTACCAACGAGTCTATTGGAACATTTGAAA 2819

RESULT 10
US-09-180-439-2
; Sequence 2, Application US/09180439
; Patent No. 6225532
; GENERAL INFORMATION:
; APPLICANT: Dixon, Mark S
; APPLICANT: Hatzixanthis, Kostas
; APPLICANT: Jones, David A
; APPLICANT: Jonathan DG
; TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof
; FILE REFERENCE: 620 - 53
; CURRENT APPLICATION NUMBER: US/09/180,439
; EARLIER FILING DATE: 1998-12-06
; EARLIER APPLICATION NUMBER: PCT/GB97/01249
; EARLIER FILING DATE: 1997-05-08
; EARLIER APPLICATION NUMBER: GB 9609681.3
; EARLIER FILING DATE: 1996-05-09
; EARLIER APPLICATION NUMBER: GB 9619924.5
; EARLIER FILING DATE: 1996-09-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 3979
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-09-180-439-2

Alignment Scores:
Pred. No.: 0.0162 Length: 3979
Score: 99.50 Matches: 66
Percent Similarity: 39.57% Conservative: 44
Best Local Similarity: 23.74% Mismatches: 85
Query Match: 9.51% Indels: 83
DB: 4 Gaps: 16

US-09-697-089-2_COPY_762_965 (1-204) x US-09-180-439-2 (1-3979)
QY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluAlaAspAlaIle 20
Db 2013 CTGAGTCTCTCTACTGAACTATTTTGGGTAATACTCTCTTAATGGCTCTATTCCT 2072
QY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHis----- 36
```

```

Db 2073 TCATTTGGGG---AATCTAAMACACTGTGATGGTTGATCTTTACAAATATACCTTTCT 2129
QY 37 -----LeuThrHisLeuSerAsp 42
Db 2130 GGCCTATCTCTGCTTCACTTTGGCAATATGGAATCTGCAAACTCTGTTCTGATGAT 2189
QY 43 -----IleGlyGluGlyMetAspTyrIleValLysSerLeuSerGlu----- 57
Db 2190 AACGATCTCATTTGGGAAATTCCTTCATTTGTGACATTTGACATCTGACCTGAGTGTG 2249
QY 58 -----ProCys-----AspLeuGlu 63
Db 2250 TATATGTCGAGAAACAATTTGAAGGAAAGCTCCGCAATTTGGTAAATATAGTGAC 2309
QY 64 IleGlnLeuValSerCysLeuSerAlaAsnAlaValLys-----IleLeuAlaGlnAsn 82
Db 2310 CTTCACATTTTGTG-----ATGTCACTTAATAGTTTCAAGAGAGAGCTCCCTTCATCT 2363
QY 83 LeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGluLysAsp 102
Db 2364 ATTTCCAAATTTAACATCACTAAATAACTGATTTTGGCAGAAACAATCTGGAGGAGCA 2423
QY 103 -----GLYASngluAlaLeuHisgluLeuIleAspArgMetAsnValLeu 117
Db 2424 ATACCAAAATTTTGGCAATATTAGTAGCCTCCAGGTTTGGATATGACAGAAAT----- 2477
QY 118 GluInleuThrAlaLeuMetLeuProTyrPglYcysAspValGlnGlySerLeuSerSer 137
Db 2478 AACAACTTCTTGGG---ACTCTTCCAAACAATTTTAGCATTTGATGTCTACGTATAGT 2534
QY 138 LeuLeuLysHis-----LeuGluGluValPro----- 146
Db 2535 CTCACATTCGACGCAATGAACATGAGATGAATCCCTCGCTCTTGGCAATTTGCAAA 2594
QY 147 GluInleuValLysLeuGlyLeuLysAsnTyrParGlyLeuThrAspThr----- 161
Db 2595 AAGCTGCAAGTCTTGATTTAGAGACATCACTCAACGACACATTTCCCATGTGGTGG 2654
QY 162 -----GluIleArgIleLeuGlyAlaPhePheGlyLys-----AsnProLeu 175
Db 2655 GGAATCTTGCCAGAGCTGAGAGTTTAAAGTTGACATCGAATTAATTCATGACGACCTATA 2714
QY 176 Lys-----AsnPheGlnGlnLeuAsnLeuAlaGlyAsn 186
Db 2715 AGATCATCAGGGGCTGAATCATGTTCCTGATCTCCGAATCATAGATCTCTCGCAAT 2774
QY 187 ArgValSerSerAspGlyTyrPheAlaPheMetGlyValPheGluAsnLeuLys 204
Db 2775 GCATTCCTCGCAAGAC-----TTACCAACGAGTCTATTGGAACATTTGAAA 2819

RESULT 11
US-09-180-439-2
; Sequence 7, Application US/09180439
; Patent No. 6225532
; GENERAL INFORMATION:
; APPLICANT: Dixon, Mark S
; APPLICANT: Hatzixanthis, Kostas
; APPLICANT: Jones, David A
; APPLICANT: Jonathan DG
; TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof
; FILE REFERENCE: 620 - 53
; CURRENT APPLICATION NUMBER: US/09/180,439
; EARLIER FILING DATE: 1998-12-06
; EARLIER APPLICATION NUMBER: PCT/GB97/01249
; EARLIER FILING DATE: 1997-05-08
; EARLIER APPLICATION NUMBER: GB 9609681.3
; EARLIER FILING DATE: 1996-05-09
; EARLIER APPLICATION NUMBER: GB 9619924.5
; EARLIER FILING DATE: 1996-09-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
```

:	LENGTH: 4123	
:	TYPE: DNA	
:	ORGANISM: Lycopersicon esculentum	
:	US-09-180-439-7	
Alignment Scores:		
Pred. NO.:	0.0172	Length: 4123
Score:	99.50	Matches: 66
Percent Similarity:	39.57%	Conservative: 44
Best Local Similarity:	23.74%	Mismatches: 85
Query Match:	9.51%	Indels: 83
DB:	4	Gaps: 16
US-09-697-089-2_COPY_762_965 (1-204) x US-09-180-439-7 (1-4123)		
QY	1	LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIle 20
DB	2157	CTGAGTCTCTTACTGACATATTTTGGTAATTAACCTCTTAATAGGCTATTCCTCT 2216
QY	21	LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHis----- 36
DB	2217	TCATTTGGG---AATCTAAACACCTGTCTAGGTGTATCTTTACAAATACAGCTTCT 2273
QY	37	-----LeuThrHisLeuSerAsp 42
DB	2274	GGCTATATTCCTCTTCATTTGGCAATATGAGAAATCTGCAAACTCTGTTCCTCAGTAT 2333
QY	43	-----IleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGlu----- 57
DB	2334	AAGCATCTCATTTGGGAAATTCCTTATTTGTGTGCAATTTACATTCACAGTGGAGTTCG 2393
QY	58	-----ProCys-----AspLeuGlu 63
DB	2394	TATATGCGAGAAACAATTGTAAGGAGAAAGTTCCGCAATGTTGGTAATATCAGTGAC 2453
QY	64	IleIleIleuValSerCysCysLeuSerAlaAsnAlaValLys---IleLeuAlaIAsn 82
DB	2454	CTTCACATTTTGTGCG---ATGTGATCTAATAGTTTCAGAGAGACCTCCCTTCATCT 2507
QY	83	LeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGluLysAsp 102
DB	2508	ATTTCACATTTTAAACATCACTAAATTAATCTGATTTTGGCAGAAACAATCTGGAGGACCA 2567
QY	103	-----GlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeu 117
DB	2568	ATACCAACAATTTTGGCATAATATTAAGTACCTCCAGGTTTGGATATGCAGAT----- 2621
QY	118	GluGluLeuThrAlaLeuMetLeuProTrrGlyCysAspValGlnGlySerLeuSerSer 137
DB	2622	AACAAACTTCTCTGG---ACTCTTCCACAAATTTTACAGATTGATGTTCACTGATAGT 2678
QY	138	LeuLeuLysHis-----LeuGluGluValPro----- 146
DB	2679	CTCAACTTCGATGGCAATGACACTAGCAGATGAATTCCTCGCTCTTGGACAAATTGCAAA 2738
QY	147	GlnLeuValLysLeuGlyLeuLysAsnTrrPargLeuThrAspThr----- 161
DB	2739	AAGCTGCAATTTCTTGATTTTAGAGACACATCAACTCAACGACACATTTCCATGTGGTGG 2798
QY	162	-----GluIleArgIleLeuGlyAlaPhePheGlyLys-----AsnProLeu 175
DB	2799	GGAATTTTGCCAGAGCTGAGAGTTTAAAGTTTGACATCGAATAAATTCATGACAGCTATA 2858
QY	176	Lys-----AsnPheGlnGlnLeuAsnLeuAlaGlyAsn 186
DB	2859	AGATCATCAGAGGCTGAATCATGTTTCTGTGATCTCCGACATCATGATGATCTTCGCAAT 2918
QY	187	ArgValSerSerAspGlyTrrPheAlaPheMetGlyValPheGluAsnLeuLys 204
DB	2919	GCATTCCTCGCAAGAC-----TTACCAAGAGATCTATTGAAACATTTGAAA 2963
RESULT 12		
CCT-US95-10509-1		

```

; Sequence 1, Application PC/TUS9510509
; GENERAL INFORMATION:
; APPLICANT: Campbell, Priscilla
; APPLICANT: Potter, Terry
; APPLICANT: Sawyer, Richard
; APPLICANT: Drevets, Douglas
; APPLICANT: Freed, John
; TITLE OF INVENTION: INTERNALIN PRODUCTS AND PROCESSES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, 35th Floor
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10509
; FILING DATE: 18 AUGUST 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2879-11-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303/863-9700
; TELEFAX: 303/863-0223
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2241 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2241
; PCT-US95-10509-1
;
Alignment Scores:
Pred. No.: 0.00753 length: 2241
Score: 99.00 Matches: 55
Percent Similarity: 41.43% Conservative: 32
Best Local Similarity: 26.19% Mismatches: 65
Query Match: 9.46% Indels: 58
DB: 5 Gaps: 11
US-09-697-089-2_COPY_762_965 (1-204) x PCT-US95-10509-1 (1-2241)
QY 1 LeuIysAsnLeuThrIleuLleuMetAspAsnIleuLysMetaSngluGlu----- 17
| | | | | : | | | | | : | | | | |
Db 184 CTTAAGATTAACTAAGTAGT-----CATATTTGAATGATATAATCAAAATGACA 237
| | | | | : | | | | | : | | | | |
QY 18 AspaIalIeLysIleuaIaIngLuIyeuLysAsnLeuLysIuLysMeCysIleupe----- 35
| | | | | : | | | | | : | | | | |
Db 238 GATATATACGTCCGCTAGCT---AATTTGCAGATCTACTCGTGGTTCGTCACACAT 294
| | | | | : | | | | | : | | | | |
QY 36 -----HisIeuThrhIsIeuSeTaSpriIegIyGluGly 46
| | | | | : | | | | | : | | | | |
Db 235 CAGATACAGATATAGACCCTTAATAATATCAACAAATTTAAATCGCGCTAGAACATATCT 354
| | | | | : | | | | | : | | | | |
QY 47 MetaSpTyrlle-----ValIysSerIeuSeuSerGlupProCysAspIeugluGluIlle 64
| | | | | : | | | | | : | | | | |
Db 355 AGTACACAGATTAGATATTAAGTGCGCTTCACGT-----TTAATAATCTA 402
| | | | | : | | | | | : | | | | |
QY 65 GlInIeuValSerCysCysIeuSeRalasnaIValIysIleIeuaIagIlnasnIeunHs 84
| | | | | : | | | | | : | | | | |
Db 403 CAGCAATATATCTTTTGGTAATCAAGTGACAGATTTAAACCAATAGT----- 450

```


Oy	149	VaLysLeuGluIleuLysAsnTrpArgLeuThrAspThrGluIleArgTyrLeuGlyAla	168
Dd	2275	ACCAATTGGGTATTATACAACAACCAGATCCGATGTGGAGCCCGTAGCTACCCAAA	2334
Oy	169	Phe-----PheGlyLysAsnProLeu-----	175
Dd	2335	ATCCTGATGATGAACAAGGCCTCACAGCATCTTTAAACTGGGAAAAAACAAATAACACAGT	2394
Oy	176	-----LysAsnPheGlnGlnLeuAsn	182
Dd	2395	GAAAGAGGAATGATCTCGCCCTGCGCTGTGAAGAACAACGAAATCATCTCTGAGGTTGGG	2454
Oy	183	LeuAlaGlyAsnArgValSerSerAspGlyTyrPleuAlaPheMetGlyValPheGluAsn	202
Dd	2455	ATGTGGGGCATCAAGTTTGGGGATGAAGAAGCAAAAAGCCTTGCGAAGAGCTTCGGCGAAC	2514

```

RESULT 15
US-09-207-359B-9
: Sequence 9, Application US/09207359B
: Patent No. 6469140
: GENERAL INFORMATION:
: APPLICANT: Berlin, John
: TITLE OF INVENTION: NOVEL MOLECULES OF THE CARP-RELATED
: TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
: FILE REFERENCE: 07334-112001
: CURRENT APPLICATION NUMBER: US/09/207,359B
: CURRENT FILING DATE: 1998-12-08
: PRIOR APPLICATION NUMBER: US 09/099,041
: PRIOR FILING DATE: 1998-06-17
: PRIOR APPLICATION NUMBER: US 09/019,942
: PRIOR FILING DATE: 1998-02-06
: NUMBER OF SEQ ID NOS: 47
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 9
: LENGTH: 2859
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-207-359B-9

```

Alignment Scores:	
Pred. No.:	0.0203
Score:	97.00
Percent Similarity:	35.00%
Best Local Similarity:	23.33%
Query Match:	9.27%
DB:	4
Gaps:	5
Length:	2859
Matches:	42
Conservative:	21
Mismatches:	65
Indels:	52

US-09-697-089-2_COPY_762_965 (1-204) X US-09-207-359B-9 (1-2859)

Oy	65	GlnLeuValSerIleCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsp-----	82
		:::: :: : : :	
Db	2005	CAGCTGGCGGCCAAGGGGCATCTGGCCCAACTACCTTAAGCTAACTACTGCAAGCCCTGC	2064
Oy	83	-----LeuHisAsnLeuValLysLeuSerIleLeu	92
Db	2065	TTCGGCGACATGCAGCGCCCTCTCTGTCTGCATCACTTCCCAGAGGGCGTCCCTA	2124
Oy	93	AspLeuSerGluAsnTrpTyrLeuGlnLysAspGlyAsnGluAlaLeuHisGluLeuIleasp	112
Db	2125	GACCTAGACAACAACCATCTCAACGACATACGGCGTGCGGAGCCTGAGCCCTGCTTACG	2184
Oy	113	ArgMetAsnValLeu-----GluGlnLeuThrAlaLeuMetLeuProTrpIcy	128
		:::: : : :	
Db	2185	CGCCTACCTGCTTCACAGACTCACGTAAACACGATCACT-----	2223
Oy	129	CysAspValGlnGlySerLeuSerSerLeuLeuLysHisLeuGluGluValProGlnLeu	148
		::: :::: : : : :	
Db	2224	-----GACGGTGGGGTAAAGGTCTTAAGCGGAAGACCTGACCAAAATAATTATG	2274
Oy	149	ValLysLeuGlnLeuLysAsnTrpArgLeuThrAspThrGluIleArgIleLeuGlyLa	168
		: : : : :	
Db	2275	ACCAATTATTTGGTTTATACCAACCAACCAAGTACCAGATGTGCGAACCGAGTACGCCAAD	2334

Qy	169	Phe-----	PhcglYLyAsnProLeu-----	175
Db	2335	ATCTGGATGATGACAAAGGCGTCACGCATCTTTAACTGGGAAAAACAAATAACAACT	2394	
Qy	176	-----	LyAsnPhcglnoLnuAsn	182
Db	2395	GAAGGAGGAAGTATCTCGCCCTGGCTGTGACAGCAACGAAATTCATCTCTGAGGTTGGG	2454	
Qy	183	LeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyValPheGluAsn	202	
		:::		
Db	2455	ATGTGGGCAATCAAGTTGGGGGATGAAGAGCAAAAGCCTTGCGACAGGCTCGGGGAAC	2514	

Search completed: January 31, 2003, 15:16:46
Job time : 51.1802.secs

THIS PAGE BLANK (USPTO)

LENGTH: 618
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(618)
US-09-864-921-181

Alignment Scores:

Pred. No.: 3,76e-126 Length: 618
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-697-089-2_copy_762_965 (1-204) x US-09-864-921-181 (1-618)

QY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIle 20
Db 7 TTGAAGAAGCTTACAAAGCTCATATGATGATTAAGATGAAGATGAAGATGCTATA 66
QY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeu 40
Db 67 AAAGTAGCTGAAGGCTGAAAAACCTGAAGAGATGCTTTATTTTCATTGACCCACTTG 126
QY 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60
Db 127 TCTGCATTTGAGAGAGGAATGATGATTAAGCTCTGTCAGTGAAGACCTGTCAC 186
QY 61 LeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80
Db 187 CTGGAAGAATTCATTAATGATCTCTGCTGCTGCTGCTGCAAAATGCAAGTAAATCCTACT 246
QY 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100
Db 247 CAGAAATCTTCACATTTGTCGCAAACTGAGCATTTCTGATTTATTCAGAAAAATTCCTGAA 306
QY 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120
Db 307 AAAGATGAATGAAGGCTCTTCATGAATGATGACAGAGATGAAGAGCTGCTGAAGACGCTC 366
QY 121 ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140
Db 367 ACCGACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 426
QY 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160
Db 427 CATTTGGAGAGGTCCTCCCAACTGCTCAAGCTTGAGTTGAAAAAACTGGAGACTCAGAT 486
QY 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln 180
Db 487 ACAGAGATTAGAAATTTTGTGTCATTTTGTGAAGAACCCTGTGAAGAACTTCACAGAG 546
QY 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPheAlaPheMetGlyValPhe 200
Db 547 TTGATTTTGGGGGAAATCGTGTGAGCAGTATGATGATGCTTGCCTCATGGGTCTATT 606
QY 201 GluAsnLeuLys 204
Db 607 GAGAAATCTTAAG 618

RESULT 2

US-09-864-921-98
Sequence 98, Application US/09864921
Patent No. US20020176853A1

GENERAL INFORMATION:

APPLICANT: Reed, John C.
APPLICANT: Pilo, Frederick F.
APPLICANT: Godzik, Adam
APPLICANT: Stehlik, Christian
APPLICANT: Damiano, Jason S.
APPLICANT: Lee, Sung-Hyun

APPLICANT: Oliveira, Vasco A.
APPLICANT: Hayashi, Hideki
APPLICANT: Pawlowski, Krzysztof
TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use
FILE REFERENCE: P-LJ 4752
CURRENT APPLICATION NUMBER: US/09/864,921
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 09/579,240
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/686,347
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 60/275,980
PRIOR FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 195
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 98

LENGTH: 1395
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (277)...(1353)
US-09-864-921-98

Alignment Scores:

Pred. No.: 1.33e-125 Length: 1395
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-697-089-2_copy_762_965 (1-204) x US-09-864-921-98 (1-1395)

QY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIle 20
Db 565 TTGAAGAAGCTTACAAAGCTCATATGATGATTAAGATGAAGATGAAGATGCTATA 624
QY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeu 40
Db 625 AAAGTAGCTGAAGGCTGAAAAACCTGAAGAGATGCTTTATTTTCATTGACCCACTG 684
QY 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60
Db 685 TCTGCATTTGAGAGAGGAATGATGATTAAGCTCTGTCAGTGAAGACCTGTCAC 744
QY 61 LeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80
Db 745 CTGGAAGAATTCATTAATGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 804
QY 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100
Db 805 CAGAAATCTTCACATTTGTCGCAAACTGAGCATTTCTGATTTATTCAGAAAAATTCCTGAA 864
QY 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120
Db 865 AAAGATGAATGAAGGCTCTTCATGAATGATGACAGAGATGAAGAGCTGCTGAAGACGCTC 924
QY 121 ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140
Db 925 ACCGACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 984
QY 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160
Db 985 CATTTGGAGAGGTCCTCCCAACTGCTCAAGCTTGAGTTGAAAAAACTGGAGACTCAGAT 1044
QY 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln 180
Db 1045 ACAGAGATTAGAAATTTTGTGTCATTTTGTGAAGAACCCTGTGAAGAACTTCACAGAG 1104
QY 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPheAlaPheMetGlyValPhe 200

```
Db 1105 TTGAATTTGGCGGAAATCGTGTGAGACGTGATGATGGCTTGCTTCATGGGTATATT 1164
QY 201 GIUASnLeuLys 204
Db 1165 GAGAAATCTTAAG 1176

RESULT 3
US-09-841-739-3
; Sequence 3, Application US/09841739
; Patent No. US20020034784A1
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/09/841,739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3072
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-841-739-3

Alignment Scores:
Pred. No.: 4,51e-125 Length: 3072
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-697-089-2_COPY_762_965 (1-204) x US-09-841-739-3 (1-3072)
QY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluLysAlaIle 20
Db 2284 TTGAAGAACCTTACAAAGCTCATTAATGATTAACATAAAGATGAAGAGAGATGCTATA 2343
QY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40
Db 2344 AACCTAGCTGGAAGGCGCTGAAAAAAGCTGAAGAGATGCTGTTATTTTCATTGACCCACTTG 2403
QY 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60
Db 2404 TCTGACATTGGAGAGAGGATGATTAACATGATCAAGTCTCTCTCAAGTGAACCCCTGTGAC 2463
QY 61 LeuGluGluIleGluLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80
Db 2464 CTTGAAGAAATTCATTAATGATCTCCCTGCTGCTTGCAAAATGACAGTGAATTCCTAGCT 2523
QY 81 GluAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100
Db 2524 CAGAATCTTCCACATTTGGTCAAACTGAGACATTTGATTATTCAGAAAATTAACCTGGAA 2583
QY 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120
Db 2584 AAAGATGGAATAATGAAGCTTCTCATGACTGACAGAGATGAAGCTGCTGATGAACAGCTC 2643
QY 121 ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLys 140
Db 2644 ACCGACATGATGCTCCCTGGGGCTGTGACGTGCAAGCAGAGCCTGAGCAGCTGTTGAAA 2703
QY 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160
Db 2704 CATTGGAGGAGAGTCCCACTCAAGCTTGAGGTTGAAAAATGGAGACTCAAGAT 2763
QY 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln 180
Db 2764 ACAGAGATTAGAAATTTAGGTGCAATTTTGGAAAGAACCCCTCTGAAAAAATCTCCAGCAG 2823
```

```
QY 181 LeuAsnLeuAlaGlyAsnArgValSerAspGlyTyrPheAlaPheMetGlyValPhe 200
Db 2824 TTGAATTTGGCGGAAATCGTGTGAGACGTGATGATGGCTTGCTTCATGGGTATATT 2883
QY 201 GIUASnLeuLys 204
Db 2884 GAGAAATCTTAAG 2895

RESULT 4
US-09-841-739-1
; Sequence 1, Application US/09841739
; Patent No. US20020034784A1
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/09/841,739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3133
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)...(3107)
US-09-841-739-1

Alignment Scores:
Pred. No.: 4,65e-125 Length: 3133
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-697-089-2_COPY_762_965 (1-204) x US-09-841-739-1 (1-3133)
QY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluLysAlaIle 20
Db 2319 TTGAAGAACCTTACAAAGCTCATTAATGATTAACATTAAGATGAATGAAGAGAGATGCTATA 2378
QY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40
Db 2379 AACCTAGCTGGAAGGCGCTGAAAAAAGCTGAAGAGATGCTGTTATTTTCATTGACCCACTTG 2438
QY 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60
Db 2439 TCTGACATTGGAGAGAGGATGATTAACATGATCAAGTCTCTCTCAAGTGAACCCCTGTGAC 2498
QY 61 LeuGluGluIleGluLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80
Db 2499 CTTGAAGAAATTCATTAATGATCTCCCTGCTGCTTGCAAAATGACAGTGAATTCCTAGCT 2558
QY 81 GluAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100
Db 2559 CAGAATCTTCCACATTTGGTCAAACTGAGACATTTGATTATTCAGAAAATTAACCTGGAA 2618
QY 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120
Db 2619 AAAGATGGAATAATGAAGCTTCTCATGACTGACAGAGATGAAGCTGCTGATGAACAGCTC 2678
QY 121 ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLys 140
Db 2679 ACCGACATGATGCTCCCTGGGGCTGTGACGTGCAAGCAGAGCCTGAGCAGCTGTTGAAA 2738
QY 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160
```

```
|||||
Db 2739 CATTGGAGAGGTCCCAACTGCTCAAGCTGGGTTGAAAACCTGAGACTCAGAT 2798
Qy 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln 180
Db 2799 ACAGAGATTAGATTGTTAGTGTCATTTTGTGAAAGAACCCCTGTAACCTCCAGCAG 2858
Qy 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPleuAlaPheMetGlyValPhe 200
Db 2859 TTGAATTTGGCGGGAATCGTGTGAGCAGTGTGATGGATGGCTTGCTCATGGGTATTT 2918
Qy 201 GluAsnLeuLys 204
Db 2919 GAGAACTTTAAG 2930

RESULT 5
US-09-864-921-96
: Sequence 96, Application US/09864921
: Patent No. US20020176853A1
: GENERAL INFORMATION:
: APPLICANT: Reed, John C.
: APPLICANT: Pio, Frederick F.
: APPLICANT: Godzik, Adam
: APPLICANT: Stehlik, Christian
: APPLICANT: Damiano, Jason S.
: APPLICANT: Lee, Sug-Hyung
: APPLICANT: Oliveira, Vasco A.
: APPLICANT: Hayashi, Hideki
: APPLICANT: Pawlowski, Krzysztof
: TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
: TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use
: FILE REFERENCE: P-LJ 4752
: CURRENT APPLICATION NUMBER: US/09/864, 921
: PRIOR FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 09/579,240
: PRIOR FILING DATE: 2000-05-24
: PRIOR APPLICATION NUMBER: US 09/686,347
: PRIOR FILING DATE: 2000-10-10
: PRIOR APPLICATION NUMBER: US 60/275,980
: PRIOR FILING DATE: 2001-03-14
: NUMBER OF SEQ ID NOS: 195
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 96
: LENGTH: 3396
: TYPE: DNA
: ORGANISM: Homo sapien
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (277)...(3348)
US-09-864-921-96

Alignment Scores:
Pred. No.: 5,27e-125 Length: 3396
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 9

US-09-697-089-2_copy_762_965 (1-204) x US-09-864-921-96 (1-3396)

Qy 1 LeuLysAsnLeuThrLysLeuIleMetLysAsnIleLysMetAsnGluLysAlaIle 20
Db 2560 TTGAAGAACCCTTAACAACCTCATATGATGAATAAAGATGAATGAAGAAGATGCTATA 2619
Qy 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40
Db 2620 AAACCTAGCTGAAGGCGCTGAAAAACCTGAAGAAGATGTGTATTTCATTGACCCACTTG 2679
Qy 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60
Db 2680 TCTGACATTGGAGAGGGAATGATTAATAGTCAAGTCTGTCTCAAGTGAACCCCTGTAC 2739
```

```
Qy 61 LeuGluGluIleGlnLeuValSerCysLeuSerAlaAsnAlaValLysIleLeuAla 80
Db 2740 CTTGAAGAAATTCATATTGATCTCCGCTGCTGTCTGCCAAATGCAGTGAATCCTAGCT 2799
Qy 81 GluAsnLeuHisAsnLeuValLysLeuSerIleLeuAsnLeuSerGluAsnTyrLeuGlu 100
Db 2800 CAGAACTTTCACAAATTTGTCAAACTGACATTTCTTGATTTATCGAAGAAATTTACCTGAA 2859
Qy 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120
Db 2860 AAAGATGAATGAAAGCTCTTCATGAATCATGATCGACAGAGATGAAGCTGTGAACAGCTC 2919
Qy 121 ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLys 140
Db 2920 ACCGCACATGATGCTGCCCTGGGGGCTGTGACGTGCAAGCAGCCTGAGAGCTGTGAAA 2979
Qy 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160
Db 2980 CATTGGAGAGGTCCCAACTGCTCAAGCTTGGGTTGAAAACCTGAGACTCAGAT 3039
Qy 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln 180
Db 3040 ACAGAGATTAGATTGTTAGTGTCATTTTGTGAAAGAACCCCTGTAACCTCCAGCAG 3099
Qy 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPleuAlaPheMetGlyValPhe 200
Db 3100 TTGAATTTGGCGGGAATCGTGTGAGCAGTGTGATGGATGGCTTGCTCATGGGTATTT 3159
Qy 201 GluAsnLeuLys 204
Db 3160 GAGAACTTTAAG 3171

RESULT 6
US-09-841-739-6
: Sequence 6, Application US/09841739
: Patent No. US20020034784A1
: GENERAL INFORMATION:
: APPLICANT: Berlin, John
: TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH
: FILE REFERENCE: 07334-328001
: CURRENT APPLICATION NUMBER: US/09/841,739
: CURRENT FILING DATE: 2001-08-29
: PRIOR APPLICATION NUMBER: US 09/697,089
: PRIOR FILING DATE: 2000-10-26
: PRIOR APPLICATION NUMBER: US 60/161,822
: PRIOR FILING DATE: 1999-10-27
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 6
: LENGTH: 3612
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-841-739-6

Alignment Scores:
Pred. No.: 5,79e-125 Length: 3612
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 10

US-09-697-089-2_copy_762_965 (1-204) x US-09-841-739-6 (1-3612)

Qy 1 LeuLysAsnLeuThrLysLeuIleMetLysAsnIleLysMetAsnGluLysAlaIle 20
Db 2755 TTGAAGAACCCTTAACAACCTCATATGATGAATAAAGATGAATGAAGAAGATGCTATA 2814
Qy 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40
Db 2815 AAACCTAGCTGAAGGCGCTGAAAAACCTGAAGAAGATGTGTATTTCATTGACCCACTTG 2874
Qy 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60
```

```
|||||
Db 2875 TCTGACATTGGAGAGGAGGATGATTACATAGTCATCTCTGCAAGTGACACCTGTGAC 2934
QY 61 LeuGlUGluIleGlnLeuValSerCysLeuSerAlaAsnAlaValLysIleLeuAla 80
Db 2935 CTTGGAAGAAATTCATTAAGTCTCTGCTGCTGTGCAAAATGACAGTAAATCCTAGCT 2994
QY 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGlnLysnTrpLeuGlu 100
Db 2995 CAGAAATCTTCACAAATTTGGTCAAACTGACACATCTTGATTTTTCAGAAAAATTAACCTGGAA 3054
QY 101 LysAspGlyAsnGluAlaLeuHisGlnLeuIleAspArgMetAsnValLeuGlnGlnLeu 120
Db 3055 AAAGATGGAATGAAGACCTTCTATGACATCGACAGCATTAACCTGTAGAACGCTC 3114
QY 121 ThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140
Db 3115 ACCGCACTGATGCTGCCCTGGGGCTGTGACGTGCAAGCAGCAGCTGAGCAGCCTGTTGAAA 3174
QY 141 HisLeuGlnGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAsp 160
Db 3175 CATTTGGAGAGAGTCCCAACACTGCTCAAGCTTGGGTTGAAAAACTGGAGACTCACAGAT 3234
QY 161 ThrGluIleArgIleLeuGlnValAlaPhePheGlyLysAsnProLeuLysAsnPhenGln 180
Db 3235 ACAGAGATTAGAAATTTTAGTGTCATTTTGGAAAAACCCCTGAAAAACTTCCAGCAG 3294
QY 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyValPhe 200
Db 3295 TTGAATTTGGCGGGAATCGTGTGACAGTGTGATGGCTTGCCCTTCATGGGTGTATTT 3354
QY 201 GlnAsnLeuLys 204
Db 3355 GAGAAATCTTAAG 3366
```

RESULT 7

US-09-841-739-4
; Sequence 4, Application US/09841739
; Patent No. US20020034784A1

GENERAL INFORMATION:

; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/09/841,739
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 3615
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3612)
US-09-841-739-4

Alignment Scores:

Pred. No.: 5.8e-125 Length: 3615
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-697-089-2_COPY_762_965 (1-204) x US-09-841-739-4 (1-3615)

```
QY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGlnGluLysAlaIle 20
Db 2755 TTGAAGAACCTTACAAAGCTCATTAATGATATACATTAAGATGAATGAGAGAGTGTATATA 2814
```

```
QY 21 LysLeuAlaGlnGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40
Db 2815 AAACCTGCTGAAGGCTGAAAAACCTGAAGAAACATGTGTTATTTATTTGACCCACTTG 2874
QY 41 SerAspIleGlyGlnLeuMetAspTrpIleValLysSerLeuSerSerGlnLysProCysAsp 60
Db 2875 TCTGACATTGGAGAGGAAATGATTCATTAAGTCTCTGCAAAATGACAGTAAATCCTAGCT 2934
QY 61 LeuGlnGluIleGlnLeuValSerCysLeuSerAlaAsnAlaValLysIleLeuAla 80
Db 2935 CTTGGAAGAAATTCATTAAGTCTCTGCTGCTGTGCAAAATGACAGTAAATCCTAGCT 2994
QY 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGlnLysnTrpLeuGlu 100
Db 2995 CAGAAATCTTCACAAATTTGGTCAAACTGACACATCTTGATTTTTCAGAAAAATTAACCTGGAA 3054
QY 101 LysAspGlyAsnGluAlaLeuHisGlnLeuIleAspArgMetAsnValLeuGlnGlnLeu 120
Db 3055 AAAGATGGAATGAAGACCTTCTATGACATCGACAGCATTAACCTGTAGAACGCTC 3114
QY 121 ThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140
Db 3115 ACCGCACTGATGCTGCCCTGGGGCTGTGACGTGCAAGCAGCAGCCTGAGCAGCCTGTTGAAA 3174
QY 141 HisLeuGlnGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAsp 160
Db 3175 CATTTGGAGAGAGTCCCAACACTGCTCAAGCTTGGGTTGAAAAACTGGAGACTCACAGAT 3234
QY 161 ThrGluIleArgIleLeuGlnValAlaPhePheGlyLysAsnProLeuLysAsnPhenGln 180
Db 3235 ACAGAGATTAGAAATTTTAGTGTCATTTTGGAAAAACCCCTGAAAAACTTCCAGCAG 3294
QY 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyValPhe 200
Db 3295 TTGAATTTGGCGGGAATCGTGTGACAGTGTGATGGCTTGCCCTTCATGGGTGTATTT 3354
QY 201 GlnAsnLeuLys 204
Db 3355 GAGAAATCTTAAG 3366
```

RESULT 8

US-09-841-739-12/c
; Sequence 12, Application US/09841739
; Patent No. US20020034784A1

GENERAL INFORMATION:

; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/09/841,739
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 3615
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-841-739-12

Alignment Scores:

Pred. No.: 5.8e-125 Length: 3615
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-697-089-2_COPY_762_965 (1-204) x US-09-841-739-12 (1-3615)

QY	1	LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluLysAlaIle	20
Db	861	TTGAAGAACCTTACAAAGCTCATATGCATACATAAAGATGAAGAAGATGCTRTA	802
QY	21	LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu	40
Db	801	AAACTAGCGTAAGGCCCTGAAAAACCTGGAAGACATGTATTATTTCATTGGACCACCTG	742
QY	41	SerAspIleGlyGluGlyMetAspIyrIleValLysSerLeuSerSergIuProCysAsp	60
Db	741	TCTGCATTGGAGAGGGAATGTGATTACATAGTCAGTCAAGCTCTGTCCAAAGTGAACCTTGAC	682
QY	61	LeuGluGluIleGlnLeuValSerCysCysLeuSerLysAsnAlaValLysIleLeuAla	80
Db	661	CTTGAGAAATTCATATTAGTCTCTCTCTGCTGTGCTGCAATGCAAGTGAACCTTCACT	622
QY	81	GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrlLeuGlu	100
Db	621	CAGATCTTCACAAATTTGGTCAAACCTGACGATCTTGATTTATCACAAAATTAACCTGAA	562
QY	101	LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu	120
Db	561	AAAGATGGAATGAAGCTCTTCATGAACTGATGACAGATGAACGTCGTAGAACAGCTC	502
QY	121	ThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSergLeuLys	140
Db	501	ACCGCATGTATCTGCCCCGCGGGCTGTGACGTCCAAAGGCCCTGACAGCTCTTGAAA	442
QY	141	HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAsp	160
Db	441	CATTGGAGAGAGCTCCCAACAACCTGTCAGACTGTGGGTGAAAACCTGAGACTACAGAT	382
QY	161	ThrgluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln	180
Db	381	ACAGAGATTAGATTTTTAGTGTGATTTTTGGAAAAGAACCTCGAAAACCTTCACAGAG	322
QY	181	LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyValPhe	200
Db	321	TTGAATTTGGCGGGAATGCTGTGACAGATGATGATGGCTTGCTTCATGGGTGATTT	262
QY	201	GluAsnLeuLys	204
Db	261	GAGAACTCTTAAG	250
RESULT 9			
US-09-864-761-4236			
: Sequence 4236, Application US/09864761			
: Patent No. US20020048763A1			
GENERAL INFORMATION:			
: APPLICANT: Penn, Sharon G.			
: APPLICANT: Rank, David R.			
: APPLICANT: Hanzel, David K.			
: APPLICANT: Chen, Wensheng			
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR			
: FILE REFERENCE: Aecmice-X-1			
: CURRENT APPLICATION NUMBER: US/09/864,761			
: PRIOR FILING DATE: 2001-05-23			
: PRIOR APPLICATION NUMBER: US 60/180,312			
: PRIOR FILING DATE: 2000-02-04			
: PRIOR APPLICATION NUMBER: US 60/207,456			
: PRIOR FILING DATE: 2000-05-26			
: PRIOR APPLICATION NUMBER: US 09/632,366			
: PRIOR FILING DATE: 2000-08-03			
: PRIOR APPLICATION NUMBER: GB 24263.6			
: PRIOR FILING DATE: 2000-10-04			
: PRIOR APPLICATION NUMBER: US 60/236,359			
: PRIOR FILING DATE: 2000-09-27			
: PRIOR APPLICATION NUMBER: PCT/US01/00666			
: PRIOR FILING DATE: 2001-01-30			
: PRIOR APPLICATION NUMBER: PCT/US01/00667			
: PRIOR FILING DATE: 2001-01-30			
: PRIOR APPLICATION NUMBER: PCT/US01/00666			

```

PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00669
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00665
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00668
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00663
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00662
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00661
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00670
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: US 60/234,687
PRIORITY FILING DATE: 2000-09-21
PRIORITY APPLICATION NUMBER: US 09/608,408
PRIORITY FILING DATE: 2000-06-30
PRIORITY APPLICATION NUMBER: US 09/774,203
PRIORITY FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
SEQ ID NO 4236
LENGTH: 421
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC011232.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 16
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
US-09-864-761-4236

Alignment Scores:
Pred. No.: 2,79e-17 Length: 421
Score: 202.00 Matches: 38
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 19.31% Indels: 0
Gaps: 10

US-09-697-089-2_COPY_762_965 (1-204) x US-09-864-761-4236 (1-421)
QY 167 GYALAPHEGGLYLYSASnProLeuLySAnPheGInGInLeuASnLeuAlaGlyASn 186
|||
Db 181 GGTGATTTTTTGGAAAGAACCTCTGAAAACCTTCCAGCAGCTTGATTTGGCGGGAAT 240
|||
QY 187 ArgValSerAspGlyTTPLeuAlaPheMetGlyAlaPheGInLeuLyS 204
|||
Db 241 CGTGAGCACTGATGATGATGCTTGCCCTTCATGGGTGATTTGGAATCTTAAG 294
|||

RESULT 10
US-09-986-224-20
Sequence 20, Application US/09986224
Patent No. US20020150920A1
GENERAL INFORMATION:
APPLICANT: Bertin, John
APPLICANT: Wang, Weiye
APPLICANT: Blatcher, Maria
TITLE OF INVENTION: NOVEL MOLECULES OF THE NBS/LRR PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-333001
CURRENT APPLICATION NUMBER: US/09/986,224
2001-10-22
CURRENT FILING DATE: 2001-10-22
PRIORITY APPLICATION NUMBER: US 09/848,035

```

[illegible][illegible]

QY 171 GlyLysAsnProLeuLysAsnPhenGlnGlnLeuAsnLeuAlaGlyAsnArgValSerSer 190
Db 2788 AGCAGCAGCT-----AAGAGCCTGCTCAATCTGAACCTTCTAGGCAATGAAATGTGACT 2841

QY 191 AspGly 192
Db 2842 GATGCT 2847

RESULT 12
US-09-938-842A-1194
; Sequence 1194, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938, 842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227, 866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264, 647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300, 111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1194
; LENGTH: 1581
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1194

Alignment Scores:
Pred. No.: 8.69e-06 Length: 1581
Score: 120.00 Matches: 58
Percent Similarity: 40.08% Conservative: 41
Best Local Similarity: 23.48% Mismatches: 82
Query Match: 11.47% Indels: 66
DB: 9 Gaps: 11

US-09-697-089-2_COPY_762_965 (1-204) x US-09-938-842A-1194 (1-1581)

QY 3 AsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGlnGluAspAlaIleLysLeu 22
Db 628 AATTTCAGCAGCAGGCTATGATGATCAGCTCAATGGCTCCGGATTCTCTAGGCAAGTTA 687

QY 23 AlaGlnGlyLeuLys--AsnLeuLysLysMetCysLeuPheHisLeu----- 37
Db 688 TCGAGTCTTTCAGGCTAGTCTCTCTGAGAATGTATCATGCTACTACCGGCAACATA 747

QY 38 -----ThrHisLeuSerAspIleGlyGlu----- 45
Db 748 GGAGGGCTAATTCTTTCAGCAGGCTGATTGCAATGCAATAGAAATGGTCAGCTCCCT 807

QY 46 -----GlyMetAspTyrIleValLysSerLeuSer 55
Db 808 GAGCTCTAAGAGATTTCTTAACCTGCTCAACCTGAATCTTAGTGGAAACCAATTATCA 867

QY 56 SerGluProCysAspLeuGlu-----IleGlnLeuValSerCysCysLeuSerAlaAsn 74
Db 868 TCTCTTCATGCTGCTAATTATAGATGATGATCATCTTGGAGAACTGATTGGCTCTAAC 927

QY 75 AlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeu 94
Db 928 AGCCTCTCTATTCCTCCCGAATCTAATGTCTCTCTGAGACCTAAGAGAGCTCGATGTT 987

QY 95 SerGluAsnTyrLeuGlnLys----- 101
Db 988 GAAACAAATTAACATCGAAGAGATTCACATAGATATCTGCTGCTTCTTCATGGAGAAGA 1047

QY 102 -----AspGlyAsn-----GluAlaLeuHisGlnLeuIleAspArgMetAsnVal 116
Db 1048 CTCCTGCAAGATTTCACAAAGACTTAACACTCTTCCAGAAAGCTGTTGGGAAATTATCTACC 1107

QY 117 LeuGlnGlnLeuThrAla-----LeuMetLeuProTyrPglyCysAspVal 131
Db 1108 TTAGAGATTCTGACTGCTCGTTAATAATCAATTCGGACGCTACCCACAAACATGCTCTCC 1167

QY 132 GlnGlySerLeuSerSerLeu-----LeuLysHisLeuGlnGluValProGln--- 147
Db 1168 ATGCTTAACCTCAAAAGACTGAGTGTCAACGAGCTTGAAGTCACTCCAGAGAGT 1227

QY 148 -----LeuValLysLeuGlyLeuLysAsnTyrPargLeuThrAspThr 161
Db 1228 TTATGTTATGCCAAACACCTTGTTAAGCTTAAACATCGGGAAC-----AATTTCGC 1278

QY 162 GluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPhenGlnLeu 181
Db 1279 AACCTTAAGTCACTCCCGGATTATAGCAAC-----CTTGAGAACCTAAGAGAGCTT 1332

QY 182 AsnLeuAlaGlyAsnArgVal 188
Db 1333 GATATGAGCAATTAACAGATC 1353

RESULT 13
US-09-905-291A-27
; Sequence 27, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Flivarov, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertschen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paonl, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905, 291A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143, 048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145, 698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146, 222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090


```

1 PRIOR FILING DATE: 1999-09-15
2 PRIOR APPLICATION NUMBER: PCT/US99/21547
3 PRIOR FILING DATE: 1999-09-15
4 PRIOR APPLICATION NUMBER: PCT/US99/23089
5 PRIOR FILING DATE: 1999-10-05
6 PRIOR APPLICATION NUMBER: PCT/US99/28214
7 PRIOR FILING DATE: 1999-11-29
8 PRIOR APPLICATION NUMBER: PCT/US99/28313
9 PRIOR FILING DATE: 1999-11-30
10 PRIOR APPLICATION NUMBER: PCT/US99/28564
11 PRIOR FILING DATE: 1999-12-02
12 PRIOR APPLICATION NUMBER: PCT/US99/28565
13 PRIOR FILING DATE: 1999-12-02
14 PRIOR APPLICATION NUMBER: PCT/US99/30095
15 PRIOR FILING DATE: 1999-12-16
16 PRIOR APPLICATION NUMBER: PCT/US99/30911
17 PRIOR FILING DATE: 1999-12-20
18 PRIOR APPLICATION NUMBER: PCT/US99/30999
19 PRIOR FILING DATE: 1999-12-20
20 PRIOR APPLICATION NUMBER: PCT/US00/00219
21 PRIOR FILING DATE: 2000-01-05
22 NUMBER OF SEQ ID NOS: 423
23 SEQ ID NO 27
24 LENGTH: 2479
25 TYPE: DNA
26 ORGANISM: Homo sapiens
27 OS-09-905-291A-27

```

PRIOR FILING DATE: 1998-09-10	PRIOR APPLICATION NUMBER: 60/099811
PRIOR FILING DATE: 1998-09-10	PRIOR APPLICATION NUMBER: 60/099812
PRIOR FILING DATE: 1998-09-10	PRIOR APPLICATION NUMBER: 60/099813
PRIOR FILING DATE: 1998-09-10	PRIOR APPLICATION NUMBER: 60/099814
PRIOR FILING DATE: 1998-09-17	PRIOR APPLICATION NUMBER: 60/100858
PRIOR FILING DATE: 1998-09-17	PRIOR APPLICATION NUMBER: 60/101922
PRIOR FILING DATE: 1998-09-24	PRIOR APPLICATION NUMBER: 60/106032
PRIOR FILING DATE: 1998-10-28	PRIOR APPLICATION NUMBER: 60/109304
PRIOR FILING DATE: 1998-11-20	PRIOR APPLICATION NUMBER: 60/125778
PRIOR FILING DATE: 1999-03-23	PRIOR APPLICATION NUMBER: 60/139695
PRIOR FILING DATE: 1999-06-15	PRIOR APPLICATION NUMBER: 60/145070
PRIOR FILING DATE: 1999-07-20	PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26	PRIOR APPLICATION NUMBER: 60/149396
PRIOR FILING DATE: 1999-08-17	PRIOR APPLICATION NUMBER: 60/164945
PRIOR FILING DATE: 1999-12-07	PRIOR APPLICATION NUMBER: 60/1918874
PRIOR FILING DATE: 1997-08-26	PRIOR APPLICATION NUMBER: 88/933821
PRIOR FILING DATE: 1997-09-19	PRIOR APPLICATION NUMBER: 88/960507
PRIOR FILING DATE: 1997-10-29	PRIOR APPLICATION NUMBER: 89/114844
PRIOR FILING DATE: 1998-07-14	PRIOR APPLICATION NUMBER: 89/136801
PRIOR FILING DATE: 1998-08-19	PRIOR APPLICATION NUMBER: 89/136804
PRIOR FILING DATE: 1998-08-19	PRIOR APPLICATION NUMBER: 89/136828
PRIOR FILING DATE: 1998-08-19	PRIOR APPLICATION NUMBER: 89/158342
PRIOR FILING DATE: 1998-09-21	PRIOR APPLICATION NUMBER: 89/180997
PRIOR FILING DATE: 1998-09-10	PRIOR APPLICATION NUMBER: 89/202088
PRIOR FILING DATE: 1998-12-08	PRIOR APPLICATION NUMBER: 89/254311
PRIOR FILING DATE: 1999-03-03	PRIOR APPLICATION NUMBER: 89/254460
PRIOR FILING DATE: 1999-03-09	PRIOR APPLICATION NUMBER: 89/254465
PRIOR FILING DATE: 1999-03-05	PRIOR APPLICATION NUMBER: 89/284663
PRIOR FILING DATE: 1999-04-15	PRIOR APPLICATION NUMBER: 89/332928
PRIOR FILING DATE: 1999-06-14	PRIOR APPLICATION NUMBER: 89/333077
PRIOR FILING DATE: 1999-06-14	PRIOR APPLICATION NUMBER: 89/333077
PRIOR FILING DATE: 1999-08-25	PRIOR APPLICATION NUMBER: 89/360138
PRIOR FILING DATE: 1999-08-25	PRIOR APPLICATION NUMBER: 89/360138
PRIOR FILING DATE: 1999-08-25	PRIOR APPLICATION NUMBER: 89/360139
PRIOR FILING DATE: 1999-10-18	PRIOR APPLICATION NUMBER: 89/403297
PRIOR FILING DATE: 1999-10-18	PRIOR APPLICATION NUMBER: 89/403297
PRIOR FILING DATE: 1999-11-10	PRIOR APPLICATION NUMBER: 89/423741

```

: PRIOR APPLICATION NUMBER: 09/423844
: PRIOR FILING DATE: 1999-11-12
: PRIOR APPLICATION NUMBER: 09/522342
: PRIOR FILING DATE: 2000-03-09
: PRIOR APPLICATION NUMBER: 09/548815
: PRIOR FILING DATE: 2000-04-13
: PRIOR APPLICATION NUMBER: 09/664610
: PRIOR FILING DATE: 2000-09-18
: PRIOR APPLICATION NUMBER: 09/665350
: PRIOR FILING DATE: 2000-09-18
: PRIOR APPLICATION NUMBER: 09/709238
: PRIOR FILING DATE: 2000-11-08
: PRIOR APPLICATION NUMBER: 09/767609
: PRIOR FILING DATE: 2001-01-22
: PRIOR APPLICATION NUMBER: 09/802706
: PRIOR FILING DATE: 2001-03-09
: PRIOR APPLICATION NUMBER: 09/808689
: PRIOR FILING DATE: 2001-03-14
: PRIOR APPLICATION NUMBER: 09/866028
: PRIOR FILING DATE: 2001-05-25
: PRIOR APPLICATION NUMBER: 09/870574
: PRIOR FILING DATE: 2001-05-30
: PRIOR APPLICATION NUMBER: 09/872035
: PRIOR FILING DATE: 2001-06-01
: PRIOR APPLICATION NUMBER: 09/886342
: PRIOR FILING DATE: 2001-06-19
: PRIOR APPLICATION NUMBER: PCT/US98/14552
: PRIOR FILING DATE: 1998-07-14
: PRIOR APPLICATION NUMBER: PCT/US98/18824
: PRIOR FILING DATE: 1998-09-10
: PRIOR APPLICATION NUMBER: PCT/US98/19093
: PRIOR FILING DATE: 1998-09-14
: PRIOR APPLICATION NUMBER: PCT/US98/19330
: PRIOR FILING DATE: 1998-09-16
: PRIOR APPLICATION NUMBER: PCT/US98/19437
: PRIOR FILING DATE: 1998-09-17
: PRIOR APPLICATION NUMBER: PCT/US98/24855
: PRIOR FILING DATE: 1998-11-20
: PRIOR APPLICATION NUMBER: PCT/US98/25108
: PRIOR FILING DATE: 1998-12-01
: PRIOR APPLICATION NUMBER: PCT/US98/25190
: PRIOR FILING DATE: 1998-11-25
: PRIOR APPLICATION NUMBER: PCT/US99/05028
: PRIOR FILING DATE: 1999-03-08
: PRIOR APPLICATION NUMBER: PCT/US99/12252
: PRIOR FILING DATE: 1999-06-02
: PRIOR APPLICATION NUMBER: PCT/US99/20111
: PRIOR FILING DATE: 1999-09-01
: PRIOR APPLICATION NUMBER: PCT/US99/20594
: PRIOR FILING DATE: 1999-09-08
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/21547

Alignment Scores:
Pred. No.:      4.95e-05      Length:      2479
Score:          116.50      Matches:      46
Percent Similarity: 44.59%      Conservative: 20
Best Local Similarity: 31.08%      Mismatches:  59
Query Match:    11.14%      Indels:      23
DB:              9      Gaps:          7

US-09-697-089-2_COPY_762_965 (1-204) x US-10-066-500-114 (1-2479)

QY      1  LeuylsAnleuThrlylsleuIlleMeAsp---AsnIllelysmetksnclugltnuaspala 19
      |||  ::::|::|  ::::|::|::|::|::|  ||:::  ||:::|
Db      870  CTCACGACCTTGAGGCGCTATTATGTGTGACGAGACCTCCTGACCAACAG----- 920

QY      20  IllelyslleuIlleagluylleuylsAnleuIllelysmetkylsleuThheHlsleuThrls 39
      |||  ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      921  ---GGTATCGCGCGAGGCG-----ACCTTGACGCATCTCACCAAG 956

40  LeuSerAspIleGlygluylMetAspTyrIlleValylSerLeuSerIupProCys 59

```

```

Db 957 CTCACGAA-----TTTCAATTGACGTAATTCGCTGCCACCCCTCCTCC 1004
QY 60 ASPLLEUGLUUILLGLINLEUVALSERCYSLSEUSERALASNAIValys---Ile 78
Db 1005 GATCTCCAGGACGATCGATCTGATGAGCTCTATTGACGACGACCAAGTAACCAACAT 1064
QY 79 LEUAlAGLInASnLEuHISnLEuVALysSerLIEuASpLEuSERGLuAsnTYr 98
Db 1065 CCTTGACAGCCTTCTCAATTCGCTGATAGCTGGAACGCTGATATATCAACACCAA 1124
QY 99 LEUGLUYASpGLYASnGLUAlALEuHISGLUEuLIEASpARGMETASnVALLeuGIU 118
Db 1125 CTGCGGATG-----CTGACTCAAGGGGTTTTTGATATATCTCCAACCTGAAG 1172
QY 119 GINLEUTHALeUmetLEUProTIPGLYCYASpVALGInGLYSerLEuSERSerLEU 138
Db 1173 CAGCTCAGCTCGGAAATACCTTGCTTTGTGACTGC-----AGTATTAATGGGTC 1226
QY 139 LEUYSHISLEUGLUValPro 146
Db 1227 ACAGATGGCTCAAAATATATCCCT 1250

RESULT 15
US-09-902-853-27
: Sequence 27, Application US/09902853
: Publication No. US20020192659A1
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, A.
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth, J.
: APPLICANT: Kijavir, Ivar J.
: APPLICANT: Mathier, Jennie P.
: APPLICANT: Pan, James
: APPLICANT: Paonli, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William, I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE OF INVENTION: Acids Encoding the Same
: FILE REFERENCE: 10466-14
: CURRENT APPLICATION NUMBER: US/09/902,853
: PRIOR APPLICATION NUMBER: US/09/665,350
: PRIOR FILING DATE: 2000-09-18
: PRIOR APPLICATION NUMBER: US 60/143,048
: PRIOR FILING DATE: 1999-07-07
: PRIOR APPLICATION NUMBER: US 60/145,698
: PRIOR FILING DATE: 1999-07-26
: PRIOR APPLICATION NUMBER: US 60/146,222
: PRIOR FILING DATE: 1999-07-28
: PRIOR APPLICATION NUMBER: PCT/US99/20594
: PRIOR FILING DATE: 1999-09-08
: PRIOR APPLICATION NUMBER: PCT/US99/20944
: PRIOR FILING DATE: 1999-09-13
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/21547

```

```

: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/23089
: PRIOR FILING DATE: 1999-10-05
: PRIOR APPLICATION NUMBER: PCT/US99/28214
: PRIOR FILING DATE: 1999-11-29
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: 1999-11-30
: PRIOR APPLICATION NUMBER: PCT/US99/28564
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/28565
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: PCT/US99/30911
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US99/30999
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US00/00219
: PRIOR FILING DATE: 2000-01-05
: NUMBER OF SEQ ID NOS: 423
: SEQ ID NO 27
: LENGTH: 2479
: TYPE: DNA
: ORGANISM: Homo Sapien
: US-09-902-853-27

Alignment Scores:
Pred. No.: 4.95e-05 Length: 2479
Score: 116.50 Matches: 46
Percent Similarity: 44.59% Conservative: 20
Best Local Similarity: 31.08% Mismatches: 59
Query Match: 11.14% Indels: 23
Gaps: 7

US-09-697-089-2_COPY_762_965 (1-204) x US-09-902-853-27 (1-2479)
QY 1 LEUYSASnLEUTHrLYSLEuLIEuMetASP---ASnILEYSEuMetASnGLUASpAlA 19
Db 870 CTCACGAGCTTGAGGCGTCTTATTGTGGACGGGACCTCTGACCAACAG----- 920
QY 20 ILEYSLEuAlAGLUGLYLeuLYSASnLEuLYSMETCYSLSEuHISLEUTHrHIS 39
Db 921 ---GGTATCGCCGAGGCG-----ACCTTCAGCCATCTGACCAAG 956
QY 40 LEUSERASpLIEGLYSLUuLYMetASpTYRILEVALYSerLEuSERSerGLUPROCYS 59
Db 957 CTCACGAA-----TTTCAATTGACGTAATTCGCTGCCACCCCTCCTCC 1004
QY 60 ASPLLEUGLUUILLGLINLEUVALSERCYSLSEUSERALASNAIValys---Ile 78
Db 1005 GATCTCCAGGACGATCGATCTGATCAGGCTCTATTGACGACGACCAAGTAACCAACAT 1064
QY 79 LEUAlAGLInASnLEuHISnLEuVALysSerLIEuASpLEuSERGLuAsnTYr 98
Db 1065 CCTTGACAGCCTTCTCAATTCGCTGATAGCTGGAACGCTGATATATCAACACCAA 1124
QY 99 LEUGLUYASpGLYASnGLUAlALEuHISGLUEuLIEASpARGMETASnVALLeuGIU 118
Db 1125 CTGCGGATG-----CTGACTCAAGGGGTTTTTGATATATCTCCAACCTGAAG 1172
QY 119 GINLEUTHALeUmetLEUProTIPGLYCYASpVALGInGLYSerLEuSERSerLEU 138
Db 1173 CAGCTCAGCTCGGAAATACCTTGCTTTGTGACTGC-----AGTATTAATGGGTC 1226
QY 139 LEUYSHISLEUGLUValPro 146
Db 1227 ACAGATGGCTCAAAATATATCCCT 1250

```

Search completed: January 31, 2003, 18:05:20
 Job time : 61.4923 secs

THIS PAGE BLANK (uspto)

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 31, 2003, 13:16:47 ; Search time 2594.61 Seconds
(without alignments)
1976.816 Million cell updates/sec

Title: US-09-697-089-2_COPY_762_965
Sequence: 1 LKNTKLIMNIRKIMEDAT.....GNRVSSDGMFLMGVFNELK 204
1046

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

MODEL=frame+_p2n.model DEV=xlh
-O=/cgn2_1/USPTO_SPOOL/US09697089/turnat_29012003_092754_19749/app_query.fasta.1.981
-DB=Pending_Patents_NA_Main -QFMT=fastap -SUFFIX=p2n.rpnm -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=Blomsum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09697089@cgn_1_1.3083@turnat_29012003_092754_19749
-NCPU=6 -ICPU=3 -NO_XLPHY -NO_MAP -LARGQUERY -NEG_SCORES=0 -WAIT -LONGIOG
-DEV_TIMEOUT=130 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Pending_Patents_NA_Main:**
1: /cgn2_6/ptodata/2/pna/US0978_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US082_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US083_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US084_COMB.seq:*
8: /cgn2_6/ptodata/2/pna/US085_COMB.seq:*
9: /cgn2_6/ptodata/2/pna/US086_COMB.seq:*
10: /cgn2_6/ptodata/2/pna/US087_COMB.seq:*
11: /cgn2_6/ptodata/2/pna/US088_COMB.seq:*
12: /cgn2_6/ptodata/2/pna/US089_COMB.seq:*
13: /cgn2_6/ptodata/2/pna/US090_COMB.seq:*
14: /cgn2_6/ptodata/2/pna/US091_COMB.seq:*
15: /cgn2_6/ptodata/2/pna/US092_COMB.seq:*
16: /cgn2_6/ptodata/2/pna/US093_COMB.seq:*
17: /cgn2_6/ptodata/2/pna/US094_COMB.seq:*
18: /cgn2_6/ptodata/2/pna/US095_COMB.seq:*
19: /cgn2_6/ptodata/2/pna/US095B_COMB.seq:*
20: /cgn2_6/ptodata/2/pna/US095C_COMB.seq:*
21: /cgn2_6/ptodata/2/pna/US095D_COMB.seq:*
22: /cgn2_6/ptodata/2/pna/US095E_COMB.seq:*
23: /cgn2_6/ptodata/2/pna/US096B_COMB.seq:*
24: /cgn2_6/ptodata/2/pna/US096C_COMB.seq:*
25: /cgn2_6/ptodata/2/pna/US096D_COMB.seq:*
26: /cgn2_6/ptodata/2/pna/US096E_COMB.seq:*
27: /cgn2_6/ptodata/2/pna/US097A_COMB.seq:*
28: /cgn2_6/ptodata/2/pna/US097A_COMB.seq:*

Result No.	Score	Query Match	Length	DB ID	Description
1	1046	100.0	618	33	US-09-864-921-181
2	1046	100.0	1395	27	US-09-866-347-98
3	1046	100.0	1395	33	US-09-864-921-98
4	1046	100.0	2950	1	PCT-US00-35017A-416
5	1046	100.0	3072	1	PCT-US00-29643-3
6	1046	100.0	3072	27	US-09-697-089-3

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

```
7 1046 100.0 3072 32 US-09-841-739-3 Sequence 3, App11
8 1046 100.0 3075 41 US-10-156-733-1 Sequence 1, App11
9 1046 100.0 3133 1 PCT-US00-29643-1 Sequence 1, App11
10 1046 100.0 3133 27 US-09-697-089-1 Sequence 1, App11
11 1046 100.0 3133 32 US-09-841-739-1 Sequence 1, App11
12 1046 100.0 3152 18 US-09-471-275-7095 Sequence 7095, Ap
13 1046 100.0 3213 1 PCT-US01-07143-23 Sequence 23, App1
14 1046 100.0 3213 42 US-10-221-097-23 Sequence 23, App1
15 1046 100.0 3219 41 US-10-156-733-14 Sequence 14, App1
16 1046 100.0 3260 1 PCT-US01-14826-66 Sequence 66, App1
17 1046 100.0 3260 26 US-09-667-298-66 Sequence 66, App1
18 1046 100.0 3396 27 US-09-686-347-96 Sequence 96, App1
19 1046 100.0 3396 33 US-09-664-921-96 Sequence 96, App1
20 1046 100.0 3545 18 US-09-491-404-1319 Sequence 1319, Ap
21 1046 100.0 3545 34 US-09-922-279-1319 Sequence 1319, Ap
22 1046 100.0 3545 34 US-09-922-279A-1319 Sequence 1319, Ap
23 1046 100.0 3612 27 US-09-697-089-6 Sequence 6, App11
24 1046 100.0 3612 32 US-09-841-739-6 Sequence 6, App11
25 1046 100.0 3615 1 PCT-US00-29643-4 Sequence 4, App11
26 1046 100.0 3615 1 PCT-US00-29643-6 Sequence 6, App11
27 1046 100.0 3615 27 US-09-697-089-4 Sequence 4, App11
28 1046 100.0 3615 27 US-09-697-089-12 Sequence 12, App1
29 1046 100.0 3615 32 US-09-841-739-4 Sequence 4, App11
30 1046 100.0 3615 32 US-09-841-739-12 Sequence 12, App1
31 1046 100.0 4626 1 PCT-US02-09921-429 Sequence 429, App
32 905 86.5 6012 22 US-09-557-676-911 Sequence 911, App
33 905 86.5 6012 22 US-09-557-676-917 Sequence 917, App
34 905 86.5 6012 38 US-10-042-938-917 Sequence 917, App
35 905 86.5 6012 38 US-10-042-938-917 Sequence 917, App
36 737 70.5 642 18 US-09-404-284-4030 Sequence 4030, Ap
37 737 70.5 642 19 US-09-524-038-4030 Sequence 4030, Ap
38 737 70.5 642 38 US-10-011-154-4030 Sequence 4030, Ap
39 645 61.7 407 17 US-09-359-067-46762 Sequence 46762, A
40 645 61.7 4275 76 US-60-324-185-22577 Sequence 22577, A
41 626 59.8 2735 1 PCT-US00-26524B-1253 Sequence 1253, Ap
42 626 59.8 2735 40 US-10-106-698-1263 Sequence 1263, Ap
43 622 59.5 791 1 PCT-US01-14826-498 Sequence 498, App
44 622 59.5 791 18 US-09-489-036-31154 Sequence 31154, A
45 622 59.5 791 22 US-09-577-408-3075 Sequence 3075, Ap
```

ALIGNMENTS

```
RESULT 1
US-09-864-921-181
: Sequence 181, Application US/096864921
: GENERAL INFORMATION:
: APPLICANT: Reed, John C.
: APPLICANT: Pio, Frederick F.
: APPLICANT: Godzik, Adam
: APPLICANT: Stehlik, Christian
: APPLICANT: Damiano, Jason S.
: APPLICANT: Lee, Sug-Hyung
: APPLICANT: Oliveira, Vasco A.
: APPLICANT: Hayashi, Hioki
: APPLICANT: Pawlowski, Krzysztof
: TITLE OF INVENTION: Novel Card Domain Containing
: FILE REFERENCE: P-LJ 4752
: CURRENT APPLICATION NUMBER: US/09/864,921
: CURRENT FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 09/579,240
: PRIOR FILING DATE: 2000-05-24
: PRIOR APPLICATION NUMBER: US 09/686,347
: PRIOR FILING DATE: 2000-10-10
: PRIOR APPLICATION NUMBER: US 60/275,980
: PRIOR FILING DATE: 2001-03-14
: NUMBER OF SEQ ID NOS: 195
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 181
: LENGTH: 618
: TYPE: DNA
: ORGANISM: Homo sapiens
```

```
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)...(618)
US-09-864-921-181
Alignment Scores:
Pred. No.: 2,11e-98 Length: 618
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
```

US-09-697-089-2_COPY_762_965 (1-204) x US-09-864-921-181 (1-618)

```
QY 1 LeuysanleuThrlyleuIleMetAspanslleYmetAsnlgluIleuAlaile 20
DB 7 TTGAAGAACCCTTACAAAGCTCATATGATACATTAAGATGAATGAAGAAATGCTATA 66
QY 21 LysleuAlagluIleuLysAsnleuLysMetCysleuPheHisleuThrHisleu 40
DB 67 AAACCTAGCTGAAGCCTGAAAACCTGAAGAAGATGCTTATTTCAATTCAGCCACTTG 126
QY 41 SerAspIleGlyIleuMetAspTyrIleVallySerLeuSerSerGluProCysasp 60
DB 127 TCTGACATTTGAGAGGGAGATGATTACATCAAGTCTCTGTAAGTGAACCTGTAGAC 186
QY 61 LeuGluGluIleGluIleuValSerCysSerleuSerAlaAsnAlaVallyIleuAla 80
DB 187 CTTGAGAGAAATTCATTTAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 246
QY 81 GluAsnleuHisAsnleuVallySerleuSerleuSerleuSerleuSerleuSerleu 100
DB 247 CAGAAATCTTCAAAATTTGCTCAAACTGACATCTTGTATATGAGAAATTAACCTGGA 306
QY 101 LysAspGlyAsnGluAlaIleuHisGluIleuIleAspArgMetAsnValleuGluIleu 120
DB 307 AAAGTGAATGAAGCCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 366
QY 121 ThrAlaIleuMetLeuProTyrGlyCysAspValGlnGlySerleuSerleuSerleu 140
DB 367 ACCGACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 426
QY 141 HisleuGluIleuValProGluIleuVallySerleuGlyleuLysAsnTyrPArgThrAsp 160
DB 427 CATTGGAGAGGATGCCCACTGCTCAAGCTTGCTGGAATAAAGTGAAGTCAAGAT 486
QY 161 ThrGluIleArgIleleuGlyAlaIlePheGlyLysAsnProleuLysAsnPhelGln 180
DB 487 ACAGAGATTGAATTTTAGTGTCATTTTGTGAAAGAACTCTGAAAACTCCAGCAG 546
QY 181 LeuAsnleuAlaGlyAsnArgValSerSerAspGlyTyrPleuAlaPheMetGlyValPhe 200
DB 547 TTGAATTTGGCGGGAATTCGTGACAGCATGATGATGATGATGATGATGATGATGATGAT 606
QY 201 GluAsnleuLys 204
DB 607 GAGAAATCTTAG 618
RESULT 2
US-09-686-347-98
: Sequence 98, Application US/09686347
: GENERAL INFORMATION:
: APPLICANT: Reed, John C.
: APPLICANT: Pio, Frederick F.
: APPLICANT: Godzik, Adam
: APPLICANT: Oliveira, Vasco A.
: APPLICANT: Lee, Sug Hyung
: APPLICANT: Stehlik, Christian
: TITLE OF INVENTION: Novel Card-Domain Containing
: FILE REFERENCE: P-LJ 4211
: CURRENT APPLICATION NUMBER: US/09/686,347
```

;; CURRENT FILING DATE: 2000-10-10
;; PRIOR APPLICATION NUMBER: US 09/579,240
;; PRIOR FILING DATE: 2000-05-24
;; NUMBER OF SEQ ID NOS: 109
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 98
;; LENGTH: 1395
;; TYPE: DNA
;; ORGANISM: Homo sapien
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (277)...(1353)
US-09-686-347-98

Alignment Scores:

Pred. NO.:	5.89e-98	Length:	1395
Score:	1046.00	Matches:	204
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	27	Gaps:	0

US-09-697-089-2_copy_762_965 (1-204) x US-09-686-347-98 (1-1395)

Qy 1 LeuTysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIle 20
|||||
Db 565 TTGAAGAACCCTTACAAAGCTCATATGATACATTAAGATGATGAAGAGATGCTATA 624
Qy 21 LysLeuAlaGluGlyLeuLysAsnLeuLysMetCysLeuPheHisLeuThrHisLeu 40
|||||
Db 625 AAACAGCTGAAGGCTGAAAGAACTGAAAGAGATGCTTTATTTTCATTGACCCACTTG 684
Qy 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProcysasp 60
|||||
Db 665 TCTGCATTGGAGAGGAGGATGATTACATGCAAGTCTCTCTCAAGTGAACCCCTGTGAC 744
Qy 61 LeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80
|||||
Db 745 CTGGAAGAAATTCATTGATGTCCTCGCTGCTGCTGCAAAAGCAGTGAATTCCTAGCT 804
Qy 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGln 100
|||||
Db 805 CAGATCTTCAACAATTTGGTCAAACTGAGACATTTTGATTTATCGAAAAATTAACCTGGA 864
Qy 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120
|||||
Db 865 AAAGATTGGAATGGAAGCTCTTCATGAACTGACAGAGATGAACGCTGTAGAACAGCTC 924
Qy 121 ThrAlaLeuMetLeuProTirpGlyCysAspValGlnGlySerLeuSerSerLeuLys 140
|||||
Db 925 ACCGCACTGATGCTGCCCTGGGGCTGTGACGTGCAAGGAGGCTGAGCGCTGTGAAA 984
Qy 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTirpArgLeuThrAsp 160
|||||
Db 985 CATTGGAGAGAGGTCCCAACACTGCTCAAGCTTGCGTTGGAAGAAATGAGAGATCACAGAT 1044
Qy 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln 180
|||||
Db 1045 ACAGAGATTAGAAATTTAGTGTCATTTTGGAAAGAACCCCTGAAAAAATCTCAGCAG 1104
Qy 101 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTirpLeuAlaPheMetGlyValPhe 200
|||||
Db 1105 TTGAATTTGGCGGGAATCGTGTGAGCAGTGATGATGGCTTGCTTCATGGGTATATT 1164
Qy 201 GlnAsnLeuLys 204
|||||
Db 1165 GAGATCTTAAAG 1176

RESULT 3
US-09-864-921-98
; Sequence 98, Application us/09864921
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.

;; APPLICANT: Plo, Frederick F.
;; APPLICANT: Godzik, Adam
;; APPLICANT: Stehlik, Christian
;; APPLICANT: Damiano, Jason S.
;; APPLICANT: Lee, Sug-Hyung
;; APPLICANT: Oliveira, Vasco A.
;; APPLICANT: Hayashi, Hideki
;; APPLICANT: Pawlowski, Krzysztof
;; TITLE OF INVENTION: Novel Card Domain Containing
;; TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use
;; FILE REFERENCE: P-IJ 4752
;; CURRENT APPLICATION NUMBER: US/09/864,921
;; PRIOR FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 09/579,240
;; PRIOR FILING DATE: 2000-05-24
;; PRIOR APPLICATION NUMBER: US 09/686,347
;; PRIOR FILING DATE: 2000-10-10
;; PRIOR APPLICATION NUMBER: US 60/275,980
;; PRIOR FILING DATE: 2001-03-14
;; NUMBER OF SEQ ID NOS: 195
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 98
;; LENGTH: 1395
;; TYPE: DNA
;; ORGANISM: Homo sapien
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (277)...(1353)
US-09-864-921-98

Alignment Scores:

Pred. NO.:	5.89e-98	Length:	1395
Score:	1046.00 <td>Matches:</td> <td>204</td>	Matches:	204
Percent Similarity:	100.00% <td>Conservative:</td> <td>0</td>	Conservative:	0
Best Local Similarity:	100.00% <td>Mismatches:</td> <td>0</td>	Mismatches:	0
Query Match:	100.00% <td>Indels:</td> <td>0</td>	Indels:	0
DB:	33	Gaps:	0

US-09-697-089-2_copy_762_965 (1-204) x US-09-864-921-98 (1-1395)

Qy 1 LeuTysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIle 20
|||||
Db 565 TTGAAGAACCCTTACAAAGCTCATATGATACATTAAGATGATGAAGAGATGCTATA 624
Qy 21 LysLeuAlaGluGlyLeuLysAsnLeuLysMetCysLeuPheHisLeuThrHisLeu 40
|||||
Db 625 AAACAGCTGAAGGCTGAAAGAACTGAAAGAGATGCTTTATTTTCATTGACCCACTTG 684
Qy 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProcysasp 60
|||||
Db 665 TCTGCATTGGAGAGGAGGATGATTACATGTCAGTCTCTGCAAAAGCAGTGAATTCCTAGCT 744
Qy 61 LeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80
|||||
Db 745 CTGGAAGAAATTCATTGATGTCCTCGCTGCTGCTGCAAAAGCAGTGAATTCCTAGCT 804
Qy 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGln 100
|||||
Db 805 CAGATCTTCAACAATTTGGTCAAACTGAGACATTTTGATTTATCGAAAAATTAACCTGGA 864
Qy 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120
|||||
Db 865 AAAGATTGGAATGGAAGCTCTTCATGAACTGACAGAGATGAACGCTGTAGAACAGCTC 924
Qy 121 ThrAlaLeuMetLeuProTirpGlyCysAspValGlnGlySerLeuSerSerLeuLys 140
|||||
Db 925 ACCGCACTGATGCTGCCCTGGGGCTGTGACGTGCAAGGAGGCTGAGCGCTGTGAAA 984
Qy 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTirpArgLeuThrAsp 160
|||||
Db 985 CATTGGAGAGAGGTCCCAACACTGCTCAAGCTTGCGTTGGAAGAAATGAGAGATCACAGAT 1044
Qy 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln 180

Db	1045	ACAGAGATTGAAATTTTAGTGCATTTTTTGGAANAACCCTGTGAANAACCTCCAGAG	1104
Qy	181	LeuAnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetcIylAlaPhe	200
Db	1105	TTCGATTTGGCGGGAAMTCGTGAGCAGTGAAGATGAGTGCCTTGCCCTCATGGGTATTT	1164
Qy	201	GluAnLeuLys	204
Db	1165	GAGATCTTAAG	1176

```

RESULT 4
PCT-US00-35017A-416
: Sequence 416, Application PC/TUS0035017A
: GENERAL INFORMATION:
: APPLICANT: Hyseq Inc
: TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
: FILE REFERENCE: 784PCT
: CURRENT APPLICATION NUMBER:
: CURRENT FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: US09/488,725
: PRIOR FILING DATE: 2000-01-21
: PRIOR APPLICATION NUMBER: US09/552,317
: PRIOR FILING DATE: 2000-04-25
: NUMBER OF SEQ ID NOS: 1478
: SEQ ID NO 416
: LENGTH: 2950
: TYPE: DNA
: ORGANISM: Homo sapiens
PCT-US00-35017A-416

```

Alignment Scores:	
Pred. No.:	1 51e-97
Score:	1046.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	1
	Gaps: 0
	Indels: 0
	Mismatches: 0
	Conservative: 0
	Matches: 204
	Length: 2950

US-09-697-089-2_COPY_762_965 (1-204) x PCT-US00-35017A-416 (1-2950)

QY	1	LeuYsAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluLysAlaIle	20
Db	1139	TTGAGAGACCTTACAAAAGCTCAATAAGGATTAACATAAATAAAGAAAGATCTCTATA	1198
QY	21	LysLeuAlaGluGlyLeuLysAsnLeuLysMetCysLeuPheHisLeuThrHisLeu	40
Db	1199	AAACTACTGAGAGCCCGAAGAAAACCGAGAGAGATGTGTTATTTCATTGTGACCCACTTG	1258
QY	41	SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp	60
Db	1259	TCTACACTTGGAGAGGAAAGATTCACATAGTCACACTCTCTCAAGTGAAACCTGTGAC	1318
QY	61	LeuGluGluIleGluLeuValSerCysCysLeuSerLeuAsnAlaValLysIleLeuAla	80
Db	1319	CTTGAGAAATTCATTATTAAGTCTCTGCTGCTTGTCTGCAGAAATGCAGTGAATTCCTACT	1378
QY	81	GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu	100
Db	1379	CAGATCTTACAAATTTGGTCAAACTGAGCATCTTGATTATTCAGAAAATTAACCTGGAA	1438
QY	101	LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAspValLeuGluGluLeu	120
Db	1439	AAAGATGAAATGAAAGCTCTTCTCAATGAAAGATGACAGAGATGAACCTGTAAACAGCTC	1498
QY	121	ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys	140
Db	1499	ACCGCACTGATGATCGCCCTGGGGCTGTGAAGTGCACAGCAGCGCTAGCAGCCTGTGGAA	1558
QY	141	HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp	160
Db	1559	CATTGGAGAGAGGTCCCAACATCTGTCAAGCTGTGGTTTAAAGTGGAGATCTCAAGAT	1618

QY	161	ThrgluilearqllleuleuGlyAlaPhePheGlyLysAsnProLeuLysAsnPhelngIn	180
Db	1619	ACAGAGATTGAATTTTAGGTCGATTTTTTGGAAAGACCCCTCGAAAACTTCCAGCAG	1678
QY	181	LeuAsnLeuAlaGlyAsnArqValSerSerAspGlyTyrLeuAlaPheMetCylValCHe	200
Db	1679	TTGCAATTTGGGGGGAATTCGTGTGAGACGTGAGTGGTGGCTTGCCTTCATGGGTCTATT	1738
QY	201	GlusnLeuLys 204	
Db	1739	GAGAACTCTTAAG 1750	

```

RESULT 5
PCT-US00-29643-3
; Sequence 3, Application PC/TUS0029643
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-136W01
; CURRENT APPLICATION NUMBER: PCT/US00/29643
; CURRENT FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3072
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US00-29643-3

```

Alignment Scores:	
Pred. No.:	1.59e-97
Score:	1046.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	1
DB:	1
Gaps:	0
Length:	3
Matches:	2
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-697-089-2_COPY_762_965 (1-204) x PCT-US00-29643-3 (1-3072)

OY	1	LeuYysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluLysAlaIle	20
Db	2284	TTGAGAGAACCTTACAAAGCCATTAAGGATTAACATAAAGTAAAGAAAGATGCTATA	2343
OY	21	LysLeuAlaGluGlyLeuLysAsnLeuLysMetCysLeuPheHisLeuThrHisLeu	40
Db	2344	AAATCTAGCTGAAGGCCCGAAGAAACCGTAAGAGATGTGTATTCTCATTTGACCCACTTG	2403
OY	41	SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp	60
Db	2404	TCTGACATTTGGAGGGGAAAGATTTCAATAGTCAGATCTCTCTCAAGTGAACCCGTGTAC	2463
OY	61	LeuGluGluIleGluLeuValSerCysCysLeuSerAlaAsnAlaValLysIleIleuAla	80
Db	2464	CTTGAAGAAATTCATTATTAAGTCTCTCTGCTGCTGTCTGCGAAATGCAGTGAATCTCTACT	2523
OY	81	GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu	100
Db	2524	CAGATCTTCACAAATTTGGTCAACACGACACTTCTGATTATTCAGAAAAATTACTCGTGA	2583
OY	101	LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGluLeu	120
Db	2584	AAAGATGAAATGAAGCTCTTTCATGACATGCATGCAGATGAACGATCAAGCTCTTGAAACAGCTC	2643
OY	121	ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys	140
Db	2644	ACCCGACTGANTCGTCCCTCGGGCTGTGACGTGCAGACGAGCGCTAGCAGCCTGTGTAA	2703
OY	141	HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp	160
Db	2704	CATTGGAGAGAGGTCCCAACACTGTGTCAAGCTTGGGTTGAAAAACGTGAGACTCAACAT	2763

QY 161 ThrGluIleArgIleLeuGluValAlaPhePheGlyLysAsnProLeuLysAsnPhgInGln 180
|
DB 2764 ACAGAGATTAGATTAGATTTTGGAGAAAGACCTCTGAAACACTTCCAGCAG 2823
QY 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPleuAlaPheMetGlyValPhe 200
|
DB 2824 TTGAATTTGGCGGGAATCGTGTGACAGTGTGATGATGCTTGCCTTCATGGGTGATATT 2883
QY 201 GluAsnLeuLys 204
|
DB 2884 GAGAACTTTAAG 2895
RESULT 6
US-09-697-089-3
; Sequence 3, Application US/09697089
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-136001
; CURRENT APPLICATION NUMBER: US/09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3072
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-697-089-3

Alignment Scores:
Pred. No.: 1,59e-97 Length: 3072
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 27 Gaps: 0

US-09-697-089-2_COPY_762_965 (1-204) x US-09-697-089-3 (1-3072)

QY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluLysAlaIle 20
|
DB 2284 TTGAAGAACCTTACAAAGCTCATATGATTAACATTAAGATGAAGAAATGATGCTATA 2343
QY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40
|
DB 2344 AAACCTAGCTGAAGGCTGAAAAAAGCTGAAGAGATGTGTTTATTCATTGACCCACTTG 2403
QY 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60
|
DB 2404 TCTGACATTGGAGAGGAGATGATTAACATAGTCAGTCTCTCAAGTAAACCTGTGAC 2463
QY 61 LeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80
|
DB 2464 CTTGAAGAAATTCATTAATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2523
QY 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100
|
DB 2524 CAGAAATCTTCACAAATTTGGTCAAACTGACATCTTGATTTATTCAGAAATTAACCTGGA 2583
QY 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120
|
DB 2584 AAAGATGGAATGAAGAGCTTCTCATGATGATGACAGATGACAGATGATGATGATGATGAT 2643
QY 121 ThrAlaLeuMetLeuProTyrPheLysAspValGlnGlySerLeuSerSerLeuLeuLys 140
|
DB 2644 ACCGACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2703
QY 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160

DB 2704 CATTGGAGAGAGTCCCAACATCGTCAAGCTTGGGTGAAAAAAGTGAAGACTCACAGAT 2763
|
QY 161 ThrGluIleArgIleLeuGluValAlaPhePheGlyLysAsnProLeuLysAsnPhgInGln 180
|
DB 2764 ACAGAGATTAGATTAGATTTTGGAGAAAGACCTCTGAAACACTTCCAGCAG 2823
QY 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPleuAlaPheMetGlyValPhe 200
|
DB 2824 TTGAATTTGGCGGGAATCGTGTGACAGTGTGATGATGCTTGCCTTCATGGGTGATATT 2883
QY 201 GluAsnLeuLys 204
|
DB 2884 GAGAACTTTAAG 2895
RESULT 7
US-09-841-739-3
; Sequence 3, Application US/09841739
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/09/841,739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3072
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-841-739-3

Alignment Scores:
Pred. No.: 1,59e-97 Length: 3072
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 32 Gaps: 0

US-09-697-089-2_COPY_762_965 (1-204) x US-09-841-739-3 (1-3072)

QY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluLysAlaIle 20
|
DB 2284 TTGAAGAACCTTACAAAGCTCATATGATTAACATTAAGATGAAGAAATGATGCTATA 2343
QY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40
|
DB 2344 AAACCTAGCTGAAGGCTGAAAAAAGCTGAAGAGATGTGTTTATTCATTGACCCACTTG 2403
QY 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60
|
DB 2404 TCTGACATTGGAGAGGAGATGATTAACATAGTCAGTCTCTGCAAGTAAACCTGTGAC 2463
QY 61 LeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80
|
DB 2464 CTTGAAGAAATTCATTAATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2523
QY 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100
|
DB 2524 CAGAAATCTTCACAAATTTGGTCAAACTGACATCTTGATTTATTCAGAAATTAACCTGGA 2583
QY 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120
|
DB 2584 AAAGATGGAATGAAGAGCTTCTCATGATGATGACAGATGACAGATGATGATGATGATGAT 2643
QY 121 ThrAlaLeuMetLeuProTyrPheLysAspValGlnGlySerLeuSerSerLeuLeuLys 140
|
DB 2644 ACCGACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2703

Oy	141	HisLeuGIuGIuValProGIuLeuValLysLeuGIuLeuLysAsnTrpArgLeuThrAsp	160
Db	2704	CAITTTGGAGGAGGTCCACACACTGTGCATACCTGGTGTAAAAACGGAGACTCACAAAT	2763
Oy	161	ThrGIuLeuArgIleLeuGIuValAlaPhePheGIuLysAsnProLeuLysAsnPheGln	180
Db	2764	ACAGAGATTAGAAATTTTAGGTGCATTTTTTGGAAAGAACCTGTGAAAACCTTCCAGAG	2823
Oy	181	LeuAsnLeuAlaGIuAsnArgValSerSerAspGIuTrpLeuAlaPheMetGIuAlaPhe	200
Db	2824	TTGAAATTGGCGGGGAAATCGTGTGAGCAGTGATGATGAGCTTGCCCTTCATGGGTATT	2883
Oy	201	GIuAsnLeuLys	204
Db	2884	GAGAACTCTTAAG	2895
RESULT 8			
US-10-156-733-1			
: Sequence 1, Application US/10156733			
: GENERAL INFORMATION:			
: APPLICANT: Alnemir, Emed S.			
: TITLE OF INVENTION: IPAT, AN ICE-PROTEASE ACTIVATING			
: TITLE OF INVENTION: FACTOR			
: FILE REFERENCE: 480140.477			
: CURRENT APPLICATION NUMBER: US/10/156,733			
: CURRENT FILING DATE: 2002-05-24			
: NUMBER OF SEQ. ID NOS: 14			
: SOFTWARE: FastSeq for Windows Version 4.0			
: SEQ. ID NO 1			
: LENGTH: 3075			
: TYPE: DNA			
: ORGANISM: Homo sapiens			
: FEATURE:			
: NAME/KEY: CDS			
: LOCATION: (1)...(3075)			
US-10-156-733-1			
Alignment Scores:			
Pred. NO.:			
Score: 1.59e-97			
Percent Similarity: 1046.00			
Best Local Similarity: 100.00%			
Query Match: 100.00%			
DB: 41			
Gaps: 0			
US-09-697-089-2_COPY_762_965 (1-204) x US-10-156-733-1 (1-3075)			
Oy	1	LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGIuAspAlaIle	20
Db	2284	TTTGAGGAACCTTACAAAAGCCATTAATGATTAACATTAACATTAAGAGAGAGATGCTATTA	2343
Oy	21	LysLeuAlaGIuGIuLysLysAsnLeuLysMetCysLeuPheHisLeuThrHisLeu	40
Db	2344	AAACTAGCTGAAGGCCCTGAAAAACCTGAGACAGATGTGTTTATTTCATTGTGACCCACTTG	2403
Oy	41	SerAspIleGIuGIuLysIleMetAspTrpIleValLysSerLeuSerSerGIuProCysAsp	60
Db	2404	TCTGCACATGGAGAGGGAATGATTAACATAGTCAAGTCTCTGCAAGTAACCTCGTAGC	2463
Oy	61	LeuGIuGIuIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla	80
Db	2464	CTTGAGAGAAATTCAAATTAAGTCTGCTGCTGTGCTGCAAAAGCAGTGAATAATCTTACT	2523
Oy	81	GIuAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGIuAspTrpLeuGlu	100
Db	2524	CAGAACTTCTCAATTTTGGTCAACATGAGCATTTTGATTATTCAGAAAATTAATCTGAA	2583
Oy	101	LysAspGIuAsnGIuAlaLeuHisGIuLeuIleAspArgMetAsnValLeuGIuGIuLeu	120
Db	2584	AAAGATGGAAATGAAGCTCTTCATTAAGAACTGATGACAGGATGAACGCTGTAAACAGCTC	2643
Oy	121	ThrAlaLeuMetLeuProTrpGIuCysAspValGlnGIuSerLeuSerSerLeuLeuLys	140

Db	2644	ACCGCAGTGAAGCTGCGCCCTGGGGCTGTGAGCTGCACGAGCGCTGAGCGCTGTGGAA	2703
QY	141	HisLeuGlugluValProGlnLeuValLysLeuGlyLeuLysAsnTPRArgLeuThrAsp	160
Db	2704	CATTGGAGGAGGCTCCACACAACTGCACAGCTGGGCTGAAAACTGGAGACTCACAGAT	2763
QY	161	ThrGluLeuArgIleLeuGlyValAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln	180
Db	2764	ACAGAGATTGGAATTTTGAAGTGAATTTTGGAAAAACCCCTGTGAAAACTTCCAGCAG	2823
QY	181	LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTPRLeuAlaPheMetGlyValPhe	200
Db	2824	TTGAATTTGGCGGGAATTCGTGTGAGAGAGTGAATGATGCTTGCCATTATGGGTATATT	2883
QY	201	GluAsnLeuLys 204	
Db	2884	GAGATCTTAG 2895	
RESULT 9			
PCT-US00-29643-1			
; Sequence 1, Application PC/TUS0029643			
; GENERAL INFORMATION:			
; APPLICANT: Millennium Pharmaceuticals, Inc.			
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED			
; TITLE OF INVENTION: PROTEIN FAMILY AND USGS THEREOF			
; FILE REFERENCE: 07334-136M01			
; CURRENT APPLICATION NUMBER: PCT/US00/29643			
; PRIOR FILING DATE: 2000-10-26			
; PRIOR APPLICATION NUMBER: US 60/161,822			
; PRIOR FILING DATE: 1999-10-27			
; NUMBER OF SEQ ID NOS: 11			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 1			
; LENGTH: 3133			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (36)...(3107)			
PCT-US00-29643-1			
Alignment Scores:			
Pred. No.: 1 63e-97 length: 3133			
Score: 1046.00 Matches: 204			
Percent Similarity: 100.00% Conservative: 0			
Best Local Similarity: 100.00% Mismatches: 0			
Query Match: 100.00% Indels: 0			
DB: 1 Gaps: 0			
US-09-697-089-2_COPY_762_965 (1-204) x PCT-US00-29643-1 (1-3133)			
QY	1	LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIle	20
Db	2319	TTGGAAGAACCTTACAAAGCTCATATATGATTAACATATAATGAATGAAGAATCTCTATA	2378
QY	21	LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu	40
Db	2379	AAACTACTGAGAGCGCTGAAGAAAACCTGAAGAAAGATGTGTTTATTCATTGACCCACTTG	2438
QY	41	SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerGluProCysAsp	60
Db	2439	TCTGACATTGGAGAGGGAATGGATTTCATATGTCATCAACTCTCTCAAGTCGAACCTGTGAC	2498
QY	61	LeuGluGluIleGlnIleuValSerCysLeuSerAlaAsnAlaValLysIleLeuAla	80
Db	2499	CTTGAAGAAATTCATTATAGTCTCCTGCTGTGTCTGTCAAAATGACAGTGAATTCCTACT	2558
QY	81	GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu	100
Db	2559	CAGATCTTCACATTTTGGTGCACAACTGAGAGATCTTGATTTATCAGAAAAATTACTGGAA	2618
QY	101	LysAspLysGluAlaLeuHisGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu	120

|||||
Db 2619 AAGATGGAATGAAAGCTTCATGACACTGATCGACAGATGAAAGCTGCTGAGAACGCTC 2678
Oy 121 ThrAlaLeuMetLeuProTfPcIycysAspValGInglySerLeuSerSerLeuLeuLys 140
Db 2679 ACCGACATGAACTGACCTCCCTGGGGCTGTGACGTGCACAGCAGCCTGTTGAAA 2738
Oy 141 HIsLeuGInGluValProGInLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAsp 160
Db 2739 CATTTGGAGGAGGTCCACAACTGCTCAAGCTTGGGTTGAAAACCTGGAGACTCACAGAT 2798
Oy 161 ThrGluIleArgIleLeuGlyValAlaPhePheGlyLysAsnProLeuLysAsnPhelGIn 180
Db 2799 ACAGAGATTAGAAATTTTGGTGCATTTTGGAAAGAACCTCTGAAAACTTCCAGCAG 2858
Oy 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyValPhe 200
Db 2859 TTGAATTTGGCGGAAATCGTGTGAGCAGTGTGATGATGCGCTTGCTCATGGGTGTAATT 2918
Oy 201 GluAsnLeuLys 204
Db 2919 GAGAACTTTAAG 2930

RESULT 10

US-09-697-089-1
; Sequence 1, Application US/09697089
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-136001
; CURRENT APPLICATION NUMBER: US/09/697, 089
; CURRENT FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3133
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)...(3107)
US-09-697-089-1

Alignment Scores:

Pred. No.:	1,63e-97	Length:	3133
Score:	1046.00	Matches:	204
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	27	Gaps:	0

US-09-697-089-2_COPY_762_965 (1-204) x US-09-697-089-1 (1-3133)

Oy 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIle 20
Db 2319 TTGAAGAACCTTACAAAGCTCATATGATGATTAACATTAAGATGAAGAGATGCTATTA 2378
Oy 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40
Db 2379 AAACTAGCTGAAGGCCCTGAAAAAAGCTGAAGAGATGTGTTTATTTTCATTTTGACCCACCTTG 2438
Oy 41 SerAspIleGlyGluGlyMetAspTrpIleValLysSerLeuSerSerGluProCysAsp 60
Db 2439 TCTGCATTTGGAGAGGAAATGATGATTACATGCAAGTCTCTGTCAAGTGAACCCGTGTGAC 2498
Oy 61 LeuGluGluIleGlnLeuValSerCysLeuSerAlaAsnAlaValLysIleLeuAla 80
Db 2499 CTTGAAGAAATTCATATGCTCTCCGTGCTGCTGCAAAATGACGTAAGTCTAGCT 2558

Oy 81 GluAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTrpLeuGlu 100
Db 2559 CAGAACTTTCACAAATTTGGTCAAACTGACATTTTGATTTATCGAAAAATTAACCTGGAA 2618
Oy 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120
Db 2619 AAGATGGAATGAAAGCTCTTCATGACATGATCGACAGATGAAGTGTATGAACAGCTC 2678
Oy 121 ThrAlaLeuMetLeuProTfPcIycysAspValGInglySerLeuSerSerLeuLeuLys 140
Db 2679 ACCGACATGACCTCCCTCCCTGGGGCTGTGACGTGCACAGCAGCCTGTTGAAA 2738
Oy 141 HIsLeuGInGluValProGInLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAsp 160
Db 2739 CATTTGGAGGAGGTCCACAACTGCTCAAGCTTGGGTTGAAAACCTGGAGACTCACAGAT 2798
Oy 161 ThrGluIleArgIleLeuGlyValAlaPhePheGlyLysAsnProLeuLysAsnPhelGIn 180
Db 2799 ACAGAGATTAGAAATTTTGGTGCATTTTGGAAAGAACCTCTGAAAACTTCCAGCAG 2858
Oy 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyValPhe 200
Db 2859 TTGAATTTGGCGGAAATCGTGTGAGCAGTGTGATGATGCGCTTGCTCATGGGTGTAATT 2918
Oy 201 GluAsnLeuLys 204
Db 2919 GAGAACTTTAAG 2930

RESULT 11

US-09-841-739-1
; Sequence 1, Application US/09841739
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/09/841,739
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697, 089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3133
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)...(3107)
US-09-841-739-1

Alignment Scores:

Pred. No.:	1,63e-97	Length:	3133
Score:	1046.00	Matches:	204
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	32	Gaps:	0

US-09-697-089-2_COPY_762_965 (1-204) x US-09-841-739-1 (1-3133)

Oy 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIle 20
Db 2319 TTGAAGAACCTTACAAAGCTCATATGATGATTAACATTAAGATGAAGAGATGCTATTA 2378
Oy 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40
Db 2379 AAACTAGCTGAAGGCCCTGAAAAAAGCTGAAGAGATGTGTTTATTTTCATTTTGACCCACCTTG 2438
Oy 41 SerAspIleGlyGluGlyMetAspTrpIleValLysSerLeuSerSerGluProCysAsp 60
Db 2439 TCTGCATTTGGAGAGGAAATGATGATTACATGCAAGTCTCTGTCAAGTGAACCCGTGTGAC 2498

```
QY 61 LeuGlucIuIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80
;
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)...(1903)
; OTHER INFORMATION: similar to g15932010 in the genepept database release 114,
; US-09-471-275-7095
QY 2499 CTTGAAGAAATTCATATAGTCTCTGCTGCTGTCTGCAGAAATGAGTGAATCTTACT 2558
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
QY 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGlnAsnTyrLeuGln 100
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
Db 2559 CAGAAATCTTCACAAATTTGGTGAACCTGAGCATCTTGTATATCAGAAATTTACCTGGAA 2618
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
QY 101 LysAspGlnAsnGlnAlaLeuHisGlnLeuIleAspArgMetAsnValLeuGlnLeu 120
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
Db 2619 AAAGATGGAAATGAAGCTTTCATGAACTGATTCGACAGATGAACGTCGTGAACAGCTC 2678
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
QY 121 ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
Db 2679 ACCGACATGATGCTGCTGCTGGGCTGTGACCTGCAGAGCAGCAGCCTGTGAAA 2738
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
QY 141 HisLeuGlnGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
Db 2739 CATTGGAGGAGGTCCCAACCTGTCAGAGCTTG6GTTGAAAACCTGAGACTCAGCAT 2798
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
QY 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln 180
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
Db 2799 ACAGAGATTAGAAATTTTAGTGTCATTTTGGAAAAGAACCTTGAAAACCTTCCAGCAG 2858
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
QY 181 LeuAsnLeuAlaGlnAsnArgValSerSerAspGlyTyrPheAlaPheMetGlyValPhe 200
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
Db 2859 TTGATTTGGCGGGAATTCGTGTGAGCAGTGTGATGATGCTTGCCCTCATGGGTATATT 2918
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
QY 201 GluAsnLeuLys 204
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
Db 2919 GAGAAATCTTAAG 2930
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
```

RESULT 12

```
; Sequence 7095, Application US/09471275
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE REFERENCE: 782
; CURRENT APPLICATION NUMBER: US/09/471,275
; EARLIER APPLICATION NUMBER: US 09/235,076
; EARLIER FILING DATE: 1999-01-20
; EARLIER APPLICATION NUMBER: US 09/234,611
; EARLIER FILING DATE: 1999-01-22
; EARLIER APPLICATION NUMBER: US 09/240,371
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: US 09/277,227
; EARLIER FILING DATE: 1999-03-25
; EARLIER APPLICATION NUMBER: US 09/271,490
; EARLIER FILING DATE: 1999-03-18
; EARLIER APPLICATION NUMBER: US 09/293,972
; EARLIER FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: US 09/274,861
; EARLIER FILING DATE: 1999-03-23
; EARLIER APPLICATION NUMBER: US 60/125,453
; EARLIER FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: US 60/126,605
; EARLIER FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: US 09/306,350
; EARLIER FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/399,720
; EARLIER FILING DATE: 1999-09-21
; EARLIER APPLICATION NUMBER: US 09/404,284
; EARLIER FILING DATE: 1999-09-21
; EARLIER APPLICATION NUMBER:
; EARLIER FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 10451
; SOFTWARE: pt.ct_genes Version 1.0
; SEQ ID NO 7095
; LENGTH: 3152
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)...(1903)
; OTHER INFORMATION: similar to g15932010 in the genepept database release 114,
; US-09-471-275-7095
Alignment Scores:
Pred. No.: 1,64e-97 Length: 3152
Score: 1046.00 Matches: 204
Percent Similarity: 100.008 Conservative: 0
Best Local Similarity: 100.008 Mismatches: 0
Query Match: 100.008 Indels: 0
DB: Gaps: 0
```

US-09-697-089-2_COPY_762_965 (1-204) x US-09-471-275-7095 (1-3152)

```
QY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGlnGluAspAlaIle 20
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
Db 1139 TTGAAGAACTTACAAAGCTCATATGATGATTAACATAAAGATGAAGAAGATGCTATA 1198
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
QY 21 LysLeuAlaGlnGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
Db 1199 AAACATAGCTGAAGGCTGGAACCTGAAAGAGATGTGTTATTTCAATTTGACCCACTTG 1258
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
QY 41 SerAspIleGlyGlnGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
Db 1259 TCTGACATGGAGAGGAGGATGATGATTAATCAAGTCTGTCTGAAGTGAACCTGTGAC 1318
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
QY 61 LeuGlnGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
Db 1319 CTTGAAGAAATTCATATAGTCTCTGCTGCTGTGTCTGCAGAAATGAGTGAATCTTACT 1378
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
QY 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGlnAsnTyrLeuGln 100
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
Db 1379 CAGAAATCTTCACAAATTTGGTGAACCTGAGCATCTTGTATATCAGAAATTTACCTGGAA 1438
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
QY 101 LysAspGlnAsnGlnAlaLeuHisGlnLeuIleAspArgMetAsnValLeuGlnLeu 120
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
Db 1439 AAAGATGGAAATGAAGCTTTCATGAACTGATTCGACAGATGAACGTCGTGAACAGCTC 1498
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
QY 121 ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
Db 1499 ACCGACATGATGCTGCTGCTGGGCTGTGACCTGCAGAGCAGCAGCCTGTGAAA 1558
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
QY 141 HisLeuGlnGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
Db 1559 CATTGGAGGAGGTCCCAACCTGTCAGAGCTTG6GTTGAAAACCTGAGACTCAGCAT 1618
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
QY 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln 180
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
Db 1619 ACAGAGATTAGAAATTTTAGTGTCATTTTGGAAAAGAACCTTGAAAACCTTCCAGCAG 1678
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
QY 181 LeuAsnLeuAlaGlnAsnArgValSerSerAspGlyTyrPheAlaPheMetGlyValPhe 200
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
Db 1679 TTGATTTGGCGGGAATTCGTGTGAGCAGTGTGATGATGATGCTTGCCCTCATGGGTATATT 1738
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
QY 201 GluAsnLeuLys 204
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
Db 1739 GAGAAATCTTAAG 1750
;
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
```

RESULT 13

```
; Sequence 23, Application PC/TUS0107143
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.L.C.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50016
; CURRENT APPLICATION NUMBER: PCT/US01/07143
; CURRENT FILING DATE: 2001-03-08
```

```
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 3213
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-07143-23

Alignment Scores:
Pred. No.: 1,68e-97 Length: 3213
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-697-089-2_COPY_762_965 (1-204) x PCT-US01-07143-23 (1-3213)
QY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIle 20
DB 2422 TTGAAGAACCTTACAAAGCTCAATGATGATACATTAAGATGAAGATGAAGATGCTATA 2481
QY 21 LysIleuAlaGluGluLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40
DB 2482 AACTAGCTGGAAGGCTGAAAAACCTGAAGAGATGTGTTATTCATTGACCCACTG 2541
QY 41 SerAspIleGluGluGlyMetAspTyrIleValLysSerLeuSerSerGluProcysAsp 60
DB 2542 TCTGACATTGGAGAGGAGATGATGATACATGCAAGTCTCTCAAGTGAACCTGTGAC 2601
QY 61 LeuGluGluIleGluLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80
DB 2602 CTTGAAGAAATTCATTAATGCTCTGCTGCTGCTGCAAAATGCAAGTGAATCCTAGCT 2661
QY 81 GluAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100
DB 2662 CAGAATCTTCACAAATTTGGTCAACTGACACTTTGATTATTCGAAAAATTAACCTGGA 2721
QY 101 LysAspGluAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGluLeu 120
DB 2722 AAAGATGGAATGAAGCTCTTCATGACATGACAGATGACAGATGCTGTAGAACGCTC 2781
QY 121 ThrAlaLeuMetLeuProTropGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140
DB 2782 ACCGACACTGATCTGCTCCCTGGGGCTGTGACGCAAGGACGCTGACGCTGTGAAA 2841
QY 141 HisLeuGluGluValProGluLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160
DB 2842 CATTGGAGAGAGTCCCACTCACTCTCAAGCTTGGGTTGAAAACCTGGAGACTCACAGAT 2901
QY 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln 180
DB 2902 ACAGAGATTAGAAATTTAGTGCATTTTGGAAAGAACCTCTGAAAAAATTCACGACG 2961
QY 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPheAlaPheMetGlyValPhe 200
DB 2962 TTGAATTTGGCGGAAATCGTGTGAGCAGTGTGATGATGCTGCTTCATGAGGTGTATTT 3021
QY 201 GluAsnLeuLys 204
DB 3022 GAGAAATCTTAAG 3033

RESULT 14
US-10-221-097-23
; Sequence 23, Application US/10221097
```

```
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdock, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50016
; CURRENT APPLICATION NUMBER: US/10/221,097
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: PCT/US01/07143
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 3213
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-221-097-23

Alignment Scores:
Pred. No.: 1,68e-97 Length: 3213
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 42 Gaps: 0

US-09-697-089-2_COPY_762_965 (1-204) x US-10-221-097-23 (1-3213)
QY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIle 20
DB 2422 TTGAAGAACCTTACAAAGCTCAATGATGATACATTAAGATGAAGATGAAGATGCTATA 2481
QY 21 LysIleuAlaGluGluLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40
DB 2482 AACTAGCTGGAAGGCTGAAAAACCTGAAGAGATGTGTTATTCATTGACCCACTG 2541
QY 41 SerAspIleGluGluGlyMetAspTyrIleValLysSerLeuSerSerGluProcysAsp 60
DB 2542 TCTGACATTGGAGAGGAGATGATGATACATGCAAGTCTCTCAAGTGAACCTGTGAC 2601
QY 61 LeuGluGluIleGluLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80
DB 2602 CTTGAAGAAATTCATTAATGCTCTGCTGCTGCTGCAAAATGCAAGTGAATCCTAGCT 2661
QY 81 GluAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100
DB 2662 CAGAATCTTCACAAATTTGGTCAACTGACACTTTGATTATTCGAAAAATTAACCTGGA 2721
QY 101 LysAspGluAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGluLeu 120
DB 2722 AAAGATGGAATGAAGCTCTTCATGACATGACAGATGACAGATGCTGTAGAACGCTC 2781
QY 121 ThrAlaLeuMetLeuProTropGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140
DB 2782 ACCGACACTGATCTGCTCCCTGGGGCTGTGACGCAAGGACGCTGACGCTGTGAAA 2841
QY 141 HisLeuGluGluValProGluLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160
DB 2842 CATTGGAGAGAGTCCCACTCACTCTCAAGCTTGGGTTGAAAACCTGGAGACTCACAGAT 2901
QY 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln 180
DB 2902 ACAGAGATTAGAAATTTAGTGCATTTTGGAAAGAACCTCTGAAAAAATTCACGACG 2961
```


GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 31, 2003, 13:24:32 : Search time 191.895 Seconds
(without alignments)
1295.994 Million cell updates/sec

Title: US-09-697-089-2_COPY_762_965

Perfect score: 1046
Sequence: 1 LKNLTKLMDIKMNEEDAI.....GNRVSSDDGLAFMGVFENLK 204

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2500250 seqs, 609544256 residues

Total number of hits satisfying chosen parameters: 5000500

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL-frame.p2n.model -DEV-xlh
-Q/cgn2_1/USPTO_spool/US09697089/runat_29012003_092755_19775/app_query.fasta.1.981
-DB-Pending_Patents_NA_New -OFMT-fastap -SUFFIX-p2n.rnph -MINMATCH-0.1
-LOOPEXT-0 -LOOPEXT-0 -UNITS-bits -START-1 -END-1 -MATRIX-biosum62
-TRANS-human40.cdi -LIST-45 -DOCLIGN-200 -THR SCORE-pct -THR_MAX-100
-THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFMT-pto NOR-ext HEAPSIDE-500 -MINLEN-0
-MAXLEN-2000000000 -USER-US09697089_0CGN_1.1_91_etunat_29012003_092755_19775
-NCPD-6 -ICPD-3 -NO_XLPXY -NO_MAMP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7

Database :

Pending_Patents_NA_New.*
1: /cgn2_6/ptodata/2/pna/PCF_NEW_COMB.seq.*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq.*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq.*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq.*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq.*
7: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1046	100.0	3075	1	PCF-US02-21946A-1
2	1046	100.0	3219	1	PCF-US02-21946A-14
3	1046	100.0	3545	6	US-10-276-781-111
4	202	19.3	421	6	US-10-203-138A-4307
5	126	12.0	2142	6	US-10-161-493-5
6	120.5	11.5	8722	6	US-10-194-163-263
7	118	11.3	916	5	US-09-724-676-19376
8	118	11.3	916	5	US-09-724-676A-19376
9	118	11.3	945	5	US-09-724-676-19370
10	118	11.3	945	5	US-09-724-676A-19370
11	118	11.3	1012	5	US-09-724-676-19364

12	118	11.3	1012	5	US-09-724-676A-19364	Sequence 19364, A
13	118	11.3	1103	5	US-09-724-676-19382	Sequence 19382, A
14	118	11.3	1103	5	US-09-724-676A-19382	Sequence 19382, A
15	118	11.3	1132	5	US-09-724-676-19395	Sequence 19395, A
16	118	11.3	1132	5	US-09-724-676A-19395	Sequence 19395, A
17	118	11.3	1170	5	US-09-724-676-19390	Sequence 19390, A
18	118	11.3	1170	5	US-09-724-676A-19390	Sequence 19390, A
19	118	11.3	1176	5	US-09-724-676-19375	Sequence 19375, A
20	118	11.3	1176	5	US-09-724-676A-19375	Sequence 19375, A
21	118	11.3	1199	5	US-09-724-676-19359	Sequence 19359, A
22	118	11.3	1199	5	US-09-724-676A-19359	Sequence 19359, A
23	118	11.3	1205	5	US-09-724-676-19369	Sequence 19369, A
24	118	11.3	1205	5	US-09-724-676A-19369	Sequence 19369, A
25	118	11.3	1272	5	US-09-724-676-19363	Sequence 19363, A
26	118	11.3	1272	5	US-09-724-676A-19363	Sequence 19363, A
27	118	11.3	1363	5	US-09-724-676-19380	Sequence 19380, A
28	118	11.3	1363	5	US-09-724-676A-19380	Sequence 19380, A
29	118	11.3	1392	5	US-09-724-676-19394	Sequence 19394, A
30	118	11.3	1392	5	US-09-724-676A-19394	Sequence 19394, A
31	118	11.3	1430	5	US-09-724-676-19389	Sequence 19389, A
32	118	11.3	1430	5	US-09-724-676A-19389	Sequence 19389, A
33	118	11.3	1459	5	US-09-724-676-19358	Sequence 19358, A
34	118	11.3	1459	5	US-09-724-676A-19358	Sequence 19358, A
35	118	11.3	1489	5	US-09-724-676-19373	Sequence 19373, A
36	118	11.3	1489	5	US-09-724-676A-19373	Sequence 19373, A
37	118	11.3	1518	5	US-09-724-676-19367	Sequence 19367, A
38	118	11.3	1518	5	US-09-724-676A-19367	Sequence 19367, A
39	118	11.3	1585	5	US-09-724-676-19361	Sequence 19361, A
40	118	11.3	1585	5	US-09-724-676A-19361	Sequence 19361, A
41	118	11.3	1645	5	US-09-724-676-19374	Sequence 19374, A
42	118	11.3	1645	5	US-09-724-676A-19374	Sequence 19374, A
43	118	11.3	1674	5	US-09-724-676-19368	Sequence 19368, A
44	118	11.3	1674	5	US-09-724-676A-19368	Sequence 19368, A
45	118	11.3	1676	5	US-09-724-676-19378	Sequence 19378, A

ALIGNMENTS

RESULT 1
PCT-US02-21946A-1
; Sequence 1, Application PC/TUS0221946A
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING
; TITLE OF INVENTION: FACTOR
; FILE REFERENCE: 480140.477PC
; CURRENT APPLICATION NUMBER: PCT/US02/21946A
; CURRENT FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3075
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3075)
PCT-US02-21946A-1

Alignment Scores:

Pred. No.: 9,43e-109
Score: 1046.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 1
Length: 3075
Matches: 204
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-09-697-089-2_COPY_762_965 (1-204) x PCT-US02-21946A-1 (1-3075)

QY 1 LeuLYASnleThrystleuileMeTASpAnileLYMeASnclnJusPlarie 20
DB 2284 TTGAGACCTTCAACAGCTCAATGATTAACATTAAGATGATGAAGAGATCTATA 2343

QY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40
|||||
Db 2344 AAGATAGCTGAGAGGCGCTGAAAAACCTGAGAGAGATGTCTTTATTTTCATTGACCCACTTG 2403
QY 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60
|||||
Db 2404 TCTGACATTTGGAGAGGAGATGATTTACATAGTCAAGTCTCTGCAAGTGAACCTGTGAC 2463
QY 61 LeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80
|||||
Db 2464 CTGGAAGAAATTCATTAATCT 2523
QY 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100
|||||
Db 2524 CAGAATCTTCACAAATTTGGTCAAACTGACACATTTCTGATTTTCACAAAATTAACCTGGA 2583
QY 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120
|||||
Db 2584 AAGATGGAATGAAAGCTCTTCATGAACTGACAGATGAACTGCTAGAACAGCTC 2643
QY 121 ThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140
|||||
Db 2644 ACCGCACTGATGCTGCCCTGGGGCTGTGACGTGCAAGCAGCCTGAGCCTGTGAAA 2703
QY 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160
|||||
Db 2704 CATTTGGAGAGAGTCCCAACACTCGTCAAGCTTGGGTTGAAAACGTGAGACTCACAGAT 2763
QY 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPhcGlnGln 180
|||||
Db 2764 ACAGAGATTTAGATTTTGTGATTTTGTGAAAGAACCCCTCTGAAAAAACTTCCAGCAG 2823
QY 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrLeuAlaPheMetGlyValPhe 200
|||||
Db 2824 TTGAATTTGGCGGGAATGCTGTGAGCATGATGATGCTGCTTCAATGGGTGATTT 2883
QY 201 GluAsnLeuLys 204
|||||
Db 2884 GAGAACTTTAAG 2895

RESULT 2

PCT-US02-21946A-14
; Sequence 14, Application PC/TUS0221946A
; GENERAL INFORMATION:
; APPLICANT: Thomas Jefferson University
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING
; TITLE OF INVENTION: FACTOR
; FILE REFERENCE: 480140.4/77PC
; CURRENT APPLICATION NUMBER: PCT/US02/21946A
; CURRENT FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 3219
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-21946A-14

Alignment Scores:

Pred. No.: 1e-108 Length: 3219
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-697-089-2_copy_762_965 (1-204) x PCT-US02-21946A-14 (1-3219)

QY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIle 20
|||||
Db 2428 TTGAAGAACCTTACAAAGCTCAATATGATTAACATTAAGATGAATGAAGAGATGCTATA 2487

QY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40
|||||
Db 2488 AAGATAGCTGAGAGGCGCTGAAAAACCTGAGAGAGATGTCTTTATTTTCATTGACCCACTTG 2547
QY 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60
|||||
Db 2548 TCTGACATTTGGAGAGGAGATGATTTACATAGTCAAGTCTCTGCAAGTGAACCTGTGAC 2607
QY 61 LeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80
|||||
Db 2608 CTGGAAGAAATTCATTAATCT 2667
QY 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100
|||||
Db 2668 CAGAATCTTCACAAATTTGGTCAAACTGACACATTTCTGATTTTCACAAAATTAACCTGGA 2727
QY 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120
|||||
Db 2728 AAGATGGAATGAAAGCTCTTCATGAACTGACAGATGAACTGCTAGAACAGCTC 2787
QY 121 ThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140
|||||
Db 2788 ACCGCACTGATGCTGCCCTGGGGCTGTGACGTGCAAGCAGCCTGAGCCTGTGAAA 2847
QY 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160
|||||
Db 2848 CATTTGGAGAGAGTCCCAACACTCGTCAAGCTTGGGTTGAAAACGTGAGACTCACAGAT 2907
QY 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPhcGlnGln 180
|||||
Db 2908 ACAGAGATTTAGATTTTGTGATTTTGTGAAAGAACCCCTCTGAAAAAACTTCCAGCAG 2967
QY 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrLeuAlaPheMetGlyValPhe 200
|||||
Db 2968 TTGAATTTGGCGGGAATGCTGTGAGCATGATGATGCTGCTTCAATGGGTGATTT 3027
QY 201 GluAsnLeuLys 204
|||||
Db 3028 GAGAACTTTAAG 3039

RESULT 3

US-10-276-781-111
; Sequence 111, Application US/10276781
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-018 (785 contig)
; CURRENT APPLICATION NUMBER: US/10/276,781
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/491,404
; NUMBER OF SEQ ID NOS: 2018
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 111
; LENGTH: 3545
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-781-111

Alignment Scores:

Pred. No.: 1.14e-108 Length: 3545
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-697-089-2_copy_762_965 (1-204) x US-10-276-781-111 (1-3545)

QY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIle 20
|||||


```
Db 2515 TTGAAGAACCTTACAAAGCTCATTAATGATTAACATTAAGATGAAGTGAAGATGCTATA 2574
Qy 21 LysleuAlaGluGlyLeuLysAsnLeuLysMetCysLeuPheHisIstLeuHrfHisLeu 40
Db 2575 AAACGTAGCTGAAGGCTGAAAAAAGCTGAAGAGATGTGTTATTTTCATTTGACCACTTG 2634
Qy 41 SerAspIleGlyGlyGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60
Db 2635 TCTGACATTTGGAGAGGAGATGATTAACATAGTCAAGTCTCTCTCAAGTGAACCTGTGAC 2694
Qy 61 LeuGluGluIleGluLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80
Db 2695 CTTGAAGAAATTCATTAAGTCTCTGCTGCTGCTGCAAAATGCAAGTGAATTCCTAGCT 2754
Qy 81 GluAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrIleGlu 100
Db 2755 CAGAAATCTTCACAAAATTTGGTCAAACTGAGACATCTTGATTTATTCAGAAAAATTAACCTGGAA 2814
Qy 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGluInleu 120
Db 2815 AAAGATGGAATGAAGACCTTCTCATAGTATGACAGAGATGAACGTGCTAGAACAGCTC 2874
Qy 121 ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140
Db 2875 ACCGACATGATGCTGCGCTGGGGCTGTGACGTGCAAGGACGCTGAGCAGCTGTGAAA 2934
Qy 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160
Db 2935 CATTTGGAGAGAGTCCACACACTGCTCAAGCTTGGGTGAAAAAACGTGAGACTCACAGAT 2994
Qy 161 ThrGluIleArgIleLeuGluValaPhePheGlyLysAsnProLeuLysAsnPhelngIn 180
Db 2995 ACAGAGATTAAGATTTTATGATGATTTTGGAAAAAGAACCTCTGAATAAACTTCCAGCAG 3054
Qy 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrLeuAlaPheMetGlyValPhe 200
Db 3055 TTGAATTTGGCGGGAATTCGTGTGAGCAGTGTATGATGATGCTGCTTATGATGCTATTT 3114
Qy 201 GluAsnLeuLys 204
Db 3115 GAGAAATCTTAAG 3126

RESULT 4
US-10-203-138A-4307
: Sequence 4307, Application US/10203138A
: GENERAL INFORMATION:
: APPLICANT: Molecular Dynamics, Inc.
: APPLICANT: Penn, Sharon G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wensheng
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
: FILE REFERENCE: PB 0004 WO 8
: CURRENT APPLICATION NUMBER: US/10/203,138A
: CURRENT FILING DATE: 2002-08-02
: PRIOR APPLICATION NUMBER: US 60/180,312
: PRIOR FILING DATE: 04 February 2000 (04.02.00)
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 26 May 2000 (26.05.00)
: PRIOR APPLICATION NUMBER: US 09/632,366
: PRIOR FILING DATE: 03 August 2000 (03.08.00)
: PRIOR APPLICATION NUMBER: GB 24263,6
: PRIOR FILING DATE: 03 October 2000 (03.10.00)
: PRIOR APPLICATION NUMBER: US 60/236,359
: PRIOR FILING DATE: 27 September 2000 (27.09.00)
: PRIOR APPLICATION NUMBER: US 60/234,687
: PRIOR FILING DATE: 21 September 2000 (21.09.00)
: PRIOR APPLICATION NUMBER: US 09/608,408
: PRIOR FILING DATE: 30 June 2000 (30.06.00)
: NUMBER OF SEQ ID NOS: 15438
: SOFTWARE: Molecular Dynamics Sequence Listing Engine
: SEQ ID NO 4307
```

```
: LENGTH: 421
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: MAP TO AC011232.3
: FEATURE:
: OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5
US-10-203-138A-4307

Alignment Scores:
Pred. No.: 8,11e-14 Length: 421
Score: 202.00 Matches: 38
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 19.31% Indels: 0
DB: 6 Gaps: 0

US-09-697-089-2_copy_762_965 (1-204) x US-10-203-138A-4307 (1-421)
Qy 167 GlyAlaPhePheGlyLysAsnProLeuLysAsnPhelngInLeuAsnLeuAlaGlyAsn 186
Db 161 GTTGCAATTTTGGAAAGAACCTCTGAAAAAATTCAGAGTGAATTTGGCGGGAAT 240
Qy 187 ArgValSerSerAspGlyTyrLeuAlaPheMetGlyValPheGluAsnLeuLys 204
Db 241 CCGTGACAGATGATGATGCTTCCCTTCATGCGTATTTGAGAAATCTTAAG 294

RESULT 5
US-10-161-493-5
: Sequence 5, Application US/10161493
: GENERAL INFORMATION:
: APPLICANT: Anderson, David W
: APPLICANT: Zernhusen, Bryan D
: APPLICANT: Li, Li
: APPLICANT: Zhong, Wei
: APPLICANT: Casman, Stacie J
: APPLICANT: Gerlach, Valerie
: APPLICANT: Shinkets, Richard A
: APPLICANT: Gorman, Linda
: APPLICANT: Pena, Carol EA
: APPLICANT: Kekuda, Ramesh
: APPLICANT: Paturajan, Meera
: APPLICANT: Spytek, Kimberly A
: APPLICANT: Leite, Mario W
: APPLICANT: Rastelli, Luca
: APPLICANT: MacDougall, John R
: APPLICANT: Taupier Jr., Raymond J
: APPLICANT: Guo, Xiaojia Sasha
: APPLICANT: Miller, Charles E
: APPLICANT: Shenoy, Suresh G
: APPLICANT: Hjal, Tord
: APPLICANT: Voss, Edward Z
: APPLICANT: Boldog, Ferenc L
: APPLICANT: Malyankar, Uriel M
: APPLICANT: Padigaru, Muralidhara
: APPLICANT: Ji, Weizhen
: APPLICANT: Smithson, Glenda
: APPLICANT: Edinger, Shlomit R
: APPLICANT: Miller, Isabelle
: APPLICANT: Ellerman, Karen
: TITLE OF INVENTION: Novel Antibodies that Bind to Antigenic Polypeptides, Nucleic
: FILE REFERENCE: 21402-377A
: CURRENT APPLICATION NUMBER: US/10/161,493
: CURRENT FILING DATE: 2002-06-03
: PRIOR APPLICATION NUMBER: 60/295,607
: PRIOR FILING DATE: 2001-06-04
: PRIOR APPLICATION NUMBER: 60/337,524
: PRIOR FILING DATE: 2001-11-16
: PRIOR APPLICATION NUMBER: 60/296,404
: PRIOR FILING DATE: 2001-06-06
: PRIOR APPLICATION NUMBER: 60/296,418
: PRIOR FILING DATE: 2001-06-06
```



```
Dh 2353 GAGGGCCGTGATAGTCTCACCCTCGTAAACAATTCTCTCTCCGATACCAATACAGT 2412
Qy 36 -----HisLeuThrHisLeuSerAspIleGlyGluGlyMetAspTyr 49
Dh 2413 AAGCTAGAGGCTTGGAAAGCTCTCCTCGTTAGGGAGCTT-----TAT 2457
Qy 50 ILeValIysSerLeuSerGluProCysAspLeuGluIle---GlnLeuValSer 68
Dh 2458 CTTTTCGATTACCAATATCAGTAACAGAGGCTCGGAAGCTCAGCTCCTTACCAACG 2517
Qy 69 CysCysLeuSerAlaAsnAlaValIysIleLeuAlaGlnAsnLeuHisAsnLeuValIys 88
Dh 2518 CTTGACATATCAGTAACCAATATCCGTAAAGCTG---GAGGGCTCGGAAGCTCTCAGCTCC 2574
Qy 89 LeuSerIleLeuAspLeuSerGluAsnTyrIleuGluIys----- 101
Dh 2575 TTACCAACGCTTGAATATCGGGTAAACCAATCCGTAAAGTAGAGGCTCGGAAGCTCTC 2634
Qy 102 -----AspGlyAsnGlu 105
Dh 2635 ACTTCGCTTAACAAGCTTCTGCTTAAGAAAGTAACCAATCACTAAGCTAAGAGGCTCGAA 2694
Qy 106 AlaLeuHisGluLeu-----IleAspArgMetAsnVal 116
Dh 2695 CGTCTCAGCTCCTTAGCAACGCTTAAGCTATCGGGTAAACCAATCCGTAAGCTGGAGGT 2754
Qy 117 LeuGluGlnLeuThrAlaLeuMetLeuProTrrpGlyCysAspValGlnGlySerLeuSer 136
Dh 2755 CTGGAACGCTCAGCTCTTCTAGCAACG-----CTTGAACGCTCGGTAACCAATC 2805
Qy 137 SerLeuLeuIysHisLeuGluIValProGlnLeuValIysLeuGlyLeuIysAsnTrrp 156
Dh 2806 AGTAAGCTAGAGGCTCGGAACGCTCTCTCTCGTTAAACAAGCTTCGCTTAAGAAGTAAAC 2865
Qy 157 ArgLeuThrAspThrGlnIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuIys 176
Dh 2866 CAGATCAGCTAAACTAGAG-----GGCTCGGAAGCTCTCACC 2901
Qy 177 AsnPheGlnGlnLeuAsnLeuAlaGlyAsnArgValSer 189
Dh 2902 TCGCTAACAAACCTTCTCTCTCGATTAACCAATACAGT 2940

RESULT 7
US-09-724-676-19376
; Sequence 19376, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19376
; LENGTH: 916
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-19376

Alignment Scores:
Pred. No.: 0.000843 Length: 916
Score: 118.00 Matches: 41
Percent Similarity: 45.96% Conserved: 33
Best Local Similarity: 25.47% Mismatches: 81
Query Match: 11.28% Indels: 6
Gaps: 4

US-09-697-089-2_COPY_762_965 (1-204) x US-09-724-676-19376 (1-916)
Qy 41 SerAspIleGlyGlu---GlyMetAspTyrIleValIysSerLeuSerGluProCys 59
Dh 353 AACGAGCTGGGCGATGTCGCGTGCATTTGCTCTCAGGGCGGACAGCCCTCTCTGC 412
```

```
Qy 60 AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValIysIleLeu 79
Dh 413 AAGATCCAGAAAGCTGAGCCTCCAGAACTGCTCGACGGGGGCCGCTGGGGGCTCTG 472
Qy 80 AlaGlnAsnLeuHisAsnLeuValIysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 99
Dh 473 TCCAGCACATACAGCAACCTCCCAACCTCGAGAGCTGCACATCAGAGCAACCTCTTG 532
Qy 100 GluIysAspGlyAsnGluAlaLeuHisGlu---LeuIleAspArgMetAsnValLeuGlu 118
Dh 533 GGGGATGGGCGCTGCAGACTCTCTCGCAAGACTCTCGAGCCCACTGCCGCTGGAA 592
Qy 119 GlnLeuThrAlaLeuMetLeuProTrrpGlyCysAspValGlnGlySerLeuSerLeu 138
Dh 593 AAG-----CTGCACCTGAGATTCAGACCTCTCGGCTGCCAGCTGGAGCCCTG 643
Qy 139 LeuIysHisLeuGluGluIValProGlnLeuValIysLeuGlyLeuIysAsnTrrpArgLeu 158
Dh 644 GCCTCCGCTGCACAGGCGCCAGCCGAGCTCAAGAGCTCAGGGTTAGCAACAGCAATC 703
Qy 159 ThrAspThrGlnIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuIysAsnPhe 178
Dh 704 AATGAGCTGCGCTCGTCTGCTGTGCTGCGCAGGCGCTGAAGAGACTCCCTGCGCAG---CTG 760
Qy 179 GlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrrpLeuAlaPheMetGly 198
Dh 761 GAGGCGCTCAAGCTGGAAGAGCTGGGGTGTGACATCAGCAACTGCCGGAGCCTGTGGCGC 820
Qy 199 Val 199
Dh 821 ATT 823

RESULT 8
US-09-724-676A-19376
; Sequence 19376, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19376
; LENGTH: 916
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-19376

Alignment Scores:
Pred. No.: 0.000843 Length: 916
Score: 118.00 Matches: 41
Percent Similarity: 45.96% Conserved: 33
Best Local Similarity: 25.47% Mismatches: 81
Query Match: 11.28% Indels: 6
Gaps: 4

US-09-697-089-2_COPY_762_965 (1-204) x US-09-724-676A-19376 (1-916)
Qy 41 SerAspIleGlyGlu---GlyMetAspTyrIleValIysSerLeuSerGluProCys 59
Dh 353 AACGAGCTGGGCGATGTCGCGTGCATTTGCTCTCAGGGCGGACAGCCCTCTCTGC 412
Qy 60 AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValIysIleLeu 79
Dh 413 AAGATCCAGAAAGCTGAGCCTCCAGAACTGCTCGACGGGGGCCGCTGGGGGCTCTG 472
Qy 80 AlaGlnAsnLeuHisAsnLeuValIysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 99
Dh 473 TCCAGCACATACAGCAACCTCCCAACCTCGAGAGCTGCACATCAGAGCAACCTCTTG 532
Qy 100 GluIysAspGlyAsnGluAlaLeuHisGlu---LeuIleAspArgMetAsnValLeuGlu 118
Dh 533 GGGGATGGGCGCTGCAGACTCTCTCGCAAGACTCTCGAGCCCACTGCCGCTGGAA 592
Qy 119 GlnLeuThrAlaLeuMetLeuProTrrpGlyCysAspValGlnGlySerLeuSerLeu 138
Dh 593 AAG-----CTGCACCTGAGATTCAGACCTCTCGGCTGCCAGCTGGAGCCCTG 643
Qy 139 LeuIysHisLeuGluGluIValProGlnLeuValIysLeuGlyLeuIysAsnTrrpArgLeu 158
Dh 644 GCCTCCGCTGCACAGGCGCCAGCCGAGCTCAAGAGCTCAGGGTTAGCAACAGCAATC 703
Qy 159 ThrAspThrGlnIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuIysAsnPhe 178
Dh 704 AATGAGCTGCGCTCGTCTGCTGTGCTGCGCAGGCGCTGAAGAGACTCCCTGCGCAG---CTG 760
Qy 179 GlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrrpLeuAlaPheMetGly 198
Dh 761 GAGGCGCTCAAGCTGGAAGAGCTGGGGTGTGACATCAGCAACTGCCGGAGCCTGTGGCGC 820
Qy 199 Val 199
Dh 821 ATT 823
```

Dh 533 GGGATCGGGGCTGCAGCTGCTCGGAGAGACTCTGCAGCCCGCCAGTCCGCTGGAA 592
Qy 119 GlnleuthralaleuMetleuprotprglyCysaspyalGlnlySerleuSerleu 138
Dh 593 AAG-----CTGCAGCTGGAGTATTGGACCTCTCGCTGCGCAGCTGGAGCCCTG 643
Qy 139 LeulshisleuGlnlualProGlnleuVallylsleuGlnlyLeuLysasnTprArgleu 158
Dh 644 GCGTCCTGCTCAGGCGCAAGCCGAGCTTCAGAGAGCTCAGGTTAGCAACACAGACATC 703
Qy 159 ThrspthrgluileargileuGlyAlaphheGlyLysasnProleuLysasnPh 178
Dh 704 AATAGGCTGGCGTCTGCTGCTGCTGCCAGGCGCTGAAGAGCTCCCTGCGAG---CTG 760
Qy 179 GlnleuLysasnleuAlaglyAsnArgValSerSeraspGlyTprleuAlaphemGly 198
Dh 761 GAGCGCTCAAGCTGGAGAGCTGGGTTGTATCATCAGACAACTCCGGGAGCTGTGGGC 820
Qy 199 Val 199
Dh 821 ATT 823

RESULT 9

US-09-724-676-19370
; Sequence 19370, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724.676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19370
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-19370

Alignment Scores:
Pred. No.: 0.000879 Length: 945
Score: 118.00 Matches: 41
Percent Similarity: 45.96% Conservative: 33
Best Local Similarity: 25.47% Mismatches: 81
Query Match: 11.28% Indels: 6
Gaps: 4

US-09-697-089-2_COPY_762_965 (1-204) x US-09-724-676-19370 (1-945)

Qy 41 Seraspilleglylu---glyMetAspTyrIleVallySerleuSerSerGluProCys 59
Dh 382 AACGAGCTGGGCGATGTCGGGCTGATTCGCTGCCAGGCGCTGCAGACCCCTCCTGC 441
Qy 60 AspleuGlnlualleuValSerCysCysleuSerAlaAsnAlaVallylsleu 79
Dh 442 AAGATCCAGAAAGCTGCAGACTGCTGAGCGGGGCGGCTGCGGGGCTCTG 501
Qy 80 AlaglnAsnleuHisasnleuVallylsleuSerlleuLysasnProleuLysasnPh 99
Dh 502 TCCAGCACACTACGACCCCTGCCACCCCTGCAGAGCTGCACCTCAGAGACACTCTTG 561
Qy 100 GlnlyAspRglYasnGlnAlaLeuHisGlu---leuLysasnArgMetAsnValleuGlu 118
Dh 562 GGGATCGGGGCTGCAGCTGCTGCGAAGAGACTCCTCGGACCCCGGCTGGAA 621
Qy 119 GlnleuthralaleuMetleuprotprglyCysaspyalGlnlySerleuSerleu 138
Dh 622 AAG-----CTGCAGCTGGAGTATTGGACCTCTCGCTGCGCAGCTGGAGCCCTG 672
Qy 139 LeulshisleuGlnlualProGlnleuVallylsleuGlnlyLysasnTprArgleu 158
Dh 673 GCGTCCTGCTCAGGCGCAAGCCGAGCTTCAGAGAGCTCAGGTTAGCAACACAGACATC 732

Qy 159 ThrspthrgluileargileuGlyAlaphheGlyLysasnProleuLysasnPh 178
Dh 733 AATAGGCTGGCGTCTGCTGCTGCTGCCAGGCGCTGAAGAGCTCCCTGCGAG---CTG 789
Qy 179 GlnleuLysasnleuAlaglyAsnArgValSerSeraspGlyTprleuAlaphemGly 198
Dh 790 GAGCGCTCAAGCTGGAGAGCTGGGTTGTATCATCAGACAACTCCGGGAGCTGTGGGC 849
Qy 199 Val 199
Dh 850 ATT 852

RESULT 10

US-09-724-676A-19370
; Sequence 19370, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724.676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19370
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-19370

Alignment Scores:
Pred. No.: 0.000879 Length: 945
Score: 118.00 Matches: 41
Percent Similarity: 45.96% Conservative: 33
Best Local Similarity: 25.47% Mismatches: 81
Query Match: 11.28% Indels: 6
Gaps: 4

US-09-697-089-2_COPY_762_965 (1-204) x US-09-724-676A-19370 (1-945)

Qy 41 Seraspilleglylu---glyMetAspTyrIleVallySerleuSerSerGluProCys 59
Dh 382 AACGAGCTGGGCGATGTCGGGCTGATTCGCTGCCAGGCGCTGCAGACCCCTCCTGC 441
Qy 60 AspleuGlnlualleuValSerCysCysleuSerAlaAsnAlaVallylsleu 79
Dh 442 AAGATCCAGAAAGCTGCAGACTGCTGAGCGGGGCGGCTGCGGGGCTCTG 501
Qy 80 AlaglnAsnleuHisasnleuVallylsleuSerlleuLysasnProleuLysasnPh 99
Dh 502 TCCAGCACACTACGACCCCTGCCACCCCTGCAGAGCTGCACCTCAGAGACACTCTTG 561
Qy 100 GlnlyAspRglYasnGlnAlaLeuHisGlu---leuLysasnArgMetAsnValleuGlu 118
Dh 562 GGGATCGGGGCTGCAGCTGCTGCGAAGAGACTCCTCGGACCCCGGCTGGAA 621
Qy 119 GlnleuthralaleuMetleuprotprglyCysaspyalGlnlySerleuSerleu 138
Dh 622 AAG-----CTGCAGCTGGAGTATTGGACCTCTCGCTGCGCAGCTGGAGCCCTG 672
Qy 139 LeulshisleuGlnlualProGlnleuVallylsleuGlnlyLysasnTprArgleu 158
Dh 673 GCGTCCTGCTCAGGCGCAAGCCGAGCTTCAGAGAGCTCAGGTTAGCAACACAGACATC 732
Qy 159 ThrspthrgluileargileuGlyAlaphheGlyLysasnProleuLysasnPh 178
Dh 733 AATAGGCTGGCGTCTGCTGCTGCTGCCAGGCGCTGAAGAGCTCCCTGCGAG---CTG 789
Qy 179 GlnleuLysasnleuAlaglyAsnArgValSerSeraspGlyTprleuAlaphemGly 198
Dh 790 GAGCGCTCAAGCTGGAGAGCTGGGTTGTATCATCAGACAACTCCGGGAGCTGTGGGC 849
Qy 199 Val 199
Dh 199 Val 199

```
Db      850 ATT 852

RESULT 11
US-09-724-676-19364
; Sequence 19364, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Comugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Comugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19364
; LENGTH: 1012
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-19364

Alignment Scores:
Pred. No.:          0.00964           Length:       1012
Score:             118.00            Matches:        41
Percent Similarity: 45.96%           Conservative:   31
Best Local Similarity: 25.47%         Mismatches:    81
Query Match:       11.28%            Indels:         6
DB:                Gaps:              4

US-09-697-089-2_COPY_762_965 (1-204) x US-09-724-676-19364 (1-1012)

QY      41 Serasplleaglylu---glymetasprtyrllevallyserserleusersergluprocys 59
Dn      449 AACGAGCTGGCGATGTGC GGCGTCATATGCTGCTCCAGGCCCTGCAGACCCCCTCCTGC 508
QY      60 AsprasplleuglnleuValserCyssseuseralAasnalValyllelu 79
Dn      509 AAGATCCAGAAGCTGAGACTCCAGAACTGCTGCTGACGGGGCGGGCTCGGGGCTCTG 568
QY      80 AlacInAsnleuHisAsnleuValLysLeuSerlleuAspsleuSergLuAsnTrLeu 99
Dn      569 TCCGACGACACTACCACCCCTCCGCCACCTCCAGGAGCTGCAGCACTGACGCAACAACCTTTG 628
QY      100 GLULysAspGLyAsnGLIALeUHLISGLU---leuILeAspRhtgmeTAsnVALleUGLU 118
Dn      629 GGGGATCGGGCGCTGCAGCTGCTCTGCGAAGAGACTCTTGGAACCCCCAGTGCCTGCCGTA 688
QY      119 GlInleuthrAlaleuMetleuProTrIPglYCysAspValGlInglSerleuSerSerleu 138
Dn      689 AAG-----CTGCAAGCTGAGGATATTGCAAGCCTCTCGGCTGCCACCTCGAGCCCTG 739
QY      139 LeuYLshSLeUGlnGLIuValProlInleuValLYSLeUGlnleuLYSLasnTPRApgleu 158
Dn      740 GCCTCCGCTGCTCAGGGCCAAAGCCGAGCTTCAAGGAGCTCACGGTTACCAACACAGACAT 799
QY      159 ThrAspThrGLIALeArGLIEUGlYALAPhePhelLYSLAsnProlEULysAsnPh 178
Dn      800 AATAGAGCTGGCGCTGCTGCTGCTGCTGCGCAGGGCCTGAAGAGACTCCCTCCACAG---CTG 856
QY      179 GlInGLInleuAsnleuAglYAsnARValserSeraspelyTrPrleuAlAPhemetGLY 198
Dn      857 GAGCGCTCAAGCTGAGAGAGCTGGGTGTGATCATCAACAACATGCGCGGAGCTGTGGCG 916
QY      199 Val 199
Dn      917 ATT 919

RESULT 12
US-09-724-676A-19364
; Sequence 19364, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Comugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Comugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
```

```

CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 19364
LENGTH: 1012
TYPE: DNA
ORGANISM: Homo sapiens
US-09-724-676A-19364

Alignment Scores:
Pred. No.: 0.00964      Length: 1012
Score: 118.00      Matches: 41
Percent Similarity: 45.96%      Conservative: 33
Best local Similarity: 25.47%      Mismatches: 81
Query Match: 11.28%      Indels: 6
Db: 5      Gaps: 4

US-09-697-089-2_COPY_762_965 (1-204) x US-09-724-676A-19364 (1-1012)

Oy 41 seraspiilegiylgu---glymetasprtyrllevallysserleuSerSergluProCys 59
      ::::::::::::::: |||::: ::::::::::: || :::: ||
Db 449 AACGAGCTGGGGCGAATGTGGCGGTGCATGGCTGCTCCAGGGCCCTGCAGACCCCTCTGC 508
      ::::::::::::::: ||| ::::| |||:::
Oy 60 AspieuglugluilegileuValSerCysCysleuSerlaalaanaValylleu 79
      ::::::::::::::: ||| ::::| |||:::
Db 509 AAGATCCGAGAGCTGAGCGCTCCAGACAGCTGCTGCAGCGGGGCGCGCTCGGGGTCTG 568
      ::::::::::::::: ||| ::::| |||:::
Oy 80 AlaglnaAnaLeuHlaAnaLeuValLysleuSerlleuAuaSpieusergluAaNTryleu 99
      :::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 569 TCCAGCACACTACGACACCCCTGCCACCCCTGCAGAGAGCTGCACCTGCAGCGACACTTGG 628
      :::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 100 gluiysasprgIyasngluaIalaLeuHlsglu--LeuileaspragmetasValleuGl 118
      ||| :::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 629 GGGGATGGGGCGCTGCACAGCTCTGCTGCAGAGAGACTCTGAGACCCCGCCAGTGGCGGCTGAA 688
      ||| :::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 119 GlnleuthrrAlaleuMetleuProTrrpelysAspylaGlnGlySerleuSerleu 138
      :::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 669 AAG-----CTGCACACTGGAATATTCAGCGCTCTGGCTGCCACTCGACCCCTTG 739
      :::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 139 LeuysHlsleugluIguIValProGlnleuValLysleuGlyleuLysAsnTrrpArgleu 158
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 740 GCGTCGCGTCGACGAGGCCAACCGGACCTTCAGAGAGCTCAACGGTATTACCAACACGACATC 799
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 159 ThrAsprhrGluileargIleleuGlyAlaIaPhehecllyLysAsnProleuLysAsnPh 178
      :::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 800 AATGAGCGCTGGCGTCGCGTGTCTGTGCCAGGGCCTGGAAGAGCTCCCTCGACAG--CTG 856
      :::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 179 GlnGlnleuAnaLeuAlaGlyAsnAraYalSerSeraspolyTrrpleuAlaIaPheMetGly 198
      :::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 857 GAGGCGCTCAAGAGCTGAGAGCTGCGGCTGTACATCAAGCAACTGCCGGAGCTGTGCGGC 916
      :::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 199 Val 199
      :::
Db 917 ATT 919

RESULT 13
US-09-724-676-19382
Sequence 19382, Application US/09724676
GENERAL INFORMATION:
APPLICANT: CompuGen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 CompuGen
CURRENT APPLICATION NUMBER: US/09/724.676
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 19382
LENGTH: 1103
TYPE: DNA
ORGANISM: Homo sapiens
US-09-724-676-19382

Alignment Scores:

```

Pred. No.: 0.00108 Length: 1103
Score: 118.00 Matches: 41
Percent Similarity: 45.96% Conservative: 33
Best Local Similarity: 25.47% Mismatches: 81
Query Match: 11.28% Indels: 6
DB: 5 Gaps: 4

US-09-697-089-2_COPY_762_965 (1-204) x US-09-724-676-19382 (1-1103)

OY 41 SeraspIleGlu---glymetAspYrIleValLysSerLeuSerSerGluProCys 59
DB 540 AACGAGCTGGGATGTCGGCTGCAATTCGCTCCAGGCGCTGCAGACCCCTCTCC 599
OY 60 AspleuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 79
DB 600 AAGATCCAAAGCTGAGCTCCAGAACTGCTGCTGACGGGGCGCGCGGCTG 659
OY 80 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnYrIleu 99
DB 660 TCCAGCACACTAGCACCTCCGCCACCTCCAGAGACTCCACTCCAGCAACAACCTCTG 719
OY 100 GluYrAspGlyAsnGlnAlaLeuHisGlu---LeuIleAspArgMetAsnValLeuGlu 118
DB 720 GGGGATCGGGCGCTGCTGCGAAGACTCTGACCCCACTGCGCCGCTGGA 779
OY 119 ThrAspThrAlaLeuMetLeuProTrrpGlyCysAspValGlnGlySerLeuSerLeu 138
DB 780 AAG-----CTGCAGCTGGAGATATTCAGACTCTCGCGCTCCAGCTCCAGCCCTG 830
OY 139 GlnLeuThrAlaLeuMetLeuProGlnLeuValLysLeuGlyLeuLysAsnTrrpArgLeu 158
DB 831 GCCTCCGCTGACGGCCCAAGCCGACTTCAAGGACTCAGCTTACAAACGACATC 890
OY 159 ThrAspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPhe 178
DB 891 AATGAGCTGGCGCTGCTGCTGCCAGGCGCTGAGAGACTCCCTGCCAG---CTG 947
OY 179 GlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrrPheuAlaPheMetGly 198
DB 948 GAGGCGCTCAAGCTGAGAGCTGCGGTGTGACATACAGAACTGCCGGGAACTGTGCGGC 1007
OY 199 Val 199
DB 1008 ATT 1010

RESULT 14

US-09-724-676A-19382
; Sequence 19382, Application US/09724676A
; GENERAL INFORMATION:

; APPLICANT: Comugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Comugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19382
; LENGTH: 1103
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-19382

Alignment Scores:

Pred. No.: 0.00108 Length: 1103
Score: 118.00 Matches: 41
Percent Similarity: 45.96% Conservative: 33
Best Local Similarity: 25.47% Mismatches: 81
Query Match: 11.28% Indels: 6
DB: 5 Gaps: 4

US-09-697-089-2_COPY_762_965 (1-204) x US-09-724-676A-19382 (1-1103)

OY 41 SeraspIleGlu---glymetAspYrIleValLysSerLeuSerSerGluProCys 59

DB 540 AACGAGCTGGGATGTCGGCTGCAATTCGCTCCAGGCGCTGCAGACCCCTCTCC 599
OY 60 AspleuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 79
DB 600 AAGATCCAAAGCTGAGCTCCAGAACTGCTGCTGACGGGGCGCGCGGCTG 659
OY 80 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnYrIleu 99
DB 660 TCCAGCACACTAGCACCTCCGCCACCTCCAGAGACTCCACTCCAGCAACAACCTCTG 719
OY 100 GluYrAspGlyAsnGlnAlaLeuHisGlu---LeuIleAspArgMetAsnValLeuGlu 118
DB 720 GGGGATCGGGCGCTGCTGCGAAGACTCTGACCCCACTGCGCCGCTGGA 779
OY 119 GlnLeuThrAlaLeuMetLeuProTrrpGlyCysAspValGlnGlySerLeuSerLeu 138
DB 780 AAG-----CTGCAGCTGGAGATATTCAGACTCTCGCGCTCCAGCTCCAGCCCTG 830
OY 139 LeuLysHisLeuGlnGluValProGlnLeuValLysLeuGlyLeuLysAsnTrrpArgLeu 158
DB 831 GCCTCCGCTGACGGCCCAAGCCGACTTCAAGGACTCAGCGTTACAAACGACATC 890
OY 159 ThrAspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPhe 178
DB 891 AATGAGCTGGCGCTGCTGCTGCCAGGCGCTGAGAGACTCCCTGCCAG---CTG 947
OY 179 GlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrrPheuAlaPheMetGly 198
DB 948 GAGGCGCTCAAGCTGAGAGCTGCGGTGTGACATACAGAACTGCCGGGAACTGTGCGGC 1007
OY 199 Val 199
DB 1008 ATT 1010

RESULT 15

US-09-724-676-19395
; Sequence 19395, Application US/09724676
; GENERAL INFORMATION:

; APPLICANT: Comugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Comugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19395
; LENGTH: 1132
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-19395

Alignment Scores:
Pred. No.: 0.00112 Length: 1132
Score: 118.00 Matches: 41
Percent Similarity: 45.96% Conservative: 33
Best Local Similarity: 25.47% Mismatches: 81
Query Match: 11.28% Indels: 6
DB: 5 Gaps: 4

US-09-697-089-2_COPY_762_965 (1-204) x US-09-724-676-19395 (1-1132)

OY 41 SeraspIleGlu---glymetAspYrIleValLysSerLeuSerSerGluProCys 59
DB 569 AACGAGCTGGGATGTCGGCTGCAATTCGCTCCAGGCGCTGCAGACCCCTCTCC 628
OY 60 AspleuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 79
DB 629 AAGATCCAAAGCTGAGCTCCAGAACTGCTGCTGACGGGGCGCGCGGCTG 688
OY 80 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnYrIleu 99
DB 689 TCCAGCACACTAGCACCTCCGCCACCTCCAGAGACTCCACTCCAGCAACAACCTCTTG 748

```
QY 100 GluLysAspGlyAsnGluAlaLeuHISGlu---LeuIleAspArgMetAsnValLeuGlu 118
Db 749 GGGGATCGGGGCTGCAAGCTGCTGCGAAGACTCTGGAACCCACAGTCCGCGCTGGAA 808
QY 119 GlnLeuThrAlaLeuMetLeuProTrrpGlyCysAspValGlnGlySerLeuSerSerLeu 138
Db 809 AAG-----CTGCAGCTGAGATATTGCAGCTCTCGCGTGCACAGCTGCGAGCCCTG 859
QY 139 LeuLysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrrpArgLeu 158
Db 860 GCCTCCGCTGCTCAGGCGCCAGCCGACTTCAGAGAGCTCAGCGTTAGCAACAACGACATC 919
QY 159 ThrAspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPhe 178
Db 920 AATGAGCTGGCGCTGCTGCTGCTGCGCCAGGCGCTGAAGAGACTCCCGCTGCCAG---CTG 976
QY 179 GlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrrpLeuAlaPheMetGly 198
Db 977 GAGGCGCTCAAGCTGAGAGCTGCGGCTGACATCATCAGACACTGCCGCGGACCTGTGCGGC 1036
QY 199 Val 199
Db 1037 ATT 1039
```

Search completed: January 31, 2003, 18:03:09
Job time : 195.895 secs

THIS PAGE BLANK (USPTO)